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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under
37 C.F.R. 1.53(b))

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First Named Inventor or
Application Identifier

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Box 1 of 3 EL290720882US (Spec pg. 1-1352)
(Sequence Listing pg. 1-1000 & CD)
Box 2 of 3 EL290720896US (pg. 1001-3500)
Box 3 of 3 EL290720905US (pg. 3501-6222)

Title of
Invention

Nucleic Acid and Amino Acid Sequences Relating to *Bacteroides Fragilis* for Diagnostics and Therapeutics

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO:

Assistant Commissioner for Patents
Box Patent Application
Washington, D.C. 20231

1. ☐ Fee Transmittal Form
(Submit an original, and a duplicate for fee processing)

6. ☐ Microfiche Computer Program (Appendix)

2. ☒ Specification **[Total Pages 1352]**

- (preferred arrangement set forth below)
- Descriptive title of the invention
- Cross References to Related Applications
- Statement Regarding Fed sponsored R & D
- Reference to microfiche Appendix
- Background of the Invention
- Summary of the Invention
- Brief Description of the Drawings
- Detailed Description
- Claim(s)
- Abstract of the Disclosure

7. ☒ Nucleotide and/or Amino Acid Sequence Submission
(if applicable, all necessary)

- a. ☒ Computer Readable Copy
- b. ☒ Paper Copy (identical to computer copy)
[1-6222] Pages
- c. ☒ Statement verifying identity of above copies

3. ☐ Drawing(s) (35 U.S.C. 113) **[Total Sheets []]**
☐ Formal ☐ Informal

8. ☐ Assignment Papers (cover sheet & documents)

9. ☐ 37 C.F.R. 3.73(b) Statement ☐ Power of Attorney
(when there is an assignee)

4. ☐ Oath or Declaration/POA **[Total Pages []]**

- a. ☐ Newly executed (original or copy)
- b. ☐ Copy from a prior application (37 C.F.R. 1.63(d))
(for continuation/divisional with Box 17 completed)
[NOTE Box 5 below]

10. ☐ English Translation Document (if applicable)

11. ☐ Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations

12. ☐ Preliminary Amendment

- i. ☐ DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. 1.63(d)(2) and 1.33(b).

13. ☒ Return Receipt Postcard (MPEP 503)
(Should be specifically itemized)

14. ☐ Small Entity Statement(s) ☐ Statement filed in prior application, status still proper and desired

5. ☐ Incorporation By Reference (useable if Box 4b is checked)
The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

15. ☐ Certified Copy of Priority Document(s)
(if foreign priority is claimed)

16. ☐ Other: _____

17. If a CONTINUING APPLICATION, check appropriate box and supply the requisite information:

☐ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No.:

Prior application information: Examiner:

Group Art Unit:

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BOX 1 OF 3	Date: <u>4/4/00</u>	Express Mail Label No. <u>EL290720882 US</u>
		Pages <u>Specification pages 1-1352; Sequence Listings pages 1-1000 and CD</u>
BOX 2 OF 3	Date: <u>4/4/00</u>	Express Mail Label No. <u>EL290720896 US</u>
		Pages <u>Sequence Listings, pages 1001-3500</u>
BOX 3 OF 3	Date: <u>4/4/00</u>	Express Mail Label No. <u>EL290720905 US</u>
		Pages <u>Sequence Listings, pages 3501-6222</u>

TITLE OF THE INVENTION

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *BACTEROIDES FRAGILIS* FOR DIAGNOSTICS AND THERAPEUTICS

INVENTOR: Gary L. Breton

RELATED APPLICATIONS:

This application claims the benefit of U.S. Provisional Application Serial Number 60/128,705, filed April 9, 1999, the entire teachings of which are incorporated herein by reference.

FIELD OF THE INVENTION

The invention relates to isolated nucleic acids and polypeptides derived from *Bacteroides fragilis* that are useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions, as well as materials and methods for the diagnosis, prevention, and amelioration of pathological conditions resulting from bacterial infection.

BACKGROUND OF THE INVENTION

The genus *Bacteroides* is a member of the family *Bacteroidaceae*. They are Gram-negative, obligately anaerobic, nonsporeforming rods. The genus contains at least 39 species, and are often isolated from sewage as well as the digestive tract of man, animals, and insects. *Bacteroides fragilis* was first described in 1898 by Veillon and Zuber, but was called *Bacillus fragilis*. In 1919, Castellani and Chalmers transferred it to the *Bacteroides* genus. The “*B. fragilis* group” refers to the saccharoclastic bacteroids that grow well in bile. Members of this group were previously subspecies of *B. fragilis* and include *B. fragilis*, *B. distasonis*, *B. ovatus*, *B. thetaiotaomicron*, and *B. vulgatus* (Castellani and Chalmers. 1984. Genus I. *Bacteroides* 1919, 959. Krieg and Holt (editors) In Bergey’s Manual of Systematic Bacteriology, 1:604-631).

Bacteroides fragilis accounts for only 1% of the normal flora of the human colon, but is the most common anaerobe isolated from clinical specimens. It is associated with soft tissue infections, abscesses and bacteremia (Moncrief J., *et al*, 1998. Infect. Immun. 66:1735-1739). *B. fragilis* has also been associated with infection of the skeletal muscle (Katagiri, K., *et al*, 1996. J. Dermatology. 23:129-132), and meningitis (Aucher, P., *et al*, 1996. Eur. J. Clin. Microbiol. Infect. Dis. 15:820-823). The *B. fragilis* group is responsible for 65% of all anaerobic bacteremia cases, with mortality rates in excess of 19% (Redondo, M., *et al*, 1995. Clinical Infectious Disease. 20:1492-1496).

In 1984, strains of *B. fragilis* were found to cause diarrhea in newborn lambs (Myers, L., *et al*, 1984. Infect. Immun. 44:241-244). Subsequently, it has been shown that *B. fragilis* is associated with diarrhea in other livestock and young children. These strains are called enterotoxigenic strains, because they produced a 20KD metalloprotease enterotoxin with intestinal secretory activity (Moncrief J., *et al*, 1995. Infect. Immun. 63:175-181).

There has been an increase in antibiotic resistance within the *Bacteroides fragilis* group. While there is still excellent activity of many antibiotics, even some of the most potent agents, the carbapenems and the β -lactamase-inhibitor combinations, are losing

activity (Snydman,D., *et al*, 1996. Clinical Infectious Diseases. 23:S54-65). The cefoxitin resistance rate has increased from 0% in 1987 to 22% in 1995 (Bianchini, H., *et al*, 1997. Clinical Infectious Diseases. 25:S268-269). Resistance to metronidazole, co-amoxiclav, and imipenem is rare, but strains have been found that are resistant to one or
 5 all of these antibiotics. (Turner,P., *et al*, 1995.The Lancet. 345:1275-1277). Clindaycin resistance has been shown to be transferred between strains by either plasmid or transposon mechanisms. (Dalmau, D., *et al*, 1997. Clinical Infectious Diseases. 24:874-877). The increasing resistance to antibiotics commonly used against *Bacteroides* species may eventually lead to failures of these treatments.

10 Sequencing and analysis of this genome is crucial for the identification of essential genes for development of drug targets and to reduce the emerging health threat this organism poses.

SUMMARY OF THE INVENTION

15 The present invention fulfills the need for diagnostic tools and therapeutics by providing bacterial-specific compositions and methods for detecting *Bacteroides* species including *B. fragilis* , as well as compositions and methods useful for treating and preventing *Bacteroides* infection, in particular, *B. fragilis* infection, in vertebrates including mammals.

20 The present invention encompasses isolated nucleic acids and polypeptides derived from *B. fragilis* that are useful as reagents for diagnosis of bacterial disease, components of effective antibacterial vaccines, and/or as targets for antibacterial drugs including anti-*B. fragilis* drugs. They can also be used to detect the presence of *B. fragilis* and other *Bacteroides* species in a sample; and in screening compounds for the
 25 ability to interfere with the *B. fragilis* life cycle or to inhibit *B. fragilis* infection. They also have use as biocontrol agents for plants.

In one aspect, the invention features compositions of nucleic acids corresponding to entire coding sequences of *B. fragilis* proteins, including surface or secreted proteins or parts thereof, nucleic acids capable of binding mRNA from *B. fragilis* proteins to

block protein translation, and methods for producing *B. fragilis* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to detect *B. fragilis* infection. In addition, vaccine compositions and methods for the protection or treatment of infection by *B.*

5 *fragilis* are within the scope of this invention.

The nucleotide sequences provided in SEQ ID NO: 1 - SEQ ID NO: 5222, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 5222 may be "provided" in a variety of medias to facilitate use thereof. As used herein, "provided" refers to a manufacture,
 10 other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NO: 1 - SEQ ID NO: 5222, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 5222. Uses for and methods for providing nucleotide sequences in a variety of media is well known in the art (see e.g.,
 15 EPO Publication No. EP 0 756 006).

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any media which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as
 20 floppy discs, hard disc storage media, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A person skilled in the art can readily appreciate how any of the presently known computer readable media can be used to create a manufacture comprising computer readable media having recorded thereon a
 25 nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable media. A person skilled in the art can readily adopt any of the presently known methods for recording information on computer readable media to

generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a person skilled in the art for creating a computer readable media having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable media. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A person skilled in the art can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable media having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NO: 1 - SEQ ID NO: 5222, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to SEQ ID NO: 1 - SEQ ID NO: 5222 in computer readable form, a person skilled in the art can routinely access the coding sequence information for a variety of purposes. Computer software is publicly available which allows a person skilled in the art to access sequence information provided in a computer readable media. Examples of such computer software include programs of the "Staden Package", "DNA Star", "MacVector", GCG "Wisconsin Package" (Genetics Computer Group, Madison, WI) and "NCBI Toolbox" (National Center For Biotechnology Information). Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Computer algorithms enable the identification of *B. fragilis* open reading frames (ORFs) within SEQ ID NO: 1 - SEQ ID NO: 5222 which contain homology to ORFs or proteins from other organisms. Examples of such similarity-search algorithms include the BLAST [Altschul et al., J. Mol. Biol. 215:403-410 (1990)] and Smith-Waterman

5 [Smith and Waterman (1981) *Advances in Applied Mathematics*, 2:482-489] search algorithms. Suitable search algorithms are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the*

10 *New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). Such algorithms are utilized on computer systems as exemplified below. The ORFs so identified represent protein encoding fragments within the *B. fragilis* genome and are useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

15 The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *B. fragilis* genome. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the

20 present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A person skilled in the art can readily appreciate that any one of the currently available computer-based systems is suitable for use in the present invention. The computer-based systems of the present invention comprise a data storage

25 means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means

which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *B. fragilis* genome which are similar to, or "match", a particular target sequence or target motif. A variety of known algorithms are known in the art and have been disclosed publicly, and a variety of commercially available software for conducting homology-based similarity searches are available and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, FASTA (GCG Wisconsin Package), Bic_SW (Compugen Bioccelerator), BLASTN2, BLASTP2, BLASTX2 (NCBI) and Motifs (GCG). Suitable software programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). A person skilled in the art can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A person skilled in the art can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that many genes are longer than 500 amino acids, or 1.5 kb in length, and that commercially important fragments of the *B. fragilis*

genome, such as sequence fragments involved in gene expression and protein processing, will often be shorter than 30 nucleotides.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are
 5 chosen based on a specific functional domain or three-dimensional configuration which is formed upon the folding of the target polypeptide. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites, membrane-spanning regions, and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible
 10 expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *B. fragilis* genome possessing varying degrees of homology to the target sequence or target motif. Such
 15 presentation provides a person skilled in the art with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *B. fragilis*
 20 genome. In the present examples, implementing software which implement the BLASTP2 and bic_SW algorithms (Altschul et al., J Mol. Biol. 215:403-410 (1990); Compugen Biocellator) was used to identify open reading frames within the *B. fragilis* genome. A person skilled in the art can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-
 25 based systems of the present invention. Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The*

Internet and the New Biology: Tools for Genomic and Molecular Research, American Society for Microbiology, Washington, D.C. (1997).

The invention features *B. fragilis* polypeptides, preferably a substantially pure preparation of an *B. fragilis* polypeptide, or a recombinant *B. fragilis* polypeptide. In preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% identical to an amino acid sequence of the invention contained in the Sequence Listing, preferably it has about 65% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing, and most preferably it has about 92% to about 99% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acid residues in length; the polypeptide includes at least about 5, preferably at least about 10, more preferably at least about 20, still more preferably at least about 50, 100, or 150 contiguous amino acid residues of the invention contained in the Sequence Listing. In yet another preferred embodiment, the amino acid sequence which differs in sequence identity by about 7% to about 8% from the *B. fragilis* amino acid sequences of the invention contained in the Sequence Listing is also encompassed by the invention.

In preferred embodiments: the *B. fragilis* polypeptide is encoded by a nucleic acid of the invention contained in the Sequence Listing, or by a nucleic acid having at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid of the invention contained in the Sequence Listing.

In a preferred embodiment, the subject *B. fragilis* polypeptide differs in amino acid sequence at about 1, 2, 3, 5, 10 or more residues from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *B. fragilis* polypeptide exhibits an *B. fragilis* biological activity, e.g., the *B. fragilis* polypeptide retains a biological activity of a naturally occurring *B. fragilis* enzyme.

In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained
5 in the Sequence Listing.

In yet other preferred embodiments, the *B. fragilis* polypeptide is a recombinant fusion protein having a first *B. fragilis* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *B. fragilis*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a
10 DNA binding domain, or a polymerase activating domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events.

In a preferred embodiment, the encoded *B. fragilis* polypeptide differs (e.g., by amino acid substitution, addition or deletion of at least one amino acid residue) in amino acid sequence at about 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that: the *B. fragilis* encoded polypeptide exhibits an *B. fragilis* biological activity, e.g., the encoded
15 *B. fragilis* enzyme retains a biological activity of a naturally occurring *B. fragilis*.

In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention
20 contained in the Sequence Listing.

The *B. fragilis* strain, 14062, from which genomic sequences have been sequenced, has been deposited on July 20, 1998, in the American Type Culture Collection and assigned the ATCC designation # 202158.

Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridize under high or low stringency conditions to a nucleic acid which encodes a polypeptide of the invention contained in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *B. fragilis* polypeptides, especially by antisera to an active site or binding domain of *B. fragilis* polypeptide. The invention also includes fragments, preferably biologically active fragments. These and other polypeptides are also referred to herein as *B. fragilis* polypeptide analogs or variants.

The invention further provides nucleic acids, e.g., RNA or DNA and their respective complements, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

In preferred embodiments, the subject *B. fragilis* nucleic acid will include a transcriptional regulatory sequence, e.g., at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *B. fragilis* gene sequence, e.g., to render the *B. fragilis* gene sequence suitable for expression in a recombinant host cell.

In yet a further preferred embodiment, the nucleic acid which encodes an *B. fragilis* polypeptide of the invention, hybridizes under stringent conditions to a nucleic acid probe corresponding to at least about 8 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least about 12 consecutive nucleotides of the invention contained in the Sequence Listing; still more preferably to at least about 20 consecutive nucleotides of the invention contained in the Sequence Listing; most preferably to at least about 40 consecutive nucleotides of the invention contained in the Sequence Listing.

In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *B. fragilis* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity; the encoded polypeptide

has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98% or 99% homologous to an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the encoded

5 polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least about 5, preferably at least about 10, more preferably at least about 20, still more preferably at least about 50, 100, or 150 contiguous amino acids of the invention contained in the Sequence Listing.

In another aspect, the invention encompasses: a vector including a nucleic acid

10 which encodes an *B. fragilis* polypeptide or an *B. fragilis* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *B. fragilis* polypeptide or *B. fragilis* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating an *B. fragilis* or *B. fragilis* polypeptide variant, e.g., from the cell or from the cell culture medium.

15 One embodiment of the invention is directed to substantially isolated nucleic acids. Nucleic acids of the invention include sequences comprising at least about 8 nucleotides in length, more preferably at least about 12 nucleotides in length, even more preferably at least about 15-20 nucleotides in length, that correspond to a subsequence of any one of SEQ ID NO: 1 - SEQ ID NO: 5222 or complements thereof. Alternatively,

20 the nucleic acids comprise sequences contained within any ORF (open reading frame), including a complete protein-coding sequence, of which any of SEQ ID NO: 1 - SEQ ID NO: 5222 forms a part. The invention encompasses sequence-conservative variants and function-conservative variants of these sequences. The nucleic acids may be DNA, RNA, DNA/RNA duplexes, protein-nucleic acid (PNA), or derivatives thereof.

25 In another aspect, the invention features a purified recombinant nucleic acid having at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% sequence identity or % homology with a sequence of the invention contained in the Sequence Listing

The invention also encompasses recombinant DNA (including DNA cloning and expression vectors) comprising these *B. fragilis* -derived sequences; host cells comprising such DNA, including fungal, bacterial, yeast, plant, insect, and mammalian host cells; and methods for producing expression products comprising RNA and

5 polypeptides encoded by the *B. fragilis* sequences. These methods are carried out by incubating a host cell comprising an *B. fragilis* -derived nucleic acid sequence under conditions in which the sequence is expressed. The host cell may be native or recombinant. The polypeptides can be obtained by (a) harvesting the incubated cells to produce a cell fraction and a medium fraction; and (b) recovering the *B. fragilis*

10 polypeptide from the cell fraction, the medium fraction, or both. The polypeptides can also be made by *in vitro* translation.

In another aspect, the invention features nucleic acids capable of binding mRNA of *B. fragilis* . Such nucleic acid is capable of acting as antisense nucleic acid to control the translation of mRNA of *B. fragilis* . A further aspect features a nucleic acid which is

15 capable of binding specifically to an *B. fragilis* nucleic acid. These nucleic acids are also referred to herein as complements and have utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *B. fragilis* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system

20 is useful for making polypeptides corresponding to *B. fragilis* nucleic acid.

In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *B. fragilis* polypeptide or an *B. fragilis* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *B. fragilis* polypeptide or *B. fragilis* polypeptide variant; including culturing

25 the cell, e.g., in a cell culture medium, and isolating the *B. fragilis* or *B. fragilis* polypeptide variant, e.g., from the cell or from the cell culture medium.

In yet another embodiment of the invention encompasses reagents for detecting bacterial infection, including *B. fragilis* infection, which comprise at least one *B. fragilis*

-derived nucleic acid defined by any one of SEQ ID NO: 1 - SEQ ID NO: 5222, or sequence-conservative or function-conservative variants thereof. Alternatively, the diagnostic reagents comprise nucleotide sequences that are contained within any open reading frames (ORFs), including preferably complete protein-coding sequences,

5 contained within any of SEQ ID NO: 1 - SEQ ID NO: 5222, or polypeptide sequences contained within any of SEQ ID NO: 5223 - SEQ ID NO: 10444, or polypeptides of which any of the above sequences forms a part, or antibodies directed against any of the above peptide sequences or function-conservative variants and/or fragments thereof.

The invention further provides antibodies, preferably monoclonal antibodies,

10 which specifically bind to the polypeptides of the invention. Methods are also provided for producing antibodies in a host animal. The methods of the invention comprise immunizing an animal with at least one *B. fragilis* -derived immunogenic component, wherein the immunogenic component comprises one or more of the polypeptides encoded by any one of SEQ ID NO: 1 - SEQ ID NO: 5222 or sequence-conservative or

15 function-conservative variants thereof; or polypeptides that are contained within any ORFs, including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 5222 forms a part; or polypeptide sequences contained within any of SEQ ID NO: 5223 - SEQ ID NO: 10444; or polypeptides of which any of SEQ ID NO: 5223 - SEQ ID NO: 10444 forms a part. Host animals include any warm blooded animal,

20 including without limitation mammals and birds. Such antibodies have utility as reagents for immunoassays to evaluate the abundance and distribution of *B. fragilis* -specific antigens.

In yet another aspect, the invention provides diagnostic methods for detecting *B. fragilis* antigenic components or anti-*B. fragilis* antibodies in a sample. *B. fragilis*

25 antigenic components may be detected by known processes, including but not limited to detection by a process comprising: (i) contacting a sample suspected to contain a bacterial antigenic component with a bacterial-specific antibody, under conditions in which a stable antigen-antibody complex can form between the antibody and bacterial

antigenic components in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of at least one bacterial antigenic component in the sample. In different embodiments of this method, the antibodies used are directed against a sequence encoded
 5 by any of SEQ ID NO: 1 - SEQ ID NO: 5222 or sequence-conservative or function-conservative variants thereof, or against a polypeptide sequence contained in any of SEQ ID NO: 5223 - SEQ ID NO: 10444 or function-conservative variants thereof.

In yet another aspect, the invention provides a method for detecting antibacterial-specific antibodies in a sample, which comprises: (i) contacting a sample suspected to
 10 contain antibacterial-specific antibodies with an *B. fragilis* antigenic component, under conditions in which a stable antigen-antibody complex can form between the *B. fragilis* antigenic component and antibacterial antibodies in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of antibacterial antibodies in the sample. In different
 15 embodiments of this method, the antigenic component is encoded by a sequence contained in any of SEQ ID NO: 1 - SEQ ID NO: 5222 or sequence-conservative and function-conservative variants thereof, or is a polypeptide sequence contained in any of SEQ ID NO: 5223 - SEQ ID NO: 10444 or function-conservative variants thereof.

In another aspect, the invention features a method of generating vaccines for
 20 immunizing an individual against *B. fragilis*. The method includes: immunizing a subject with an *B. fragilis* polypeptide, e.g., a surface or secreted polypeptide, or a combination of such peptides or active portion(s) thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention features a method of evaluating a compound, e.g.,
 25 a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *B. fragilis* polypeptide. The method includes contacting the compound to be evaluated with an *B. fragilis* polypeptide and determining if the compound binds or otherwise interacts with the *B. fragilis* polypeptide. Compounds which bind or otherwise interact with *B.*

fragilis polypeptides are candidates as modulators, including activators and inhibitors, of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

In another aspect, the invention features a method of evaluating a compound, e.g., a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *B.*

5 *fragilis* nucleic acid, e.g., DNA or RNA. The method includes contacting the compound to be evaluated with an *B. fragilis* nucleic acid and determining if the compound binds or otherwise interacts with the *B. fragilis* nucleic acid. Compounds which bind *B. fragilis* are candidates as modulators, including activators and inhibitors, of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

10 A particularly preferred embodiment of the invention is directed to a method of screening test compounds for anti-bacterial activity, which method comprises: selecting as a target a bacterial specific sequence, which sequence is essential to the viability of a bacterial species; contacting a test compound with said target sequence; and selecting those test compounds which bind to said target sequence as potential anti-bacterial
15 candidates. In one embodiment, the target sequence selected is specific to a single species, or even a single strain, such as, for example, the strain *B. fragilis* 14062. In a second embodiment, the target sequence is common to at least two species of bacteria. In a third embodiment, the target sequence is common to a family of bacteria. The target sequence may be a nucleic acid sequence or a polypeptide sequence. Methods employing
20 sequences common to more than one species of microorganism may be used to screen candidates for broad spectrum anti-bacterial activity.

The invention also provides methods for preventing or treating disease caused by certain bacteria, including *B. fragilis*, which are carried out by administering to an animal in need of such treatment, in particular a warm-blooded vertebrate, including but
25 not limited to birds and mammals, a compound that specifically inhibits or interferes with the function of a bacterial polypeptide or nucleic acid. In a particularly preferred embodiment, the mammal to be treated is human.

DETAILED DESCRIPTION OF THE INVENTION

The sequences of the present invention include the specific nucleic acid and amino acid sequences set forth in the Sequence Listing that forms a part of the present specification, and which are designated SEQ ID NO: 1 - SEQ ID NO: 10444. Use of the terms "SEQ ID NO: 1 - SEQ ID NO: 5222 ", " SEQ ID NO: 5223 - SEQ ID NO: 10444, "the sequences depicted in Table 2", etc., is intended, for convenience, to refer to each individual SEQ ID NO *individually*, and is not intended to refer to the genus of these sequences unless such reference would be indicated. In other words, it is a shorthand for listing all of these sequences individually. The invention encompasses each sequence individually, as well as any combination thereof.

DEFINITIONS

"Nucleic acid" or "polynucleotide" as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotides or mixed polyribo-polydeoxyribo nucleotides. This includes single- and double-stranded molecules, i.e., DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

A nucleic acid or polypeptide sequence that is "derived from" a designated sequence refers to a sequence that corresponds to a region of the designated sequence. For nucleic acid sequences, this encompasses sequences that are homologous or complementary to the sequence, as well as "sequence-conservative variants" and "function-conservative variants." For polypeptide sequences, this encompasses "function-conservative variants." Sequence-conservative variants are those in which a change of one or more nucleotides in a given codon position results in no alteration in the amino acid encoded at that position. Function-conservative variants are those in which a given amino acid residue in a polypeptide has been changed without altering the overall conformation and function of the native polypeptide, including, but not limited to,

replacement of an amino acid with one having similar physico-chemical properties (such as, for example, acidic, basic, hydrophobic, and the like). "Function-conservative" variants also include any polypeptides that have the ability to elicit antibodies specific to a designated polypeptide.

- 5 An "*B. fragilis* -derived" nucleic acid or polypeptide sequence may or may not be present in other bacterial species, and may or may not be present in all *B. fragilis* strains. This term is intended to refer to the source from which the sequence was originally isolated. Thus, an *B. fragilis* -derived polypeptide, as used herein, may be used, e.g., as a target to screen for a broad spectrum antibacterial agent, to search for homologous
- 10 proteins in other species of bacteria or in eukaryotic organisms such as bacteria humans, etc.

- A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally
- 15 occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least about 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains sufficient polypeptide to allow protein sequencing; at least about 1, 10, or preferably 100 mg of polypeptide.

- 20 A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least about 10%, more preferably at least about 50%, of the subject cells.

- A purified or isolated or a substantially pure nucleic acid, e.g., a substantially
- 25 pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome of the organism from which the nucleic acid is derived; or

which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a
 5 separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *B. fragilis* DNA sequence.

A "contig" as used herein is a nucleic acid representing a continuous stretch of
 10 genomic sequence of an organism.

An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from a stop to stop codon or from a start to stop codon.

As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not limited to messenger
 15 RNA, synthetic DNA, and recombinant nucleic acid sequences.

A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by
 25 a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety

capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred

5 herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art

10 using routine experimentation.

"Homologous" refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules

15 are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two sequences are matched or homologous then the two sequences are 60% homologous. By way of example, the DNA sequences ATTGCC and TATGGC

20 share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid can anneal to the other nucleic acid under defined stringency conditions. Stringency of hybridization is determined by: (a) the temperature at which hybridization and/or

25 washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. Typically, hybridization of two sequences at high

stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires that the sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65 ° C) and low stringency (such as, for example 2X SSC at 55° C) require correspondingly less overall complementarity between the

5 hybridizing sequences. (1X SSC is 0.15 M NaCl, 0.015 M Na citrate).

The terms peptides, proteins, and polypeptides are used interchangeably herein.

As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

10 A polypeptide has *B. fragilis* biological activity if it has one, two or preferably more of the following properties: (1) if when expressed in the course of an *B. fragilis* infection, it can promote, or mediate the attachment of *B. fragilis* to a cell; (2) it has an enzymatic activity, structural or regulatory function characteristic of an *B. fragilis* protein; (3) the gene which encodes it can rescue a lethal mutation in an *B. fragilis* gene.

15 A polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *B. fragilis* polypeptides of the invention contained in the Sequence Listing, or of other naturally occurring *B. fragilis* polypeptides, e.g., one

20 or more of the biological activities described herein. Especially preferred are fragments which exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO (Chinese Hamster Ovary) cells. Because peptides such as *B. fragilis*

25 polypeptides often exhibit a range of physiological properties and because such properties may be attributable to different portions of the molecule, a useful *B. fragilis* fragment or *B. fragilis* analog is one which exhibits a biological activity in any biological assay for *B. fragilis* activity. The fragment or analog possesses about 10%, preferably

about 40%, more preferably about 60%, 70%, 80% or 90% or greater of the activity of *B. fragilis*, in any *in vivo* or *in vitro* assay.

Analogues can differ from naturally occurring *B. fragilis* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogues include *B. fragilis* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *B. fragilis* polypeptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions can be made in view of the table below.

TABLE 1

CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β -Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met

Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline
Proline	P	D-Pro, L-I-thioazolidine-4-carboxylic acid, D-or L-1-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs
5 that include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to an *B. fragilis* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues,
10 preferably at least about 60 residues in length. Fragments of *B. fragilis* polypeptides can be generated by methods known to those skilled in the art. The ability of an *Bacteroides* fragment to exhibit a biological activity of *B. fragilis* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *B. fragilis* polypeptides containing residues that are not required for biological activity of
15 the peptide or that result from alternative mRNA splicing or alternative protein processing events.

An "immunogenic component" as used herein is a moiety, such as an *B. fragilis* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as an *B. fragilis* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with sufficiently high affinity to form a detectable antigen-antibody complex.

The term "antibody" as used herein is intended to include fragments thereof which are specifically reactive with *B. fragilis* polypeptides.

As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of increased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refers to cells which can

become or have been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA complement to the original
 5 parent, due to accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally
 10 include a promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

15 As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

The "metabolism" of a substance, as used herein, means any aspect of the
 20 expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a
 25 substance includes changes the substance induces in the distribution of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum,

cerebrospinal fluid, lymph, tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

Technical and scientific terms used herein have the meanings commonly understood by one of ordinary skill in the art to which the present invention pertains, unless otherwise defined. Reference is made herein to various methodologies known to those of skill in the art. Publications and other materials setting forth such known methodologies to which reference is made are incorporated herein by reference in their entireties as though set forth in full. The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See e.g.*, Sambrook, Fritsch, and Maniatis, *Molecular Cloning; Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.); *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991); *Immunology*, 2d Edition, 1989, Roitt *et al.*, C.V. Mosby Company, and New York; *Advanced Immunology*, 2d Edition, 1991, Male *et al.*, Grower Medical Publishing, New York.; *DNA Cloning: A Practical Approach*, Volumes I and II, 1985 (D.N. Glover ed.); *Oligonucleotide Synthesis*, 1984, (M.L. Gait ed); *Transcription and Translation*, 1984 (Hames and Higgins eds.); *Animal Cell Culture*, 1986 (R.I. Freshney ed.); *Immobilized Cells and Enzymes*, 1986 (IRL Press); Perbal, 1984, *A Practical Guide to Molecular Cloning*; *Gene Transfer Vectors for Mammalian Cells*, 1987 (J. H. Miller and M. P. Calos eds., Cold Spring Harbor Laboratory); Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Any suitable materials and/or methods known to those of skill can be utilized in carrying out the present invention; however, preferred materials and/or methods are described. Materials, reagents and the like to which reference is made in the following description and examples are obtainable from commercial sources, unless otherwise
 5 noted.

B. FRAGILIS GENOMIC SEQUENCE

This invention provides nucleotide sequences of the genome of *B. fragilis* which thus comprises a DNA sequence library of *B. fragilis* genomic DNA. The detailed
 10 description that follows provides nucleotide sequences of *B. fragilis* , and also describes how the sequences were obtained and how ORFs and protein-coding sequences were identified. Also described are compositions and methods of using the disclosed *B. fragilis* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of
 15 medically important sequences in this and other strains of *B. fragilis* .

To determine the genomic sequence of *B. fragilis* , DNA from strain 14062 of *B. fragilis* was isolated after Zymolyase digestion, sodium dodecyl sulfate lysis, potassium acetate precipitation, phenol:chloroform extraction and ethanol precipitation (Soll, D.R., T. Srikantha and S.R. Lockhart: Characterizing Developmentally Regulated Genes in *B. fragilis* . In Microbial Genome Methods. K.W. Adolph, editor. CRC Press. New York. p 17-37.). DNA was sheared hydrodynamically using an HPLC (Oefner, et. al., 1996) to an insert size of 2000-3000 bp. After size fractionation by gel electrophoresis the fragments were blunt-ended, ligated to adapter oligonucleotides and cloned into the pGTC (Thomann) vector to construct a "shotgun" subclone library.
 20

DNA sequencing was achieved using established ABI sequencing methods on ABI377 automated DNA sequencers. The cloning and sequencing procedures are described in more detail in the Exemplification.

Individual sequence reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). The average contig length was about 3-4 kb.

All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. The cloning and sequencing procedures are described in more detail in the Exemplification.

A variety of approaches may be used to order the contigs so as to obtain a continuous sequence representing the entire *B. fragilis* genome. Synthetic oligonucleotides are designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libraries of *B. fragilis* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that contain sequences corresponding to the junctional regions between individual contigs. Such clones are then used to isolate template DNA and the same oligonucleotides are used as primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which is then determined.

The *B. fragilis* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least 180 nucleotides. As a result of the analysis of ORFs based on stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *B. fragilis* polypeptide. These ORFs may contain start codons which indicate the initiation of protein synthesis of a naturally-occurring *B. fragilis* polypeptide. Such start codons within the ORFs provided herein were identified by those of ordinary skill in the relevant art, and the resulting ORF and the encoded *B. fragilis* polypeptide is within the scope of this invention. For example, within the ORFs a codon such as AUG or GUG (encoding methionine or valine) which is part of the initiation signal for protein synthesis were identified and the portion of an ORF to corresponding to a naturally-occurring *B. fragilis* polypeptide was recognized. The predicted coding regions were defined by evaluating the coding potential of such

sequences with the program GENEMARK™ (Borodovsky and McIninch, 1993, *Comp. .*
17:123).

Each predicted ORF amino acid sequence was compared with all sequences
 found in current GENBANK, SWISS-PROT, and PIR databases using the BLAST
 5 algorithm. BLAST identifies local alignments occurring by chance between the ORF
 sequence and the sequence in the databank (Altschall et al., 1990, *L Mol. Biol.* 215:403-
 410). Homologous ORFs (probabilities less than 10^{-5} by chance) and ORF's that are
 probably non-homologous (probabilities greater than 10^{-5} by chance) but have good
 codon usage were identified. Both homologous, sequences and non-homologous
 10 sequences with good codon usage, are likely to encode proteins and are encompassed by
 the invention.

B. FRAGILIS NUCLEIC ACIDS

The present invention provides a library of *B. fragilis* -derived nucleic acid
 15 sequences. The libraries provide probes, primers, and markers which are used as markers
 in epidemiological studies. The present invention also provides a library of *B. fragilis* -
 derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

The nucleic acids of this invention may be obtained directly from the DNA of the
 above referenced *B. fragilis* strain by using the polymerase chain reaction (PCR). See
 20 "*PCR, A Practical Approach*" (McPherson, Quirke, and Taylor, eds., IRL Press, Oxford,
 UK, 1991) for details about the PCR. High fidelity PCR is used to ensure a faithful DNA
 copy prior to expression. In addition, the authenticity of amplified products is verified by
 conventional sequencing methods. Clones carrying the desired sequences described in
 this invention may also be obtained by screening the libraries by means of the PCR or by
 25 hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or
 plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning, A Laboratory*
Manual 2nd edition, 1989, Cold Spring Harbor Press, NY).

It is also possible to obtain nucleic acids encoding *B. fragilis* polypeptides from a cDNA library in accordance with protocols herein described. A cDNA encoding an *B. fragilis* polypeptide can be obtained by isolating total mRNA from an appropriate strain. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes encoding *B. fragilis* polypeptides can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids of the invention are contained in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

In another example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 264:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

Nucleic acids isolated or synthesized in accordance with features of the present invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to such sequences. As probes, primers, capture ligands and antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability to form

stable hybridization products) of the nucleic acids of the invention contained in the Sequence Listing. These uses are described in further detail below.

PROBES

5 A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained in the Sequence Listing can be used as a probe to specifically detect *B. fragilis*. With the sequence information set forth in the present application, sequences of twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *B. fragilis*, and extraneous nucleic acids likely to be
10 encountered during hybridization conditions. More preferably, the sequence will comprise at least about twenty to thirty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules.

Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will
15 readily recognize that the nucleic acids, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with the sequence of the invention contained in the Sequence Listing can also be useful as probes to detect homologous regions (especially homologous genes) of other *Bacteroides* species using
20 appropriate stringency hybridization conditions as described herein.

CAPTURE LIGAND

For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in
25 which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing have utility to separate *B. fragilis* nucleic acid from one strain from the nucleic acid of other another strain as well as from other organisms. Nucleic acid having twenty

or more nucleotides in a sequence of the invention contained in the Sequence Listing can also have utility to separate other *Bacteroides* species from each other and from other organisms. Preferably, the sequence will comprise at least about twenty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

PRIMERS

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility as primers for the amplification of *B. fragilis* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acids in other *Bacteroides* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of ≥ 10 -15 nucleotides of the invention contained in the Sequence Listing have utility in conjunction with suitable enzymes and reagents to create copies of *B. fragilis* nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *B. fragilis* and/or other *Bacteroides* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as is described in greater detail herein.

The nucleic acids of the present invention find use as templates for the recombinant production of *B. fragilis* -derived peptides or polypeptides

ANTISENSE

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *B. fragilis* genes. These sequences also have utility as

5 antisense agents to prevent expression of genes of other *Bacteroides* species.

In one embodiment, nucleic acid or derivatives corresponding to *B. fragilis* nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA.

10 Preferably, the antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and bacterial nucleic acid and/or bacterial messenger RNA. Nucleic acid having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes

15 is known in the art as exemplified by U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

The present invention encompasses isolated polypeptides and nucleic acids derived from *B. fragilis* that are useful as reagents for diagnosis of bacterial infection, components of effective anti-bacterial vaccines, and/or as targets for anti-bacterial drugs,

20 including anti-*B. fragilis* drugs.

EXPRESSION OF *B. FRAGILIS* NUCLEIC ACIDS

Table 2, which is appended herewith and which forms part of the present specification, provides a list of open reading frames (ORFs) in both strands and a

25 putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLASTP2 algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. An ORF is a region of nucleic acid which encodes a polypeptide. This region may represent

a portion of a coding sequence or a total sequence and was determined from stop to stop codons. The first column contains a designation for the ORF ("ORF Name"). The second and third columns list the SEQ ID numbers for the nucleic acid ("NT ID") and amino acid ("AA ID") sequences corresponding to each ORF, respectively. The fourth and fifth
5 columns list the length of the nucleic acid ORF ("NT Length") and the length of the amino acid ORF ("AA Length"), respectively. The nucleotide sequence corresponding to each ORF begins at the first nucleotide immediately following a stop codon and ends at the nucleotide immediately preceding the next downstream stop codon in the same reading frame. It will be recognized by one skilled in the art that the natural translation
10 initiation sites will correspond to ATG, GTG, or TTG codons located within the ORFs. The natural initiation sites depend not only on the sequence of a start codon but also on the context of the DNA sequence adjacent to the start codon. Usually, a recognizable ribosome binding site is found within 20 nucleotides upstream from the initiation codon. In some cases where genes are translationally coupled and coordinately expressed
15 together in "operons", ribosome binding sites are not present, but the initiation codon of a downstream gene may occur very close to, or overlap, the stop codon of the an upstream gene in the same operon. The correct start codons can be generally identified without undue experimentation because only a few codons need be tested. It is recognized that the translational machinery in bacteria initiates all polypeptide chains with the amino
20 acid methionine, regardless of the sequence of the start codon. In some cases, polypeptides are post-translationally modified, resulting in an N-terminal amino acid other than methionine *in vivo*. The sixth and seventh columns provide metrics for assessing the likelihood of the homology match (determined by the BLASTP2 algorithm), as is known in the art, to the genes indicated in the description frame
25 ("Description") defined further below. These genes in the Description were identified when the designated ORF was compared against a comprehensive non-redundant protein database. Specifically, the sixth column represents the Blast Score ("Score") for the match (a higher score is a better match), and the seventh column represents the

probability ("Probability") for the match (the probability that such a match can have occurred by chance; the lower the value, the more likely the match is valid). If a BLASTP2 score of less than 100 was obtained, no value is reported in the table. The remaining fields below the columns contain additional information relating to the potential function of the sequence based on the BLASTP2 analysis. Where a match was discovered, the field "Protein name" list the protein's name identified from the match. In addition, one skilled in the art would be able to identify the match and elucidate its function using the "Locus name" and where available the accession number, "Acc#" from the database. Lastly, one skilled in the art would appreciate the "Description" field to further describe the potential function of the protein based on this analysis. This information allows one of ordinary skill in the art to determine a potential use for each identified coding sequence and, as a result, allows to use the polypeptides of the present invention for commercial and industrial purposes.

Using the information provided in SEQ ID NO: 1 - SEQ ID NO: 5222, SEQ ID NO: 5223 - SEQ ID NO: 10444 and in Table 2 together with routine cloning and sequencing methods, one of ordinary skill in the art will be able to clone and sequence all the nucleic acid fragments of interest including open reading frames (ORFs) encoding a large variety of proteins of *B. fragilis*.

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate polypeptides. The nucleic acid of the invention exemplified in SEQ ID NO: 1 - SEQ ID NO: 5222 and in Table 2 or fragments of said nucleic acid encoding active portions of *B. fragilis* polypeptides can be cloned into suitable vectors or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

The function of a specific gene or operon can be ascertained by expression in a bacterial strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large quantities in an expressing strain for use as an antigen, an

industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does not produce the same gene product(s). This includes, but is not limited to, Eucaryotic species such as the yeast *Saccharomyces cerevisiae*, *Methanobacterium* strains or other Archaea, and Eubacteria such as *E. coli*, *B. Subtilis*, *S. Aureus*, *S. Pneumonia* or *Pseudomonas putida*. In some cases the expression host will utilize the natural *B. fragilis* promoter whereas in others, it will be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *B. fragilis* promoter, a procedure such as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant plasmid containing an origin of replication that functions in the host organism and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is introduced into the host organism by, for example, electroporation and cells containing the recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

A suitable host cell for expression of a gene can be any procaryotic or eucaryotic cell. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press (1989)), and other laboratory textbooks.

5 For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding an *B. fragilis* polypeptide can be cultured under appropriate conditions to allow expression of the polypeptide to occur. Suitable media for cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art
10 for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such polypeptides. Additionally, in many situations, polypeptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

15 In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Chromatographic techniques
20 which can be used in the final purification step are known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye affinity and immunoaffinity.

One strategy to maximize recombinant *B. fragilis* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods
25 in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy would be to alter the nucleic acid encoding an *B. fragilis* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc.*

Acids Res. 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

The present invention provides a library of *B. fragilis* -derived nucleic acid sequences. The libraries provide probes, primers, and markers which can be used as markers in epidemiological studies. The present invention also provides a library of *B. fragilis* -derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

Nucleic acids comprising any of the sequences disclosed herein or sub-sequences thereof can be prepared by standard methods using the nucleic acid sequence information provided in SEQ ID NO: 1 - SEQ ID NO: 5222. For example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 264:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

Of course, due to the degeneracy of the genetic code, many different nucleotide sequences can encode polypeptides having the amino acid sequences defined by SEQ ID NO: 5223 - SEQ ID NO: 10444 or sub-sequences thereof. The codons can be selected for optimal expression in prokaryotic or eukaryotic systems. Such degenerate variants are also encompassed by this invention.

Insertion of nucleic acids (typically DNAs) encoding the polypeptides of the invention into a vector is easily accomplished when the termini of both the DNAs and the

vector comprise compatible restriction sites. If this cannot be done, it may be necessary to modify the termini of the DNAs and/or vector by digesting back single-stranded DNA overhangs generated by restriction endonuclease cleavage to produce blunt ends, or to achieve the same result by filling in the single-stranded termini with an appropriate DNA
 5 polymerase.

Alternatively, any site desired may be produced, e.g., by ligating nucleotide sequences (linkers) onto the termini. Such linkers may comprise specific oligonucleotide sequences that define desired restriction sites. Restriction sites can also be generated by the use of the polymerase chain reaction (PCR). See, e.g., Saiki *et al.*, 1988, *Science*
 10 239:48. The cleaved vector and the DNA fragments may also be modified if required by homopolymeric tailing.

The nucleic acids of the invention may be isolated directly from cells. Alternatively, the polymerase chain reaction (PCR) method can be used to produce the nucleic acids of the invention, using either chemically synthesized strands or genomic
 15 material as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

The nucleic acids of the present invention may be flanked by natural *B. fragilis*
 20 regulatory sequences, or may be associated with heterologous sequences, including promoters, enhancers, response elements, signal sequences, polyadenylation sequences, introns, 5'- and 3'- noncoding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, "caps", substitution of one or more of the naturally occurring
 25 nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoroamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.). Nucleic acids may contain one or more additional covalently

linked moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (e.g., acridine, psoralen, etc.), chelators (e.g., metals, radioactive metals, iron, oxidative metals, etc.), and alkylators. PNAs are also included. The nucleic acid may be derivatized by formation of a methyl or ethyl
 5 phosphotriester or an alkyl phosphoramidate linkage. Furthermore, the nucleic acid sequences of the present invention may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

The invention also provides nucleic acid vectors comprising the disclosed *B.*
 10 *fragilis* -derived sequences or derivatives or fragments thereof. A large number of vectors, including plasmid and bacterial vectors, have been described for replication and/or expression in a variety of eukaryotic and prokaryotic hosts, and may be used for cloning or protein expression.

The encoded *B. fragilis* polypeptides may be expressed by using many known
 15 vectors, such as pUC plasmids, pET plasmids (Novagen, Inc., Madison, WI), or pRSET or pREP (Invitrogen, San Diego, CA), and many appropriate host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not critical to the practice of the invention.

Recombinant cloning vectors will often include one or more replication systems
 20 for cloning or expression, one or more markers for selection in the host, e.g. antibiotic resistance, and one or more expression cassettes. The inserted *B. fragilis* coding sequences may be synthesized by standard methods, isolated from natural sources, or prepared as hybrids, etc. Ligation of the *B. fragilis* coding sequences to transcriptional regulatory elements and/or to other amino acid coding sequences may be achieved by
 25 known methods. Suitable host cells may be transformed/transfected/infected as appropriate by any suitable method including electroporation, CaCl₂ mediated DNA uptake, bacterial infection, microinjection, microprojectile, or other established methods.

Appropriate host cells include bacteria, archebacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. Of particular interest are *B. fragilis*, *E. coli*, *B. Subtilis*, *Saccharomyces cerevisiae*, *Saccharomyces carlsbergensis*, *Schizosaccharomyces pombe*, SF9 cells, C129 cells, 293 cells, *Neurospora*, and CHO cells, COS cells, HeLa cells, and immortalized mammalian myeloid and lymphoid cell lines. Preferred replication systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, and the like. A large number of transcription initiation and termination regulatory regions have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Examples of these regions, methods of isolation, manner of manipulation, etc. are known in the art. Under appropriate expression conditions, host cells can be used as a source of recombinantly produced *B. fragilis* -derived peptides and polypeptides.

Advantageously, vectors may also include a transcription regulatory element (i.e., a promoter) operably linked to the *B. fragilis* portion. The promoter may optionally contain operator portions and/or ribosome binding sites. Non-limiting examples of bacterial promoters compatible with *E. coli* include: b-lactamase (penicillinase) promoter; lactose promoter; tryptophan (trp) promoter; araBAD (arabinose) operon promoter; lambda-derived P₁ promoter and N gene ribosome binding site; and the hybrid tac promoter derived from sequences of the trp and lac UV5 promoters. Non-limiting examples of yeast promoters include 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) promoter, galactokinase (GAL1) promoter, galactoeprimase promoter, and alcohol dehydrogenase (ADH) promoter. Suitable promoters for mammalian cells include without limitation viral promoters such as that from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences, polyA addition sequences and enhancer sequences to increase expression. Sequences which cause amplification of the gene may also be desirable. Furthermore, sequences that facilitate secretion of the recombinant product from cells, including, but

not limited to, bacteria, yeast, and animal cells, such as secretory signal sequences and/or prohormone pro region sequences, may also be included. These sequences are well described in the art.

Nucleic acids encoding wild-type or variant *B. fragilis* -derived polypeptides may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell, and thereby effect homologous recombination at the site of an endogenous gene or a sequence with substantial identity to the gene. Other recombination-based methods such as nonhomologous recombinations or deletion of endogenous genes by homologous recombination may also be used.

The nucleic acids of the present invention find use as templates for the recombinant production of *B. fragilis* -derived peptides or polypeptides.

IDENTIFICATION AND USE OF *B. FRAGILIS* NUCLEIC ACID SEQUENCES

The disclosed *B. fragilis* polypeptide and nucleic acid sequences, or other sequences that are contained within ORFs, including complete protein-coding sequences, of which any of the disclosed *B. fragilis* -specific sequences forms a part, are useful as target components for diagnosis and/or treatment of *B. fragilis* - caused infection

It will be understood that the sequence of an entire protein-coding sequence of which each disclosed nucleic acid sequence forms a part can be isolated and identified based on each disclosed sequence. This can be achieved, for example, by using an isolated nucleic acid encoding the disclosed sequence, or fragments thereof, to prime a sequencing reaction with genomic *B. fragilis* DNA as template; this is followed by sequencing the amplified product. The isolated nucleic acid encoding the disclosed sequence, or fragments thereof, can also be hybridized to *B. fragilis* genomic libraries to identify clones containing additional complete segments of the protein-coding sequence of which the shorter sequence forms a part. Then, the entire protein-coding sequence, or fragments thereof, or nucleic acids encoding all or part of the sequence, or sequence-

conservative or function-conservative variants thereof, may be employed in practicing the present invention.

Preferred sequences are those that are useful in diagnostic and/or therapeutic applications. Diagnostic applications include without limitation nucleic-acid-based and antibody-based methods for detecting bacterial infection. Therapeutic applications include without limitation vaccines, passive immunotherapy, and drug treatments directed against gene products that are both unique to bacteria and essential for growth and/or replication of bacteria.

10 IDENTIFICATION OF NUCLEIC ACIDS ENCODING VACCINE COMPONENTS AND TARGETS FOR AGENTS EFFECTIVE AGAINST *B. FRAGILIS*

The disclosed *B. fragilis* genome sequence includes segments that direct the synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *B. fragilis*. Identification of said immunogenic components involved in the determination of the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these approaches are described briefly below.

20

HOMOLOGY TO KNOWN SEQUENCES:

Computer-assisted comparison of the disclosed *B. fragilis* sequences with previously reported sequences present in publicly available databases is useful for identifying functional *B. fragilis* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level indicates that the two proteins also possess some degree of functional homology, such as, for example, among enzymes involved in

metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for
5 covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-coding sequence. Identification of such a feature in an *B. fragilis* sequence is therefore useful in determining the function of the encoded protein and identifying useful targets of antibacterial drugs.

10 Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal peptides and hydrophobic transmembrane domains. *B. fragilis* proteins identified as containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

15 Targets for therapeutic drugs according to the invention include, but are not limited to, polypeptides of the invention, whether unique to *B. fragilis* or not, that are essential for growth and/or viability of *B. fragilis* under at least one growth condition. Polypeptides essential for growth and/or viability can be determined by examining the effect of deleting and/or disrupting the genes, i.e., by so-called gene "knockout".

20 Alternatively, genetic footprinting can be used (Smith *et al.*, 1995, *Proc. Natl. Acad. Sci. USA* 92:5479-6433; Published International Application WO 94/26933; U.S. Patent No. 5,612,180). Still other methods for assessing essentiality includes the ability to isolate conditional lethal mutations in the specific gene (e.g., temperature sensitive mutations). Other useful targets for therapeutic drugs, which include polypeptides that are not
25 essential for growth or viability *per se* but lead to loss of viability of the cell, can be used to target therapeutic agents to cells.

STRAIN-SPECIFIC SEQUENCES:

Because of the evolutionary relationship between different *B. fragilis* strains, it is believed that the presently disclosed *B. fragilis* sequences are useful for identifying, and/or discriminating between, previously known and new *B. fragilis* strains. It is

5 believed that other *B. fragilis* strains will exhibit at least about 70% sequence homology with the presently disclosed sequence. Systematic and routine analyses of DNA sequences derived from samples containing *B. fragilis* strains, and comparison with the present sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all *B. fragilis* strains.

10 In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that discriminate between different strains of *B. fragilis*. Strain-specific components can also be identified functionally by their ability to elicit or react with antibodies that selectively recognize one or more *B. fragilis* strains.

In another embodiment, the invention provides nucleic acids, including probes,

15 and peptide and polypeptide sequences that are common to all *B. fragilis* strains but are not found in other bacterial species.

B. FRAGILIS POLYPEPTIDES

This invention encompasses isolated *B. fragilis* polypeptides encoded by the

20 disclosed *B. fragilis* genomic sequences, including the polypeptides of the invention contained in the Sequence Listing. Polypeptides of the invention are preferably at least about 5 amino acid residues in length. Using the DNA sequence information provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using methods well-known in the art. It will be understood that the sequence

25 of an entire nucleic acid encoding an *B. fragilis* polypeptide can be isolated and identified based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated nucleic acid encoding

the ORF, or fragments thereof, to prime a polymerase chain reaction with genomic *B. fragilis* DNA as template; this is followed by sequencing the amplified product.

The polypeptides of the present invention, including function-conservative variants of the disclosed ORFs, may be isolated from wild-type or mutant *B. fragilis* cells, or from heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) including *B. fragilis* into which an *B. fragilis* - derived protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins.

B. fragilis polypeptides of the invention can be chemically synthesized using commercially automated procedures such as those referenced herein, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. The polypeptides are preferably prepared by solid phase peptide synthesis as described by Merrifield, 1963, *J. Am. Chem. Soc.* 85:2149. The synthesis is carried out with amino acids that are protected at the alpha-amino terminus. Trifunctional amino acids with labile side-chains are also protected with suitable groups to prevent undesired chemical reactions from occurring during the assembly of the polypeptides. The alpha-amino protecting group is selectively removed to allow subsequent reaction to take place at the amino-terminus. The conditions for the removal of the alpha-amino protecting group do not remove the side-chain protecting groups.

Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the *B. fragilis* protein contains an additional sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively,

antibodies produced against an *B. fragilis* protein or against peptides derived therefrom can be used as purification reagents. Other purification methods are possible.

The present invention also encompasses derivatives and homologues of *B. fragilis* -encoded polypeptides. For some purposes, nucleic acid sequences encoding the peptides may be altered by substitutions, additions, or deletions that provide for functionally equivalent molecules, i.e., function-conservative variants. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of similar properties, such as, for example, positively charged amino acids (arginine, lysine, and histidine); negatively charged amino acids (aspartate and glutamate); polar neutral amino acids; and non-polar amino acids.

The isolated polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

To identify *B. fragilis* -derived polypeptides for use in the present invention, essentially the complete genomic sequence of a virulent, methicillin-resistant isolate of *Bacteroides fragilis* isolate was analyzed. While, in very rare instances, a nucleic acid sequencing error may be revealed, resolving a rare sequencing error is well within the art, and such an occurrence will not prevent one skilled in the art from practicing the invention.

Also encompassed are any *B. fragilis* polypeptide sequences that are contained within the open reading frames (ORFs), including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 5222 forms a part. Table 2, which is appended herewith and which forms part of the present specification, provides a putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLAST algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. As a result, one

skilled in the art can use the polypeptides of the present invention for commercial and industrial purposes consistent with the type of putative identification of the polypeptide.

The present invention provides a library of *B. fragilis* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences that are contemplated for use as components of vaccines. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended herewith and which forms part of the present specification.

The present invention also provides a library of *B. fragilis* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences lacking homology to any known prokaryotic or eukaryotic sequences. Such libraries provide probes, primers, and markers which can be used to diagnose *B. fragilis* infection, including use as markers in epidemiological studies. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended hereto and part hereof.

The present invention also provides a library of *B. fragilis* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise targets for therapeutic drugs.

SPECIFIC EXAMPLE: DETERMINATION OF *BACTEROIDES* PROTEIN ANTIGENS FOR ANTIBODY AND VACCINE DEVELOPMENT

The selection of *Bacteroides* protein antigens for vaccine development can be derived from the nucleic acids encoding *B. fragilis* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and

DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University
 5 Research Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g.
 10 probabilities lower than 1×10^{-6} that the homology is only due to random chance) to membrane or exported proteins represent protein antigens for vaccine development. Possible functions can be provided to *B. fragilis* genes based on sequence homology to genes cloned in other organisms.

Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino
 15 acid sequences. This algorithm uses the intrinsic information contained in the ORF amino acid sequence and compares it to information derived from the properties of known membrane and exported proteins. This comparison predicts which proteins will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as exported or membrane associated by this algorithm are likely protein antigens for
 20 vaccine development.

PRODUCTION OF FRAGMENTS AND ANALOGS OF *B. FRAGILIS* NUCLEIC ACIDS AND POLYPEPTIDES

Based on the discovery of the *B. fragilis* gene products of the invention provided
 25 in the Sequence Listing, one skilled in the art can alter the disclosed structure of *B. fragilis* genes, e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art
 * which allow the production and testing of fragments and analogs are discussed below.

These, or analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *B. fragilis* polypeptides. Such screens are useful for the identification of inhibitors of *B. fragilis*.

5

GENERATION OF FRAGMENTS

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments. Digestion with "end-nibbling" endonucleases can thus generate DNAs which encode an array of fragments. DNAs which encode fragments of a protein can also be generated by random shearing, restriction digestion or a combination of the above-

10 discussed methods.

Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a

15 desired length.

20

ALTERATION OF NUCLEIC ACIDS AND POLYPEPTIDES: RANDOM METHODS

Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

25

PCR MUTAGENESIS

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

SATURATION MUTAGENESIS

Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro*, and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and essentially all possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

DEGENERATE OLIGONUCLEOTIDES

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton,

Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

ALTERATION OF NUCLEIC ACIDS AND POLYPEPTIDES: METHODS FOR DIRECTED MUTAGENESIS

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

ALANINE SCANNING MUTAGENESIS

Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution.

Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit
 5 variants are screened for the optimal combination of desired activity.

OLIGONUCLEOTIDE-MEDIATED MUTAGENESIS

Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA*
 10 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the
 15 oligonucleotide primer, and will code for the selected alteration in the desired protein DNA. Generally, oligonucleotides of at least about 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the
 20 stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci. USA*, 75: 5765[1978]).

CASSETTE MUTAGENESIS

25 Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a

unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the mutated desired protein subunit DNA sequence.

COMBINATORIAL MUTAGENESIS

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related proteins are aligned, preferably to promote the highest homology possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

25

OTHER MODIFICATIONS OF *B. FRAGILIS* NUCLEIC ACIDS AND POLYPEPTIDES

It is possible to modify the structure of an *B. fragilis* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and
5 resistance to proteolytic degradation *in vivo*). A modified *B. fragilis* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition as described herein.

An *B. fragilis* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize
10 dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

In order to enhance stability and/or reactivity, an *B. fragilis* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the
15 protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, an *B. fragilis* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Sehon and co-workers (Wie et al., *supra*) to produce a protein conjugated with PEG.
20 In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *B. fragilis* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, *supra*); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA
25 (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

To facilitate purification and potentially increase solubility of an *B. fragilis* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide

backbone. For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of epitopes within an *B. fragilis* polypeptide, canonical protease sensitive sites can be engineered between regions, each comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

15 PRIMARY METHODS FOR SCREENING POLYPEPTIDES AND ANALOGS

Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *B. fragilis* polypeptide or an interacting protein, facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the techniques described below is amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

25

TWO HYBRID SYSTEMS

Two hybrid assays such as the system described below (as with the other screening methods described herein), can be used to identify polypeptides, e.g.,

fragments or analogs of a naturally-occurring *B. fragilis* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to an *B. fragilis* protein. (The *B. fragilis* domain is used as the bait protein and the library of variants are expressed as prey fusion proteins.) In an analogous fashion, a two hybrid assay (as with
 5 the other screening methods described herein), can be used to find polypeptides which bind an *B. fragilis* polypeptide.

DISPLAY LIBRARIES

In one approach to screening assays, the Bacteroides peptides are displayed on the
 10 surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and
 15 Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently labeled ligands, allows cells to be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell
 20 permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at concentrations well over
 25 10^{13} phage per milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of infection. The group of almost identical *E. coli* filamentous phages, M13, fd.,

and fl, are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH₂-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage
 5 lacking this epitope (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane
 10 protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037). Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA
 15 (Schorr et al. (1991) *Vaccines* 91, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993).
 20 Because of its role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motive organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Kuwajima et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other
 25 bacterial species have also served as peptide fusion partners. Examples include the *Staphylococcus* protein A and the outer membrane IgA protease of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme

5 uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull *et al.* (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By

10 installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stably associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA

15 complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the

20 opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull *et al.* (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89-1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the

25 C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs, the phage-

displayed peptides are presented right at the amino terminus of the fusion protein.

(Cwirla, et al. (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic activities. The phage coat proteins require transport across the inner membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7 - 10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.

In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation

of a substantial proportion of the RNA in polysomes and yielding complexes containing nascent peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound
 5 complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next round of synthesis and screening. The polysome display method can be coupled to the phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat
 10 proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the sequences of the active peptides
 15 one sequences the DNA produced by the phagemid host.

SECONDARY SCREENING OF POLYPEPTIDES AND ANALOGS

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled
 20 in the art to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated though one of the primary screens described above.

25 Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine for one skilled in the art to obtain analogs and fragments.

PEPTIDE MIMETICS OF *B. FRAGILIS* POLYPEPTIDES

The invention also provides for reduction of the protein binding domains of the subject *B. fragilis* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its counter ligand, e.g., in the case of an *B. fragilis* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *B. fragilis* polypeptide which are involved in molecular recognition of a polypeptide can be determined and used to generate *B. fragilis* -derived peptidomimetics which competitively or noncompetitively inhibit binding of the *B. fragilis* polypeptide with an interacting polypeptide (see, for example, European patent applications EP-412,762A and EP-B31,080A).

For example, scanning mutagenesis can be used to map the amino acid residues of a particular *B. fragilis* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepine or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of an *B. fragilis* polypeptide to an interacting polypeptide and thereby interfere with the function of *B. fragilis* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), b-turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and b-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and et al. (1986) *Biochem Biophys Res Commun* 134:71).

VACCINE FORMULATIONS FOR *B. FRAGILIS* NUCLEIC ACIDS AND POLYPEPTIDES

This invention also features vaccine compositions for protection against infection
 5 by *B. fragilis* or for treatment of *B. fragilis* infection. In one embodiment, the vaccine compositions contain one or more immunogenic components such as a surface protein from *B. fragilis*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids of the invention contained in the Sequence Listing which encode *B. fragilis* surface proteins.
 10 Any nucleic acid encoding an immunogenic *B. fragilis* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

One aspect of the invention provides a vaccine composition for protection against infection by *B. fragilis* which contains at least one immunogenic fragment of an *B. fragilis* protein and a pharmaceutically acceptable carrier. Preferred fragments include
 15 peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by screening polypeptides recombinantly produced from the corresponding fragment of the
 20 nucleic acid encoding the full-length *B. fragilis* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for
 25 example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at

the level of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune
 5 cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of antibodies. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this
 10 invention.

Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture.
 15 Presentation of an immunogenic *B. fragilis* peptide in association with appropriate MHC molecules to T cells in conjunction with the necessary co-stimulation has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one
 20 of several conventional assays for interleukin-2 can be employed, such as the assay described in *Proc. Natl. Acad. Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

Alternatively, a common assay for T cell proliferation entails measuring tritiated
 25 thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ³H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

Vaccine compositions of the invention containing immunogenic components (e.g., *B. fragilis* polypeptide or fragment thereof or nucleic acid encoding an *B. fragilis* polypeptide or fragment thereof) preferably include a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not
 5 cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or
 10 buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing *B. fragilis* polypeptides, the polypeptide is co-administered with a suitable adjuvant.

It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the
 15 administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or DNA.

Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular
 20 immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *B. fragilis*. Cain et. al. (1993) *Vaccine* 11: 637-642. Oral formulations
 25 include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like.

The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl--L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycolate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or genetically engineered fusions of the *B. fragilis* polypeptide with cholera toxin or its B subunit, procholeragenoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*B. fragilis* bacterial lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or immunostimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 mg to 50 mg, for example 10 mg to 35 mg. When used in the form of microcapsules, the amount used will depend on the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *B. fragilis* polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N NaHCO₃ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *B. fragilis* in an infected host, or as a therapeutic agent in the aim to induce an immune response in a susceptible host to prevent infection by *B. fragilis*. The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 mg to 10 g, preferably 10 mg to 100 mg. A suitable dosage for adults will also be in the range of 5 mg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary immunization schedule over 1 month (Boedeker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of an *B. fragilis* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *B. fragilis* infection, some are useful only for treating *B. fragilis* infection, and some are useful for both preventing and treating *B. fragilis* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *B. fragilis* infection by stimulating humoral

and/or cell-mediated immunity against *B. fragilis*. It should be understood that amelioration of any of the symptoms of *B. fragilis* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *B. fragilis*-caused disease, or an increase in the production of antibodies in the serum or mucous of patients.

5

ANTIBODIES REACTIVE WITH *B. FRAGILIS* POLYPEPTIDES

The invention also includes antibodies specifically reactive with the subject *B. fragilis* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *B. fragilis* polypeptide can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *B. fragilis* polypeptides of the invention, e.g. antigenic determinants of a polypeptide of the invention contained in the Sequence Listing, or a closely related human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least about 95% homologous). In yet a further preferred embodiment of the invention, the anti-*B. fragilis* antibodies do not substantially cross react (i.e., react specifically) with a protein which is for example, less than 80% percent homologous to a sequence of the invention contained in the Sequence Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein of the invention

contained in the Sequence Listing. In a most preferred embodiment, there is no cross-reactivity between bacterial and mammalian antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *B. fragilis* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab')₂ fragments can be generated by treating antibody with pepsin. The resulting F(ab')₂ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*B. fragilis* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *B. fragilis* polypeptides or *B. fragilis* polypeptide variants, and antibody fragments such as Fab' and F(ab')₂, can be used to block the action of *B. fragilis* polypeptide and allow the study of the role of a particular *B. fragilis* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *B. fragilis* and by microinjection of anti-*B. fragilis* polypeptide antibodies of the present invention.

Antibodies which specifically bind *B. fragilis* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *B. fragilis* antigens. Anti-*B. fragilis* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *B. fragilis* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the ability to monitor *B. fragilis* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of an *B. fragilis* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*B. fragilis* antibodies can include, for example, immunoassays designed to aid in early diagnosis of *B. fragilis* infections. The

present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *B. fragilis* antigens.

Another application of anti-*B. fragilis* polypeptide antibodies of the invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λ gt11, λ gt18-23, λ ZAP, and λ ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λ gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *B. fragilis* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*B. fragilis* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *B. fragilis* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

15

KITS CONTAINING NUCLEIC ACIDS, POLYPEPTIDES OR ANTIBODIES OF THE INVENTION

The nucleic acid, polypeptides and antibodies of the invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided

25

herein, individuals skilled in art can readily assemble kits to serve their particular purpose. Kits further can include instructions for use.

BIO CHIP TECHNOLOGY

5 The nucleic acid sequence of the present invention may be used to detect *B. fragilis* or other species of *Bacteroides* acid sequence using bio chip technology. Bio chips containing arrays of nucleic acid sequence can also be used to measure expression of genes of *B. fragilis* or other species of *Bacteroides*. For example, to diagnose a patient with a *B. fragilis* or other *Bacteroides* infection, a sample from a human or animal can be
10 used as a probe on a bio chip containing an array of nucleic acid sequence from the present invention. In addition, a sample from a disease state can be compared to a sample from a non-disease state which would help identify a gene that is up-regulated or expressed in the disease state. This would provide valuable insight as to the mechanism by which the disease manifests. Changes in gene expression can also be used to identify
15 critical pathways involved in drug transport or metabolism, and may enable the identification of novel targets involved in virulence or host cell interactions involved in maintenance of an infection. Procedures using such techniques have been described by Brown *et al.*, 1995, *Science* 270: 467-470.

 Bio chips can also be used to monitor the genetic changes of potential therapeutic
20 compounds including, deletions, insertions or mismatches. Once the therapeutic is added to the patient, changes to the genetic sequence can be evaluated for its efficacy. In addition, the nucleic acid sequence of the present invention can be used to determine essential genes in cell cycling. As described in Iyer *et al.*, 1999 (*Science*, 283:83-87) genes essential in the cell cycle can be identified using bio chips. Furthermore, the
25 present invention provides nucleic acid sequence which can be used with bio chip technology to understand regulatory networks in bacteria, measure the response to environmental signals or drugs as in drug screening, and study virulence induction.

(Mons *et al.*, 1998, *Nature Biotechnology*, 16: 45-48. Patents teaching this technology include U.S. Patents 5445934, 5744305, and 5800992.

DRUG SCREENING ASSAYS USING *B. FRAGILIS* POLYPEPTIDES

5 By making available purified and recombinant *B. fragilis* polypeptides, the present invention provides assays which can be used to screen for drugs which are either agonists or antagonists of the normal cellular function, in this case, of the subject *B. fragilis* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *B. fragilis* infections in
10 humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the person skilled in the art.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free
15 systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being
20 focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *B. fragilis* polypeptide.

25 Screening assays can be constructed *in vitro* with a purified *B. fragilis* polypeptide or fragment thereof, such as an *B. fragilis* polypeptide having enzymatic activity, such that the activity of the polypeptide produces a detectable reaction product. The efficacy of the compound can be assessed by generating dose response curves from

data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example, because detection may be easily automated. A variety of synthetic or naturally occurring compounds can be tested in the assay to identify those which inhibit or potentiate the activity of the *B. fragilis* polypeptide. Some of these active compounds may directly, or with chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *B. fragilis* cells.

10

OVEREXPRESSION ASSAYS

Overexpression assays are based on the premise that overproduction of a protein would lead to a higher level of resistance to compounds that selectively interfere with the function of that protein. Overexpression assays may be used to identify compounds that interfere with the function of virtually any type of protein, including without limitation enzymes, receptors, DNA- or RNA-binding proteins, or any proteins that are directly or indirectly involved in regulating cell growth.

Typically, two bacterial strains are constructed. One contains a single copy of the gene of interest, and a second contains several copies of the same gene. Identification of useful inhibitory compounds of this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of the two strains. The method involves constructing a nucleic acid vector that directs high level expression of a particular target nucleic acid. The vectors are then transformed into host cells in single or multiple copies to produce strains that express low to moderate and high levels of protein encoding by the target sequence (strain A and B, respectively). Nucleic acid comprising sequences encoding the target gene can, of course, be directly integrated into the host cell.

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on the growth of the two strains. Agents which interfere with an unrelated target equally inhibit the growth of both strains. Agents which interfere with the function of the target at high concentration should inhibit the growth of both strains. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit the growth of strain A at a concentration of the compound that allows strain B to grow.

Alternatively, a bacterial strain is constructed that contains the gene of interest under the control of an inducible promoter. Identification of useful inhibitory agents using this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of this strain under both inducing and non-inducing conditions. The method involves constructing a nucleic acid vector that directs high-level expression of a particular target nucleic acid. The vector is then transformed into host cells that are grown under both non-inducing and inducing conditions (conditions A and B, respectively).

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on growth under these two conditions. Agents that interfere with the function of the target should inhibit growth under both conditions. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit growth under condition A at a concentration that allows the strain to grow under condition B.

LIGAND-BINDING ASSAYS

Many of the targets according to the invention have functions that have not yet been identified. Ligand-binding assays are useful to identify inhibitor compounds that interfere with the function of a particular target, even when that function is unknown.

These assays are designed to detect binding of test compounds to particular targets. The detection may involve direct measurement of binding. Alternatively, indirect indications of binding may involve stabilization of protein structure or disruption of a biological function. Non-limiting examples of useful ligand-binding assays are detailed below.

5 A useful method for the detection and isolation of binding proteins is the Biomolecular Interaction Assay (BIAcore) system developed by Pharmacia Biosensor and described in the manufacturer's protocol (LKB Pharmacia, Sweden). The BIAcore system uses an affinity purified anti-GST antibody to immobilize GST-fusion proteins onto a sensor chip. The sensor utilizes surface plasmon resonance which is an optical
10 phenomenon that detects changes in refractive indices. In accordance with the practice of the invention, a protein of interest is coated onto a chip and test compounds are passed over the chip. Binding is detected by a change in the refractive index (surface plasmon resonance).

 A different type of ligand-binding assay involves scintillation proximity assays
15 (SPA, described in U.S. Patent No. 4,568,649).

 Another type of ligand binding assay, also undergoing development, is based on the fact that proteins containing mitochondrial targeting signals are imported into isolated mitochondria *in vitro* (Hurt *et al.*, 1985, *Embo J.* 4:2061-2068; Eilers and Schatz, *Nature*, 1986, 322:228-231). In a mitochondrial import assay, expression vectors are constructed
20 in which nucleic acids encoding particular target proteins are inserted downstream of sequences encoding mitochondrial import signals. The chimeric proteins are synthesized and tested for their ability to be imported into isolated mitochondria in the absence and presence of test compounds. A test compound that binds to the target protein should inhibit its uptake into isolated mitochondria *in vitro*.

25 Another ligand-binding assay is the yeast two-hybrid system (Fields and Song, 1989, *Nature* 340:245-246). The yeast two-hybrid system takes advantage of the properties of the GAL4 protein of the yeast *Saccharomyces cerevisiae*. The GAL4 protein is a transcriptional activator required for the expression of genes encoding

enzymes of galactose utilization. This protein consists of two separable and functionally essential domains: an N-terminal domain which binds to specific DNA sequences (UAS_G); and a C-terminal domain containing acidic regions, which is necessary to activate transcription. The native GAL4 protein, containing both domains, is a potent

5 activator of transcription when yeast are grown on galactose media. The N-terminal domain binds to DNA in a sequence-specific manner but is unable to activate transcription. The C-terminal domain contains the activating regions but cannot activate transcription because it fails to be localized to UAS_G. In the two-hybrid system, a system of two hybrid proteins containing parts of GAL4: (1) a GAL4 DNA-binding domain

10 fused to a protein 'X' and (2) a GAL4 activation region fused to a protein 'Y'. If X and Y can form a protein-protein complex and reconstitute proximity of the GAL4 domains, transcription of a gene regulated by UAS_G occurs. Creation of two hybrid proteins, each containing one of the interacting proteins X and Y, allows the activation region of UAS_G to be brought to its normal site of action.

15 The binding assay described in Fodor *et al.*, 1991, *Science* 251:767-773, which involves testing the binding affinity of test compounds for a plurality of defined polymers synthesized on a solid substrate, may also be useful.

Compounds which bind to the polypeptides of the invention are potentially useful as antibacterial agents for use in therapeutic compositions.

20 Pharmaceutical formulations suitable for antibacterial therapy comprise the antibacterial agent in conjunction with one or more biologically acceptable carriers. Suitable biologically acceptable carriers include, but are not limited to, phosphate-buffered saline, saline, deionized water, or the like. Preferred biologically acceptable carriers are physiologically or pharmaceutically acceptable carriers.

25 The antibacterial compositions include an antibacterial effective amount of active agent. Antibacterial effective amounts are those quantities of the antibacterial agents of the present invention that afford prophylactic protection against bacterial infections or which result in amelioration or cure of an existing bacterial infection. This antibacterial

effective amount will depend upon the agent, the location and nature of the infection, and the particular host. The amount can be determined by experimentation known in the art, such as by establishing a matrix of dosages and frequencies and comparing a group of experimental units or subjects to each point in the matrix.

5 The antibacterial active agents or compositions can be formed into dosage unit forms, such as for example, creams, ointments, lotions, powders, liquids, tablets, capsules, suppositories, sprays, aerosols or the like. If the antibacterial composition is formulated into a dosage unit form, the dosage unit form may contain an antibacterial effective amount of active agent. Alternatively, the dosage unit form may include less
10 than such an amount if multiple dosage unit forms or multiple dosages are to be used to administer a total dosage of the active agent. Dosage unit forms can include, in addition, one or more excipient(s), diluent(s), disintegrant(s), lubricant(s), plasticizer(s), colorant(s), dosage vehicle(s), absorption enhancer(s), stabilizer(s), bactericide(s), or the like.

15 For general information concerning formulations, see, e.g., Gilman et al. (eds.), 1990, *Goodman and Gilman's: The Pharmacological Basis of Therapeutics*, 8th ed., Pergamon Press; and *Remington's Pharmaceutical Sciences*, 17th ed., 1990, Mack Publishing Co., Easton, PA; Avis et al. (eds.), 1993, *Pharmaceutical Dosage Forms: Parenteral Medications*, Dekker, New York; Lieberman et al (eds.), 1990,
20 *Pharmaceutical Dosage Forms: Disperse Systems*, Dekker, New York.

 The antibacterial agents and compositions of the present invention are useful for preventing or treating *B. fragilis* infections. Infection prevention methods incorporate a prophylactically effective amount of an antibacterial agent or composition. A prophylactically effective amount is an amount effective to prevent *B. fragilis* infection
25 and will depend upon the specific bacterial strain, the agent, and the host. These amounts can be determined experimentally by methods known in the art and as described above.

B. fragilis infection treatment methods incorporate a therapeutically effective amount of an antibacterial agent or composition. A therapeutically effective amount is an amount sufficient to ameliorate or eliminate the infection. The prophylactically and/or therapeutically effective amounts can be administered in one administration or over
 5 repeated administrations. Therapeutic administration can be followed by prophylactic administration, once the initial bacterial infection has been resolved.

The antibacterial agents and compositions can be administered topically or systemically. Topical application is typically achieved by administration of creams, ointments, lotions, or sprays as described above. Systemic administration includes both
 10 oral and parental routes. Parental routes include, without limitation, subcutaneous, intramuscular, intraperitoneal, intravenous, transdermal, inhalation and intranasal administration.

EXEMPLIFICATION

15

CLONING AND SEQUENCING *B. FRAGILIS* GENOMIC SEQUENCE

This invention provides nucleotide sequences of the genome of *B. fragilis* which thus comprises a DNA sequence library of *B. fragilis* genomic DNA. The detailed description that follows provides nucleotide sequences of *B. fragilis*, and also describes
 20 how the sequences were obtained and how ORFs (Open Reading Frames) and protein-coding sequences can be identified. Also described are methods of using the disclosed *B. fragilis* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *B. fragilis* as well as other
 25 species of *Bacteroides*.

Chromosomal DNA from strain 14062 of *B. fragilis* was isolated after Zymolyase digestion, sodium dodecyl sulfate lysis, potassium acetate precipitation, phenol:chloroform extraction and ethanol precipitation (Soll, D.R., T. Srikantha and S.R.

Lockhart: Characterizing Developmentally Regulated Genes in *B. fragilis*. In Microbial Genome Methods. K.W. Adolph, editor. CRC Press. New York. p 17-37.). Genomic *B. fragilis* DNA was hydrodynamically sheared in an HPLC and then separated on a standard 1% agarose gel. Fractions corresponding to 2500-3000 bp in length were
 5 excised from the gel and purified by the GeneClean procedure (Bio101, Inc.).

The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique *Bst*XI-linker adapters (5'-GTCTTCACCACGGGG-3' and 5'-GTGGTGAAGAC-3' in 100-1000 fold molar excess). These linkers are complimentary to the *Bst*XI-cut pGTC vector, while the
 10 overhang is not self-complimentary. Therefore, the linkers will not concatamerize nor will the cut-vector religate itself easily. The linker-adapted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adapted inserts were then ligated to *Bst*XI-cut vector to construct a "shotgun" subclone libraries.

15 Only major modifications to the protocols are highlighted. Briefly, the library was then transformed into DH5 α competent cells (Gibco/BRL, DH5 α transformation protocol). It was assessed by plating onto antibiotic plates containing ampicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Transformants were then used for plating of clones and picking for sequencing. The cultures were grown overnight at
 20 37°C. DNA was purified using a silica bead DNA preparation (Engelstein, 1996) method. In this manner, 25 μ g of DNA was obtained per clone.

These purified DNA samples were then sequenced using primarily ABI dye-terminator chemistry. All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. The ABI dye terminator sequence reads were run
 25 on ABI377 machines and the data was transferred to UNIX machines following lane tracking of the gels. Base calls and quality scores were determined using the program PHRED (Ewing et al., 1998, Genome Res. 8: 175-185; Ewing and Green, 1998, Genome Res. 8: 685-734). Reads were assembled using PHRAP (P. Green, Abstracts of DOE

Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157) with default program parameters and quality scores. The initial assembly was done at 7.8 fold coverage and yielded 223 contigs.

Finishing can follow the initial assembly. Missing mates (sequences from clones that only gave reads from one end of the *Bacteroides* DNA inserted in the plasmid) can be identified and sequenced with ABI technology to allow the identification of additional overlapping contigs.

End-sequencing of randomly picked genomic lambda was also performed. Sequencing on a both sides was done for all lambda sequences. The lambda library backbone helped to verify the integrity of the assembly and allowed closure of some of the physical gaps. Primers for walking off the ends of contigs would be selected using pick_primer (a GTC program) near the ends of the clones to facilitate gap closure. These walks can be sequenced using the selected clones and primers. These data are then reassembled with PHRAP. Additional sequencing using PCR-generated templates and screened and/or unscreened lambda templates can be done in addition.

To identify *B. fragilis* polypeptides the complete genomic sequence of *B. fragilis* were analyzed essentially as follows: First, all possible stop-to- stop open reading frames (ORFs) greater than 180 nucleotides in all six reading frames were translated into amino acid sequences. Second, the identified ORFs were analyzed for homology to known (archeabacter, prokaryotic and eukaryotic) protein sequences. Third, the coding potential of non-homologous sequences were evaluated with the program GENEMARK™ (Borodovsky and McIninch, 1993, Comp. Chem. 17:123).

IDENTIFICATION, CLONING AND EXPRESSION OF *B. FRAGILIS* NUCLEIC ACIDS

Expression and purification of the *B. fragilis* polypeptides of the invention can be performed essentially as outlined below.

To facilitate the cloning, expression and purification of membrane and secreted proteins from *B. fragilis*, a gene expression system, such as the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, is selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, is fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end is selected for fusion in order to avoid alteration of any 5' terminal signal sequence.

PCR AMPLIFICATION AND CLONING OF NUCLEIC ACIDS CONTAINING ORF'S ENCODING ENZYMES

Nucleic acids chosen (for example, from the nucleic acids set forth in SEQ ID NO: 1 - SEQ ID NO: 5222 for cloning from the 14062 strain of *B. fragilis*) are prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers specific for the 5' and 3' ends of open reading frames (ORFs) are designed and purchased from GibcoBRL Life Technologies (Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) are designed to include an NcoI cloning site at the extreme 5' terminus. These primers are designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding sequence for the remainder of the native *B. fragilis* DNA sequence. All reverse primers (specific for the 3' end of any *B. fragilis* ORF) include a EcoRI site at the extreme 5' terminus to permit cloning of each *B. fragilis* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids including six histidine residues (at the extreme C-terminus), which comprise the His-Tag.

Genomic DNA prepared from the 14062 strain of *B. fragilis* is used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *B. fragilis* ORF, genomic DNA (50 nanograms) is introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide

primers (forward and reverse primers) complementary to and flanking a defined *B. fragilis* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters.

5 Upon completion of thermal cycling reactions, each sample of amplified DNA is washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples are subjected to digestion with the restriction endonucleases, e.g., NcoI and EcoRI (New England BioLabs, Beverly, MA, USA)(Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et
10 al., eds., 1994). DNA samples are then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA is visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel is purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

15 CLONING OF *B. FRAGILIS* NUCLEIC ACIDS INTO AN EXPRESSION VECTOR

The pET-28b vector is prepared for cloning by digestion with restriction endonucleases, e.g., NcoI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). The pET-28a vector, which encodes
20 a His-Tag that can be fused to the 5' end of an inserted gene, is prepared by digestion with appropriate restriction endonucleases.

Following digestion, DNA inserts are cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously digested pET-28b expression vector. Products of the ligation reaction are then used to
25 transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.

TRANSFORMATION OF COMPETENT BACTERIA WITH RECOMBINANT PLASMIDS

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), are transformed with recombinant pET expression plasmids carrying the cloned *B. fragilis* sequences according to standard methods (Current Protocols in Molecular, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction is mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples are incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples are then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 are then picked and analyzed to evaluate cloned inserts as described below.

15 IDENTIFICATION OF RECOMBINANT EXPRESSION VECTORS WITH *B. FRAGILIS* NUCLEIC ACIDS

Individual BL21 clones transformed with recombinant pET-28b *B. fragilis* ORFs are analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *B. fragilis* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verifies the integration of the *B. fragilis* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

25 ISOLATION AND PREPARATION OF NUCLEIC ACIDS FROM TRANSFORMANTS

Individual clones of recombinant pET-28b vectors carrying properly cloned *B. fragilis* ORFs are picked and incubated in 5 mls of LB broth plus 25 microgram/ml

kanamycin sulfate overnight. The following day plasmid DNA is isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

EXPRESSION OF RECOMBINANT *B. FRAGILIS* SEQUENCES IN *E. COLI*

5 The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the *lacI* gene, the *lacUV5* promoter and the gene for T7 RNA polymerase. T7
10 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying its gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) *Meth. Enzymol.* 185, 60-89).

To express recombinant *B. fragilis* sequences, 50 nanograms of plasmid DNA
15 isolated as described above is used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). The *lacZ* gene (beta-galactosidase) is expressed in the pET-System as described for the *B. fragilis* recombinant constructions. Transformed cells are cultured in SOC medium for 1 hour, and the culture is then plated on LB plates containing 25 micrograms/ml
20 kanamycin sulfate. The following day, bacterial colonies are pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nM of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *B. fragilis* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria are pelleted by
25 centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4 °C. Pellets are resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells are then centrifuged at 2000 x g for 20 min at 4 °C. Wet pellets are weighed and frozen at -80 °C until ready for protein purification.

A variety of methodologies known in the art can be utilized to purify the isolated proteins. (Current Protocols in Protein Science, John Wiley and Sons, Inc., J. E. Coligan et al., eds., 1995). For example, the frozen cells may be thawed, resuspended in buffer and ruptured by several passages through a small volume microfluidizer (Model M-110S, 5 Microfluidics International Corporation, Newton, MA). The resultant homogenate may be centrifuged to yield a clear supernatant (crude extract) and following filtration the crude extract may be fractionated over columns. Fractions may be monitored by absorbance at OD₂₈₀ nm. and peak fractions may analyzed by SDS-PAGE

The concentrations of purified protein preparations may be quantified 10 spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations are also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

15 SDS-polyacrylamide gels of various concentrations may be purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers may include rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor 20 (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods 25 described herein. The specific embodiments described herein are offered by way of example only, and the invention is to limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled.

TABLE 2

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32245287_f2_2.....	1	5223	139	420	196	1.5e-15
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein jhp1211					pir:C71832	C71832
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10020167_c1_80	2	5224	611	1836	706	1.4e-69
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
glutaminase A					gp:AB029552	AB029552
<u>Description</u>						
Aspergillus oryzae gtaA gene for glutaminase A, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1064765_c1_89.....	3	5225	249	750	324	1.8e-28
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
alpha-1,6-mannanase					gp:AB024331	AB024331
<u>Description</u>						
Bacillus circulans aman6 gene for alpha-1,6-mannanase, completecds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10945326_f3_56.....	4	5226	481	1446		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12109430_c2_116	5	5227	788	2367	2343	4.6e-243
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
immunoreactive 89kD antigen PG87			gp:AF175722		AF175722	
<u>Description</u>						
Porphyromonas gingivalis strain W50 immunoreactive 89kD antigenPG87 gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14647327_c1_92	6	5228	837	2514	706	2.7e-76
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
glutaminase A			gp:AB029552		AB029552	
<u>Description</u>						
Aspergillus oryzae gtaA gene for glutaminase A, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19125_c1_98.....	7	5229	406	1221	760	2.6e-75
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative aldose 1-epimerase			gp:SC4A7		AL133423	
<u>Description</u>						
Streptomyces coelicolor cosmid 4A7.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19536316_c2_107.....	8	5230	1085	3258	755	1.9e-78
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22455343_c1_88	9	5231	65	198	55	0.031

Protein name

Locus Name

Acc#

gp:AP000969

AP000969

Description

Oryza sativa genomic DNA, chromosome 1, clone:P0011D01.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22457686_c2_112	10	5232	724	2175		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23492786_c3_124.....	11	5233	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23866437_c3_134.....	12	5234	493	1482	822	6.9e-82

Protein name

Locus Name

Acc#

hypothetical protein SCU4.42c

pir:T37125

T37125

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24645308_f1_20.....	13	5235	1207	3624	741	5.9e-71

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76045

S76045

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24647811_c2_108	14	5236	619	1860	126	6.0e-11
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:U96771		U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26307018_c2_119	15	5237	427	1284	351	5.6e-32
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YXAH_BACSU		P42107	
<u>Description</u>						
HYPOTHETICAL 46.2 KD PROTEIN IN ASNH-GNTR INTERGENIC REGION						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29461537_c3_138.....	16	5238	158	477		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3027177_c1_87.....	17	5239	336	1011	370	5.4e-34
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
endo-arabinase			gp:D85132		D85132	
<u>Description</u>						
Bacillus subtilis DNA for endo-arabinase, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4142127_c2_109	18	5240	147	444		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4492168_c3_125	19	5241	161	486	222	2.3e-17
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Protein name

Locus Name

Acc#

alpha-1,6-mannanase

gp:AB024331

AB024331

Description

Bacillus circulans aman6 gene for alpha-1,6-mannanase, completecds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4726687_c1_86	20	5242	240	723		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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818876_c2_110	21	5243	142	429		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12203438_c1_6	22	5244	420	1263	1627	3.4e-167
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:JQ1020		JQ1020	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26365816_f3_4	23	5245	857	2574		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32631533_f1_1	24	5246	295	885	435	2.3e-48
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
glucan 1,4-beta-glucosidase, :exo-1,4-beta-glucosidase			pir:JC4825		JC4825	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22275187_f1_1	25	5247	170	513	482	7.4e-46
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
glutathione peroxidase			gp:LLAJ109		AJ000109	
<u>Description</u>						
Lactococcus lactis carB and gpo genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24432962_f2_1	26	5248	91	273		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
311767067_f1_1	27	5249	294	885		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14257180_f2_19	28	5250	493	1482	250	6.5e-36

Protein name

Locus Name

Acc#

sp:ARSF_HUMAN

P54793

Description

ARYLSULFATASE F PRECURSOR, (ASF)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24025282_c2_75	29	5251	550	1653	1045	1.6e-105

Protein name

Locus Name

Acc#

sp:HEXA_PORGI

P49008

Description

(BETA-NAHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24486016_f2_21	30	5252	980	2943	165	1.4e-09
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
response regulator			gp:SPAJ6398		AJ006398	
<u>Description</u>						
Streptococcus pneumoniae rr09 and hk09 genes; two component system09.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25584525_f1_10	31	5253	786	2361	212	2.8e-14
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative secreted protein			gp:SCF41		AL117387	
<u>Description</u>						
Streptomyces coelicolor cosmid F41.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26209530_c3_98.....	32	5254	535	1608	280	5.0e-32
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
phosphonate monoester hydrolase			gp:BCU44852		U44852	
<u>Description</u>						
Burkholderia caryophylli PG2982 phosphonate monoester hydrolase(pehA) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
267517_f3_30.....	33	5255	60	183		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2932812_c2_68	34	5256	509	1530	258	1.4e-34

Protein name

Locus Name

Acc#

sp:ARSE_HUMAN

P51690

Description

ARYLSULFATASE E PRECURSOR, (ASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3020203_c2_67	35	5257	423	1272	666	2.3e-65

Protein name

Locus Name

Acc#

sp:HEXA_PORGI

P49008

Description

(BETA-NAHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3949012_c2_69	36	5258	487	1464	726	1.0e-71

Protein name

Locus Name

Acc#

sp:MODF_ECOLI

P31060

Description

PROTEIN PHRA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4726588_c3_86	37	5259	370	1113	1233	1.9e-125

Protein name

Locus Name

Acc#

hypothetical protein b2097

pir:H64976

H64976

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5273452_c1_61	38	5260	248	747	783	9.4e-78

Protein name

Locus Name

Acc#

sp:PMG1_ECOLI

P31217

Description

(PGAM 1) (BPG-DEPENDENT PGAM 1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10569587_c1_59	39	5261	768	2307	924	1.1e-92

Protein name

Locus Name

Acc#

melibiase

gp:TEMELA

Y08557

Description

T.ethanolicus melA and lacA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1369077_f3_49	40	5262	405	1218		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15631576_c1_74	41	5263	400	1203	111	0.0016

Protein name

Locus Name

Acc#

cytochrome-c oxidase, chain III

pir:S36954

S36954

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16532750_c2_104	42	5264	174	525	140	3.5e-08

Protein name	Locus Name	Acc#
F14N23.29	gp:AC005489	AC005489

Description

Genomic sequence for Arabidopsis thaliana BAC F14N23 fromChromosome 1, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16828427_f1_5	43	5265	422	1269	593	1.3e-57

Protein name	Locus Name	Acc#
N utilization substance protein A	pir:H72213	H72213

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19535126_f3_53.....	44	5266	284	855	820	1.1e-81

Protein name	Locus Name	Acc#
	sp:ABCX_CYAPA	P48255

Description

PROBABLE ATP-DEPENDENT TRANSPORTER YCF16

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20214450_f1_7.....	45	5267	64	195		

Protein name	Locus Name	Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2054635_f2_34	46	5268	115	348	353	3.4e-32

Protein name

Locus Name

Acc#

hypothetical protein b0866

pir:B64825

B64825

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20724002_c1_63	47	5269	553	1662	742	2.1e-73

Protein name

Locus Name

Acc#

probable secreted alpha-galactosidase

pir:T36472

T36472

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22519677_f1_3	48	5270	449	1350	1532	4.0e-157

Protein name

Locus Name

Acc#

L-fucose permease

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22917183_c1_62	49	5271	573	1722	297	9.3e-23

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encodinga major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23679512_c1_61	50	5272	555	1668	432	7.7e-42
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24490677_c3_119	51	5273	136	411	111	1.6e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable sigK protein			pir:F70830		F70830	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640927_c3_121	52	5274	616	1851	116	0.00016
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:U96771		U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24803457_c1_65	53	5275	112	339		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25963962_f2_28	54	5276	377	1134	123	0.00063

Protein name

Locus Name

Acc#

sp:TRHY_RABIT

P37709

Description

TRICHOHYALIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26212805_f2_29	55	5277	156	471	119	2.2e-07

Protein name

Locus Name

Acc#

sp:YHBC_ECOLI

P03843

Description

HYPOTHETICAL 16.8 KD PROTEIN IN NUSA-METY INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26364056_f2_31	56	5278	521	1566	1803	7.7e-186

Protein name

Locus Name

Acc#

sp:Y074_SYNY3

Q55790

Description

HYPOTHETICAL 52.8 KD PROTEIN SLR0074

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29480306_f3_51	57	5279	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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30578126_f1_4	58	5280	446	1341		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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31663925_f3_50	59	5281	89	270	76	0.0077
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Protein name

Locus Name

Acc#

probable serine proteinase

pir:T36552

T36552

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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33242938_f2_33	60	5282	456	1371	433	1.1e-40
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Protein name

Locus Name

Acc#

sp:Y076_SYNY3

Q55792

Description

HYPOTHETICAL 50.0 KD PROTEIN SLR0076

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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33448342_f1_8	61	5283	253	762		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35442313_f1_1	62	5284	292	879	864	2.4e-86

Protein name

Locus Name

Acc#

sp:FUCO_ECOLI

P11549

Description

LACTALDEHYDE REDUCTASE, (PROPANEDIOL OXIDOREDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3942813_f3_47	63	5285	215	648	1026	1.7e-103

Protein name

Locus Name

Acc#

L-fuculose-1-phosphate aldolase

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4001515_c1_60	64	5286	388	1167	135	3.7e-06

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4196001_f2_26	65	5287	488	1467	1748	5.2e-180

Protein name

Locus Name

Acc#

L-fuculose kinase

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5197137_f1_6	66	5288	1016	3051	1669	1.2e-171
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
Initiation factor IF2-alpha	gp:ECAJ2540				AJ002540	
<u>Description</u>	Escherichia coli (strain EcoAU9307) infB gene encodingtranslational initiation factor IF2.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5366453_f1_9	67	5289	416	1251	1106	5.5e-112
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
nifS-like protein					gp:MLCB22	Z98741
<u>Description</u>						
Mycobacterium leprae cosmid B22.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6252033_f2_27.....	68	5290	67	204	259	8.1e-22
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
L-fucose permease	gp:AF137263				AF137263	
<u>Description</u>						
Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10742010_c1_61.....	69	5291	695	2088	633	7.3e-62
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:PFLD_ECOLI				P32674	
<u>Description</u>						
FORMATE ACETYLTRANSFERASE 2, (PYRUVATE FORMATE-LYASE 2)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13913887_c2_82	70	5292	694	2085	564	2.7e-74

Protein name

Locus Name

Acc#

hypothetical protein TM0280

pir:F72395

F72395

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15660937_c3_108	71	5293	260	783		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20734637_c2_80	72	5294	263	792	306	3.9e-45

Protein name

Locus Name

Acc#

probable pyruvate formate-lyase activating enzyme, pflC homolog

pir:A69431

A69431

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21516933_f1_15	73	5295	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22461007_f3_37	74	5296	235	708	241	2.5e-20

Protein name

Locus Name

Acc#

probable competence protein ComF

pir:F75402

F75402

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23437627_f1_1	75	5297	88	267		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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29350677_c2_79	76	5298	1368	4107	468	1.7e-40
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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bZIP histidine kinase	gp:PPUY18245	Y18245
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Description

Pseudomonas putida todX, todF, todC1, todC2, todB, todA, todD, todE, todG, todI, todH, todS, todT genes.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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30573761_f1_4	77	5299	69	210		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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36225337_f2_19	78	5300	382	1149		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36585962_f3_35	79	5301	418	1257	722	2.7e-71

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
alpha galactosidase precursor	gp:AF061331	AF061331

<u>Description</u>
Saccharopolyspora erythraea alpha galactosidase precursor (melA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3940877_c1_67	80	5302	96	291	163	4.7e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YCNE_BACSU	P94425

<u>Description</u>
HYPOTHETICAL 10.9 KD PROTEIN IN PHRC-GDH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4094627_f1_17	81	5303	1060	3183	879	6.3e-88

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4101507_c3_101	82	5304	382	1149	842	5.2e-84

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative aldose 1-epimerase	gp:SC4A7	AL133423

<u>Description</u>
Streptomyces coelicolor cosmid 4A7.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4103812_f2_21	83	5305	271	816	360	6.2e-33

Protein name

Locus Name

Acc#

sp:SUHB_ECOLI

Description

EXTRAGENIC SUPPRESSOR PROTEIN SUHB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4422768_f1_18	84	5306	95	288		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4534660_c1_62	85	5307	443	1332	620	5.5e-78

Protein name

Locus Name

Acc#

sp:XYLE_ECOLI

P09098

Description

D-XYLOSE-PROTON SYMPORTER (D-XYLOSE TRANSPORTER)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4799033_f2_30	86	5308	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10820130_c1_218	87	5309	68	207		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11723437_c3_354	88	5310	79	240		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1207152_c3_351	89	5311	162	489	217	8.9e-18
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
unknown					gp:AF125164	AF125164
<u>Description</u>						

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12754816_f2_114	90	5312	209	630		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14296885_c1_248	91	5313	200	603	260	2.5e-22

Protein name conserved hypothetical protein AF0781
Locus Name pir:E69347
Acc# E69347

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14626317_f1_52.....	92	5314	640	1923	736	1.0e-78

Protein name
Locus Name gp:ECU89166
Acc# U89166

Description

Eikenella corrodens lysine decarboxylase (ECORLD) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14648562_f2_116.....	93	5315	579	1740	889	5.5e-89

Protein name
Locus Name pir:H69980
Acc# H69980

single-strand DNA-specific exonuclease
homolog yrvE

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15735882_c1_208.....	94	5316	400	1203	696	1.5e-68

Protein name
Locus Name pir:S75649
Acc# S75649

renin-binding protein-related protein:protein
slr1975:protein slr1975

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16016075_c2_288	95	5317	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16616302_f3_197.....	96	5318	439	1320	1138	2.3e-115

Protein name

Locus Name

Acc#

coenzyme F390 synthetase (ftsA-3) homolog

pir:D69501

D69501

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16835312_f1_34.....	97	5319	279	840		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
192693_c2_289.....	98	5320	211	636	236	1.4e-19

Protein name

Locus Name

Acc#

sp:YHCG_ECOLI

P45423

Description

HYPOTHETICAL 43.3 KD PROTEIN IN GLTF-NANT INTERGENIC REGION (0375)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19535652_c3_316	99	5321	640	1923	940	2.2e-94

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative epimerase/dehydratase WbiI	gp:AF064070	AF064070

Description

Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetrphosphatase (apaH), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2031552_c2_298	100	5322	101	306	74	0.013

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:NU3M_RAT	P05506

Description

NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20516500_c2_304	101	5323	705	2118		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
211687_c2_299	102	5324	461	1386	309	2.0e-27

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
Cap8K	gp:SAU73374	U73374

Description

Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2117305_c3_317	103	5325	856	2571	464	2.7e-56
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
otnA protein			pir:S70958		S70958	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21485952_c1_244.....	104	5326	965	2898	821	1.0e-120
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YDIJ_ECOLI		P77748	
<u>Description</u>						

HYPOTHETICAL 113.2 KB PROTEIN IN LPP-AROD INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21500933_f1_41.....	105	5327	1084	3255		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22345000_f2_88.....	106	5328	88	267		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22551562_f1_48	107	5329	143	432		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23546952_f2_106.....	108	5330	291	876		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23567187_f2_102.....	109	5331	109	330		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23609457_f1_27.....	110	5332	64	195		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23633592_c1_237.....	111	5333	64	195		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24103388_f1_71	112	5334	531	1596	831	7.7e-83
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
indolepyruvate oxidoreductase, alpha subunit	pir:G69114				G69114	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24303127_f1_33	113	5335	142	429		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24318802_f3_187	114	5336	410	1233	490	1.0e-46
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:XYLR_ANATH				Q44406	
<u>Description</u>						

XYLOSE REPRESSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24402177_f2_103	115	5337	94	285		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415908_f1_72	116	5338	195	588	310	1.2e-27

Protein name Locus Name Acc#
indolepyruvate ferredoxin oxidoreductase, subunit beta (iorB) homolog pir:E69503 E69503

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415930_c1_239.....	117	5339	322	969	937	4.5e-94

Protein name Locus Name Acc#
WbpB gp:PAU50396 U50396

Description

Pseudomonas aeruginosa Wzz (Rol) (wzz (rol)) gene, partial cds, WbpA (wbpB), WbpB (wbpB), WbpC (wbpC), WbpD (wbpD), WbpE (wbpE), Wzy (rfc) (wzy (rfc)), Wzx (wzx), HisH (hisH), HisF (hisF), WbpG (wbpG), WbpH (wbpH), WbpI (wbpI), WbpJ (wbpJ), WbpK (wbpK), WbpL (wbpL), WbpM (wbpM) and WbpN (wbpN) genes, complete cds, and UvrB (uvrB) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24426337_c1_216.....	118	5340	89	270		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24640875_c1_245.....	119	5341	376	1131	1914	1.3e-197

Protein name Locus Name Acc#
putative aminotransferase gp:AF125164 AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24651562_f1_68	120	5342	522	1569	318	3.1e-25

Protein name Locus Name Acc#
 surface antigen BspA pir:T31094 T31094

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24806502_c1_249.....	121	5343	325	978	581	2.4e-56

Protein name Locus Name Acc#
 sp:FMT_BACSU

Description

METHIONYL-TRNA FORMYLTRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25421942_c1_207.....	122	5344	181	546	152	6.9e-11

Protein name Locus Name Acc#
 unknown gp:AF048749 AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25429812_f3_171.....	123	5345	341	1026	111	0.0022

Protein name Locus Name Acc#
 sp:Y973_METJA Q58383

Description

HYPOTHETICAL PROTEIN MJ0973

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25583577_c3_356	124	5346	393	1182	172	3.4e-10
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
Cap5I	gp:SAU81973				U81973	
<u>Description</u>						
Staphylococcus aureus capsule gene cluster Cap5A through Cap5Pgenes, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25667592_c3_363	125	5347	606	1821	537	4.0e-55
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
chloride channel, probable, homolog	pir:F69426				F69426	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25676387_c3_352.....	126	5348	83	252	118	2.8e-07
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
tachylectin-3	gp:AB017484				AB017484	
<u>Description</u>						
Tachypleus tridentatus mRNA for tachylectin-3, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25976510_c2_263.....	127	5349	311	936	271	1.7e-23
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	gp:ECNPL				X03345	
<u>Description</u>						
E. coli npl gene for N-acetylneuraminate lyase subunit (EC4.1.3.3).						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26604635_c3_355	128	5350	370	1113	678	1.3e-66
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:AF144879		AF144879	
<u>Description</u>						
Leptospira interrogans rfb locus, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29305313_c1_242	129	5351	490	1473	122	0.00028
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative polysaccharide polymerase			gp:SPU09239		U09239	
<u>Description</u>						
Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cps19fABCDEFGHIJKLMNO) genes, complete cds, and aliA gene, partial cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29317660_c1_204	130	5352	125	378		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29509630_c1_217	131	5353	70	213		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30355312_c1_246	132	5354	165	498	102	1.4e-05

Protein name Locus Name Acc#
DNA-binding protein HB pir:C75600 C75600

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3.1381_c1_209.....	133	5355	416	1251	289	6.5e-24

Protein name Locus Name Acc#
sp:YYBO_BACSU P37489

Description

HYPOTHETICAL 48.2 KD PROTEIN IN COTF-TETB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3.1414025_c2_290.....	134	5356	227	684	505	2.7e-48

Protein name Locus Name Acc#
sp:3MG1_ECOLI P05100

Description

I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3.1882036_c2_271.....	135	5357	73	222		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32064137_c2_294	136	5358	209	630	120	2.3e-07

Protein name

Locus Name

Acc#

unknown

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32323912_f1_17	137	5359	411	1236		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32429512_f2_113.....	138	5360	771	2316	163	1.1e-18

Protein name

Locus Name

Acc#

DNA repair protein RAD25 homolog

pir:F69294

F69294

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32617177_f2_95.....	139	5361	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
337_c3_353	140	5362	198	597	532	3.7e-51

Protein name Locus Name Acc#
 acetyl transferase homolog pir:S70673 S70673

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34011402_f1_20.....	141	5363	74	225		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34066312_c1_238.....	142	5364	177	534		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34116277_f3_191.....	143	5365	60	183	115	5.7e-07

Protein name Locus Name Acc#

hypothetical protein 3 pir:S28487 S28487

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34167567_c2_297	144	5366	446	1341	1226	1.1e-124

Protein name

Locus Name

Acc#

ORF1P

gp:AB025970

AB025970

Description

Plesiomonas shigelloides gene for ORF1P, ORF2P, ORF3P, ORF4P, ORF5P, ORF6P, ORF7P, ORF8P, ORF9P, ORF10P, ORF11P.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36361063_c2_300	145	5367	370	1113	610	2.0e-59

Protein name

Locus Name

Acc#

WbpH

gp:PAU50396

U50396

Description

Pseudomonas aeruginosa Wzz (Rol) (wzz (rol)) gene, partial cds, WbpA (wbpB), WbpB (wbpB), WbpC (wbpC), WbpD (wbpD), WbpE (wbpE), Wzy (rfc) (wzy (rfc)), Wzx (wzx), HisH (hisH), HisF (hisF), WbpG (wbpG), WbpH (wbpH), WbpI (wbpI), WbpJ (wbpJ), WbpK (wbpK), WbpL (wbpL), WbpM (wbpM) and WbpN (wbpN) genes, complete cds, and UvrB (uvrB) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3911015_c3_358.....	146	5368	180	543	153	5.4e-11

Protein name

Locus Name

Acc#

serine O-acetyltransferase,

pir:E53402

E53402

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3948587_c2_296.....	147	5369	399	1200	1198	9.9e-122

Protein name

Locus Name

Acc#

gp:D64132

D64132

Description

Porphyromonas gingivalis PorR and PorS genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4022178_c2_262	148	5370	373	1122	86	7.1e-07

Protein name

Locus Name

Acc#

sp:YCCC_ECOLI

Description

HYPOTHETICAL 81.2 KD PROTEIN IN APPA-CSPH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4033125_c1_250	149	5371	226	681	546	1.2e-52

Protein name

Locus Name

Acc#

ribulose-5-phosphate 3-epimerase homolog ylor

pir:B69879

B69879

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4065677_f2_133.....	150	5372	348	1047	283	9.0e-25

Protein name

Locus Name

Acc#

conserved hypothetical protein BB0709

pir:D70188

D70188

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4096877_f1_69.....	151	5373	296	891	348	1.2e-31

Protein name

Locus Name

Acc#

sp:NUC_BORBU

O51372

Description

PUTATIVE ENDONUCLEASE BB0411,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4103375_c1_243	152	5374	410	1233	843	4.1e-84
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative transferase			gp:BBR007747		AJ007747	
<u>Description</u>						
Bordetella bronchiseptica cosmid BbLPS1.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4457512_f3_184	153	5375	333	1002	221	2.6e-16
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein MTH83			pir:F69210		F69210	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4459660_c2_252.....	154	5376	269	810	109	9.0e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable NADH-plastoquinone oxidoreductase subunit			pir:C71018		C71018	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4728385_f3_173.....	155	5377	724	2175	208	6.3e-13
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable purine NTPase PAB0812			pir:F75103		F75103	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4786250_f2_83	156	5378	156	471	135	4.3e-09
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein MTH658			pir:E69187		E69187	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4789066_f2_104	157	5379	71	216		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5359842_c3_319	158	5380	174	525		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5877042_c1_251	159	5381	325	975	131	3.0e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:CME3_BACSU		P39695	
<u>Description</u>						

COME OPERON PROTEIN 3

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5894001_f1_46	160	5382	83	252	65	0.020

Protein name

Locus Name

Acc#

sp:UDG_STRPY

Q07172

Description

(UDP-GLCDH) (UDPGDH)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6056562_c3_359	161	5383	204	615	406	8.3e-38

Protein name

Locus Name

Acc#

putative transferase

gp:BBR007747

AJ007747

Description

Bordetella bronchiseptica cosmid BbLPS1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6288313_f2_105.....	162	5384	308	927	407	6.5e-38

Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781512_f2_123.....	163	5385	82	249		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
962777_f1_73	164	5386	190	573	457	3.3e-43

Protein name

Locus Name

Acc#

sp:XPT_BACSU

P42085

Description

XANTHINE PHOSPHORIBOSYLTRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9765913_c1_232	165	5387	67	204	75	0.013

Protein name

Locus Name

Acc#

sp:HBB_PANPO

P04244

Description

HEMOGLOBIN BETA CHAIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10671885_c2_125.....	166	5388	123	372		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10735927_c2_130.....	167	5389	335	1008	124	3.2e-07

Protein name

Locus Name

Acc#

actinorhodin polyketide dimerase-related
protein

pir:C72410

C72410

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10757837_c1_119	168	5390	415	1248	404	1.4e-37

Protein name

Locus Name

Acc#

sp:YRKO_BACSU

P54442

Description

HYPOTHETICAL 46.4 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11953533_f1_20	169	5391	75	228	69	0.0020

Protein name

Locus Name

Acc#

sp:HXD3_BRARE

O42370

Description

HOMEBOX PROTEIN HOX-D3 (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12541502_f2_51	170	5392	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12693752_f2_64	171	5393	208	627	451	1.4e-42

Protein name

Locus Name

Acc#

putative GTP-binding protein

gp:ATAC004786

AC004786

Description

Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14642187_f2_61	172	5394	175	528	511	6.2e-49

Protein name

Locus Name

Acc#

sp:Y318_HAEIN

P43984

Description

HYPOTHETICAL PROTEIN HI0318

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15125662_c3_164	173	5395	495	1488	367	1.6e-33

Protein name

Locus Name

Acc#

gp:D90837

Description

E.coli genomic DNA, Kohara clone #347(44.2-44.5 min.).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16907762_c3_168	174	5396	360	1083	973	6.9e-98

Protein name

Locus Name

Acc#

sp:YODE_PSEAE

Q01609

Description

HYPOTHETICAL 40.7 KD PROTEIN IN OPDE 3' REGION (ORF2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20579675_c1_104	175	5397	213	642	496	2.4e-47

Protein name

Locus Name

Acc#

recR protein

pir:H75547

H75547

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20587753_c3_165	176	5398	388	1167	882	3.0e-88

Protein name

Locus Name

Acc#

sp:PATB_BACSU

Q08432

Description

PUTATIVE AMINOTRANSFERASE B,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20601437_f2_65	177	5399	204	615		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21648312_f2_62	178	5400	109	330		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22853452_c3_156	179	5401	179	540	158	1.6e-11

Protein name

Locus Name

Acc#

sp:YP20_BACLI

P05332

Description

HYPOTHETICAL P20 PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22867327_c3_155	180	5402	149	450		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23492786_f3_67	181	5403	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23945302_c2_140	182	5404	230	693	163	4.7e-12

Protein name

Locus Name

Acc#

sp:RIBD_METJA

Q58085

Description

PUTATIVE RIBOFLAVIN BIOSYNTHESIS ENZYME

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24334637_c1_122	183	5405	406	1221	223	3.6e-16

Protein name

Locus Name

Acc#

cation efflux system (czcB-like)

pir:E70342

E70342

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24416552_c1_118	184	5406	123	372	224	1.6e-18

Protein name

Locus Name

Acc#

oxidoreductase, aldo/keto reductase family

pir:H72307

H72307

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26594087_c1_109	185	5407	379	1140	896	9.9e-90
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
oxidoreductase, aldo/keto reductase family			pir:H72307		H72307	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3237755_c2_132.....	186	5408	225	678	376	1.3e-34
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
plant-metabolite dehydrogenase homolog yvgN			pir:C70040		C70040	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33392187_c1_120.....	187	5409	342	1029	608	3.3e-59
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
oxidoreductase, aldo/keto reductase family			pir:H72307		H72307	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34198387_c2_134.....	188	5410	292	879		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35313816_c1_111.....	189	5411	287	864	761	2.0e-75
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
oxidoreductase, aldo/keto reductase family			pir:A72308		A72308	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3948575_c2_123	190	5412	227	684	584	1.1e-56

Protein name

Locus Name

Acc#

sp:YF08_METJA

Q58903

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ1508

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4064178_f1_25	191	5413	455	1368	197	8.2e-13

Protein name

Locus Name

Acc#

aspartate aminotransferase

gp:AF035157

AF035157

Description

Lactococcus lactis aspartate aminotransferase (aspC) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4335425_f3_98	192	5414	498	1497	370	5.4e-34

Protein name

Locus Name

Acc#

hypothetical protein

pir:S75887

S75887

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4410135_f2_56	193	5415	141	426		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4486261_c1_121	194	5416	164	495		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4589627_f3_93	195	5417	199	600	257	5.1e-22
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
yqge hypothetical protein			pir:H72114		H72114	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
47157165_c1_100	196	5418	75	228		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
632012_f1_22	197	5419	82	249		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
969687_f1_28	198	5420	140	423		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10631882_c2_238	199	5421	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11148453_f3_122.....	200	5422	127	384	126	3.9e-08

Protein name

Locus Name

Acc#

hypothetical protein yngA

pir:F69892

F69892

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12381962_f3_134.....	201	5423	1058	3177	2370	6.3e-246

Protein name

Locus Name

Acc#

hypothetical protein mexF

pir:T30830

T30830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1256327_c3_274.....	202	5424	149	450	96	1.6e-06

Protein name

Locus Name

Acc#

ct469 hypothetical protein

pir:D72060

D72060

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12690817_c2_225.....	203	5425	141	426		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12712827_f3_120	204	5426	353	1062	276	5.0e-24
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
conserved hypothetical protein			pir:F72386			F72386
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12922202_f3_116.....	205	5427	316	951	132	3.0e-06
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein aq_380			pir:A70334			A70334
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1370468_f3_118.....	206	5428	93	282		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13878425_f2_72.....	207	5429	134	405	368	8.9e-34
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:YYAH_BACSU			P37516
<u>Description</u>						
HYPOTHETICAL 14.4 KD PROTEIN IN TETB-EXOA INTERGENIC REGION (ORFF)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14508425_c1_192.....	208	5430	236	711	166	2.3e-12
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein MTH939			pir:G69225			G69225
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14646956_c2_261	209	5431	82	249	61	0.023
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
mannanase			gp:U96771		U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14705261_f1_15	210	5432	501	1506	115	0.00082
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown protein			gp:BACCOMGA			
<u>Description</u>						
Bacillus subtilis (clone pED4) comG-(1,2,3,4,5,6,and 7) proteins in comG operon, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14744010_f3_129.....	211	5433	265	798	275	6.3e-24
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein yjka			pir:E69851		E69851	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14876313_f2_84.....	212	5434	667	2004	1443	1.1e-147
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
DNA ligase			gp:BST011676		AJ011676	
<u>Description</u>						
Bacillus stearothermophilus lig gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15641902_c3_288	213	5435	202	609	345	2.4e-31
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein AF2201			pir:A69525		A69525	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16204662_f2_65.....	214	5436	604	1815	134	3.1e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein AF1867			pir:B69483		B69483	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16828382_f3_137.....	215	5437	305	918	801	1.2e-79
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:PYRD_AQUAE				066461	
<u>Description</u>						
(DHODEHASE)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c3_307.....	216	5438	431	1296	1724	1.8e-177
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:JQ1020		JQ1020	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
188752_f1_20.....	217	5439	761	2286	380	3.5e-34
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein AF1878			pir:E69484		E69484	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
188905_c1_179	218	5440	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19645166_f3_136.....	219	5441	345	1038	244	8.2e-20

Protein name

Locus Name

Acc#

sp:YQEN_BACSU

P54459

Description

HYPOTHETICAL 40.5 KD PROTEIN IN COMEC-RPST INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2051500_c3_266.....	220	5442	777	2334	178	2.5e-23

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_1386

pir:F70420

F70420

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20741703_f2_89.....	221	5443	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2151556_f1_27	222	5444	99	300		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21541425_c2_199	223	5445	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21679062_f1_18	224	5446	283	852	206	1.3e-16

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:E72209

E72209

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
235762_f1_22	225	5447	179	540		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23625693_f2_64	226	5448	265	798		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23633312_f1_7	227	5449	248	747	193	3.1e-15

Protein name

Locus Name

Acc#

gp:APU72238

U72238

Description

Anabaena PCC7120 ORFR1, ORFR2, ORFR3, ORFR4, and ORFR5 genes, complete sequences.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23635812_f1_9	228	5450	784	2355	148	2.0e-09

Protein name

Locus Name

Acc#

conserved hypothetical protein AF1017

pir:A69377

A69377

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23884561_f1_45.....	229	5451	131	396	136	4.1e-08

Protein name

Locus Name

Acc#

63 kDa protein

gp:MBU73653

U73653

Description

Mycobacterium bovis 63 kDa protein, 47 kDa protein and clpB gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24256502_f3_115.....	230	5452	383	1152		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24316061_f1_6	231	5453	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24334393_c1_151	232	5454	98	297		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24412502_c1_196	233	5455	94	285		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24485926_f1_16	234	5456	476	1431		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24494017_c1_169	235	5457	295	888	887	8.9e-89

Protein name

Locus Name

Acc#

hypothetical protein jhp0694

pir:F71901

F71901

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24500032_f3_121	236	5458	612	1839	1501	7.7e-154

Protein name

Locus Name

Acc#

sp:SYD_BACSU

032038

Description

(ASPRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642760_c3_311	237	5459	415	1245	1990	1.2e-205

Protein name

Locus Name

Acc#

L-fucose isomerase

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24726550_f2_61	238	5460	136	411		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24804712_f3_114	239	5461	164	495	88	0.013

Protein name

Locus Name

Acc#

ATP synthase F0, subunit b'

pir:A64662

A64662

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24897943_f1_12	240	5462	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2531692_f1_21	241	5463	105	318	217	8.9e-18

Protein name

Locus Name

Acc#

gp:AB024563

AB024563

Description

Bacillus halodurans gene for YFIL, YFIM, YFIN, YHDE, HMP and ARGE, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2617125_f1_40	242	5464	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26376540_c1_194	243	5465	255	768	106	0.0015

Protein name

Locus Name

Acc#

sensory transduction system regulatory protein slr1837:protein slr1837:protein slr1837

pir:S77341

S77341

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26578375_f3_100	244	5466	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2741543_f3_111	245	5467	608	1827	111	0.0053

Protein name

Locus Name

Acc#

sp:SECY_ANTSP

Q37143

Description

PREPROTEIN TRANSLOCASE SECY SUBUNIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2851577_f1_41	246	5468	297	894	296	3.8e-26

Protein name

Locus Name

Acc#

XylR

gp:BSU15985

U15985

Description

Bacillus stearothermophilus endo-beta-1,4-xylanase (xynA) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29344652_f1_37	247	5469	279	840	433	1.1e-40

Protein name

Locus Name

Acc#

sp:PYRZ_BACSU

P25983

Description

DIHYDROOROTATE DEHYDROGENASE ELECTRON TRANSFER SUBUNIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29537532_f3_117	248	5470	101	306	113	9.3e-07
Protein name			Locus Name		Acc#	
hypothetical protein Rv2816c			pir:C70691		C70691	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33205013_c1_157	249	5471	247	744	605	6.8e-59
Protein name			Locus Name		Acc#	
			sp:TRMD_BACSU		O31741	
Description						

METHYLTRANSFERASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34015677_f3_131	250	5472	279	840	218	7.0e-18
Protein name			Locus Name		Acc#	
hypothetical protein CT398			pir:A71519		A71519	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34068760_f1_28	251	5473	452	1359	599	2.9e-58
Protein name			Locus Name		Acc#	
conserved hypothetical protein yqfO			pir:A69954		A69954	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35345057_c2_240	252	5474	63	192		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35432303_c2_228	253	5475	396	1191	778	3.2e-77

Protein name

Locus Name

Acc#

hypothetical protein HP0049

pir:A64526

A64526

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35832062...f3...108.....	254	5476	815	2448	173	2.9e-09

Protein name

Locus Name

Acc#

sp:YBJZ_ECOLI

P75831

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36362551...c2...232.....	255	5477	396	1191	801	1.2e-79

Protein name

Locus Name

Acc#

sp:BIOF_BACSH

P22806

Description

LIGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3906625...c3...309.....	256	5478	189	570		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3923465_f3_135	257	5479	261	786	510	7.9e-49
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
amp nucleosidase			pir:A72021		A72021	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3928336_g2_262.....	258	5480	464	1395		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3932756_f2_74.....	259	5481	471	1416	518	1.1e-49
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
OprM			gp:AB011381		AB011381	
<u>Description</u>						
Pseudomonas aeruginosa gene for OprM, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3942137_f2_54.....	260	5482	135	408		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3946962_c1_163	261	5483	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3985640_c2_260.....	262	5484	152	459		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4103383_c2_201.....	263	5485	125	378	164	3.7e-12

Protein name

Locus Name

Acc#

sp:YBDF_ECOLI

Description

HYPOTHETICAL 14.1 KD PROTEIN IN NFNB-ENTD INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
41307_f1_14.....	264	5486	247	744	187	1.3e-14

Protein name

Locus Name

Acc#

sp:Y978_METJA

Q58388

Description

HYPOTHETICAL PROTEIN MJ0978

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4343942_f2_75	265	5487	383	1152	443	1.0e-41

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein mexE	pir:T30829	T30829

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4531536_f3_112.....	266	5488	412	1239	150	7.0e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:YP102KB	AL031866

Description

Yersinia pestis 102 kbases unstable region: from 1 to 119443.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4535677_c1_154.....	267	5489	211	636	241	2.5e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:CAT3_ECOLI	P00484

Description

CHLORAMPHENICOL ACETYLTRANSFERASE III,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4691032_c2_233.....	268	5490	143	432		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4691061_c3_294	269	5491	94	285	72	0.020

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NADH dehydrogenase subunit 4L	gp:BMMITOCH01	AF110610

Description

Boophilus microplus NADH dehydrogenase subunit 4 (ND4) gene, partial cds; NADH dehydrogenase subunit 4L (ND4L) gene, complete cds; tRNA-Thr and tRNA-Pro genes, complete sequence; and NADH dehydrogenase subunit 6 (ND6) gene, partial cds, mitochondrial genes for mitochondrial products.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4897087_f1_19	270	5492	139	420		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4898537_f1_11	271	5493	749	2250	136	8.6e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:Y797_METJA Q58207

Description

HYPOTHETICAL PROTEIN MJ0797

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4973765_f3_104	272	5494	141	426	128	1.6e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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conserved hypothetical protein yknZ pir:E69858 E69858

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5084381_c3_310	273	5495	331	996	1166	2.4e-118

Protein name	Locus Name	Acc#
FucR	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5187812_f1_13	274	5496	228	687	596	6.1e-58

Protein name	Locus Name	Acc#
	sp:YF08_METJA	Q58903

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ1508

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5191942_f3_128	275	5497	209	630	246	7.5e-21

Protein name	Locus Name	Acc#
amino acid ABC transporter, ATP-binding protein	pir:H72356	H72356

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
547082_f1_36	276	5498	170	513	93	0.00016

Protein name	Locus Name	Acc#
gpC	gp:AF063097	

Description

Bacteriophage P2, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5859625_c3_299	277	5499	62	189		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6412812_c2_198	278	5500	686	2061	2246	8.7e-233

Protein name Locus Name Acc#

high temperature protein HtpG gp:AF176245 AF176245

Description

Porphyromonas gingivalis high temperature protein HtpG (htpG) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6723262_f2_56	279	5501	133	402		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
787567_f3_139	280	5502	303	912	659	1.3e-64

Protein name Locus Name Acc#

dlhydrodipicolinate synthase pir:B72246 B72246

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
907974_c1_149	281	5503	745	2238	1877	1.1e-193

Protein name

Locus Name

Acc#

sp:MECB_BACSU

P37571

Description

NEGATIVE REGULATOR OF GENETIC COMPETENCE MECB

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9851505_f3_113	282	5504	238	717	106	1.5e-05

Protein name

Locus Name

Acc#

hypothetical protein

gp:SEL243707

AJ243707

Description

Synechococcus elongatus petB gene, petD gene and ORF1.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10969062_f3_151	283	5505	256	771	747	6.1e-74

Protein name

Locus Name

Acc#

ATP synthase F1, subunit alpha

pir:F72231

F72231

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
133562_f3_116	284	5506	265	798	565	1.2e-54

Protein name

Locus Name

Acc#

hypothetical protein

gp:STE242827

AJ242827

Description

Streptomyces tendae aip gene and ORF2 (partial), strain Tue901/8c.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13672255_f2_95	285	5507	146	441		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14501312_c3_311	286	5508	461	1386	473	6.6e-45

Protein name

Locus Name

Acc#

conserved hypothetical integral membrane protein HP1184

pir:H64667

H64667

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14511007_f1_2	287	5509	330	993		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14645437_f3_135	288	5510	768	2307	117	0.0015

Protein name

Locus Name

Acc#

conserved hypothetical protein yknZ

pir:E69858

E69858

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14969692_f1_37	289	5511	404	1215	232	4.9e-17

Protein name

Locus Name

Acc#

antibiotic resistance protein homolog ywoG

pir:B70065

B70065

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15104137_f1_1	290	5512	466	1401		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15673443_c3_323	291	5513	464	1395	792	1.0e-78

Protein name

Locus Name

Acc#

Salmonella typhimurium transcriptional

gp:STYSTMF1

AF170176

Description

Salmonella typhimurium fragment STMF1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
158187_f3_121	292	5514	409	1230	988	1.8e-99

Protein name

Locus Name

Acc#

sp:URAA_HAEIN

P45117

Description

PROBABLE URACIL PERMEASE (URACIL TRANSPORTER)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16172682_f1_45	293	5515	310	933	532	3.4e-78

Protein name

Locus Name

Acc#

sp:ATPA_RICPR

050288

Description

ATP SYNTHASE ALPHA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16828462_f1_46	294	5516	292	879	470	1.4e-44

Protein name

Locus Name

Acc#

sp:ATPG_BACSU

P37810

Description

ATP SYNTHASE GAMMA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19945317_c2_264	295	5517	285	858	120	2.0e-05

Protein name

Locus Name

Acc#

3',5'-cyclic-nucleotide phosphodiesterase,
cpdA homolog MTH178:Icc related protein

pir:F69104

F69104

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21990930_c1_217.....	296	5518	326	981		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22464182_c1_215.....	297	5519	328	987		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2346936_f3_153	298	5520	463	1392	153	8.5e-08

Protein name

Locus Name

Acc#

HeIC

gp:LPU11704

U11704

Description

Legionella pneumophila HeIC (heIC) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23694686_f1_35	299	5521	225	678	179	9.5e-14

Protein name

Locus Name

Acc#

sp:GS1_HUMAN

Q08623

Description

GS1 PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23829510_c3_325.....	300	5522	228	687	283	9.0e-25

Protein name

Locus Name

Acc#

transcription regulator, crp family

pir:F72285

F72285

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24009530_c1_182.....	301	5523	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24010962_f1_25	302	5524	131	396		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24111375_f3_110	303	5525	68	207		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24219032_f2_97	304	5526	92	279	172	5.2e-13

Protein name Locus Name Acc#

sp:ATPL_ANASP P12409

Description

ATP SYNTHASE C CHAIN, (LIPID-BINDING PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24254417_f2_53	305	5527	379	1140	480	1.2e-45

Protein name Locus Name Acc#

sensory transduction system regulatory protein sll1229:protein sll1229:protein sll1229

pir:S75524 S75524

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24333127_c3_332	306	5528	532	1599	748	1.3e-76

Protein name

Locus Name

Acc#

sp:YIEN_ECOLI

P31473

Description

HYPOTHETICAL 56.4 KD PROTEIN IN ASNA-KUP INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24398417_c2_280	307	5529	996	2991	108	3.4e-15

Protein name

Locus Name

Acc#

hypothetical protein jhp0336

pir:C71944

C71944

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24399035_c3_312	308	5530	60	183	44	0.049

Protein name

Locus Name

Acc#

nonstructural protein

gp:AF012732

AF012732

Description

Bovine viral diarrhea virus strain Yak nonstructural protein (p125)mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24408437_c2_228	309	5531	122	369	265	7.3e-23

Protein name

Locus Name

Acc#

sp:THIO_BORBU

O51088

Description

THIOREDOXIN (TRX)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24414153_f1_20	310	5532	448	1347	83	0.0040

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24489452_c2_269	311	5533	560	1683	526	2.0e-58

Protein name

Locus Name

Acc#

long-chain-fatty-acid CoA ligase

pir:D70386

D70386

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24644068_f2_94	312	5534	83	252	158	1.6e-11

Protein name

Locus Name

Acc#

sp:ATPE_CHLLI

P35111

Description

ATP SYNTHASE EPSILON CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24808312_f1_49	313	5535	189	567	308	3.8e-26

Protein name

Locus Name

Acc#

sp:HELA_LEGPN

Q48815

Description

HELA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24875042_f3_147	314	5536	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24881577_f2_85	315	5537	248	747	210	5.1e-16

Protein name

Locus Name

Acc#

sp:XYNE_BUTF1

P26223

Description

D-XYLAN XYLANOHYDROLASE B)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25479842_c3_315	316	5538	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26446928_f3_113	317	5539	254	765	129	3.7e-05

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26831386_f3_139	318	5540	349	1050	507	1.7e-48

Protein name

Locus Name

Acc#

sp:PYRD_ECOLI

P05021

Description

(DHODEHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2942827_c3_342	319	5541	1057	3174	214	3.5e-28

Protein name

Locus Name

Acc#

probable ATP-dependent helicase

pir:A71805

A71805

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29494000_f1_48	320	5542	364	1095	309	4.8e-27

Protein name

Locus Name

Acc#

sp:CZCB_ALCSP

P94176

Description

CATION EFFLUX SYSTEM PROTEIN CZCB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29572678_f2_63	321	5543	208	627	213	5.3e-16

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29973182_c2_246	322	5544	857	2574	1042	3.4e-105

Protein name Locus Name Acc#
 (p)ppGpp synthetase gp:BSU86377 U86377

Description

Bacillus subtilis (p)ppGpp synthetase (relA) and adeninephosphoribosyltransferase (apt) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3131910_c2_268	323	5545	492	1479	832	6.0e-83

Protein name Locus Name Acc#
 sp:YCGO_ECOLI P76007

Description

PUTATIVE NA(+)/H(+) EXCHANGER YCGO

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3165800_c3_302	324	5546	103	312	134	5.5e-09

Protein name Locus Name Acc#
 ORF2 gp:AB015879 AB015879

Description

Porphyromonas gingivalis dnaK operon genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32660011_f3_150	325	5547	415	1248	276	5.8e-24

Protein name Locus Name Acc#
 sp:ATP6_RHORU P15012

Description

ATP SYNTHASE A CHAIN, (PROTEIN 6)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33240828_f2_62	326	5548	885	2658		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33788387_f2_78.....	327	5549	310	933	101	0.024

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:G72385

G72385

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33992211_c1_181.....	328	5550	132	399	200	5.6e-16

Protein name

Locus Name

Acc#

diacylglycerol kinase

gp:BSU29177

U29177

Description

Bacillus subtilis PhoH (phoH) gene, partial cds, diacylglycerolkinase (dgk) gene, complete cds, and cytidine deaminase (cdd) gene,partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34178385_f3_149.....	329	5551	511	1536	2540	6.1e-264

Protein name

Locus Name

Acc#

sp:ATPB_BACFR

P13356

Description

ATP SYNTHASE BETA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34181561_f1_19	330	5552	602	1809	452	8.9e-52

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35625000_f2_92	331	5553	530	1593		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3937751_f2_101	332	5554	864	2595	404	1.3e-36

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
DNA helicase homolog	gp:AF108138	AF108138

Description

Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4395252_c1_209	333	5555	528	1587	494	1.7e-62

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
Beta-N-Acetylglucosaminidase	gp:AB015350	AB015350

Description

Streptomyces thermoviolaceus nagB gene forBeta-N-Acetylglucosaminidase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4454637_f1_5	334	5556	315	948	1058	6.8e-107

Protein name

Locus Name

Acc#

dTDP-glucose 4-6-dehydratase:protein
slr0809:protein slr0809

pir:S75550

S75550

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4501875_f2_51	335	5557	124	375		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4553376_c1_199	336	5558	459	1380	291	2.5e-25

Protein name

Locus Name

Acc#

gp:ECOUW82

L10328

Description

E. coli; the region from 81.5 to 84.5 minutes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4881660_c2_266	337	5559	547	1644	1809	1.8e-186

Protein name

Locus Name

Acc#

sp:PRIS_DESVH

P31101

Description

PRISMANE PROTEIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5276557_f2_98	338	5560	169	510	197	1.2e-15

Protein name	Locus Name	Acc#
ATP synthase F0, subunit b	pir:H72231	H72231

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5276586_f2_99	339	5561	189	570	215	1.4e-17

Protein name	Locus Name	Acc#
F1F0-ATPase subunit delta	gp:AF098522	AF098522

Description

Lactobacillus acidophilus uracil phosphoribosyltransferase (upp) gene, partial cds; and F1F0-ATPase operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
556557_f3_134	340	5562	478	1437	136	6.4e-06

Protein name	Locus Name	Acc#
	sp:YF07_METJA	Q58902

Description

HYPOTHETICAL PROTEIN MJ1507

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5890667_c1_176	341	5563	95	288	213	2.4e-17

Protein name	Locus Name	Acc#
RNA-binding protein	gp:ANARBPD2	D49425

Description

Anabaena variabilis rbpD gene for RNA-binding protein, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6046881_f3_140	342	5564	306	921	655	3.4e-64

Protein name

Locus Name

Acc#

3-methyl-2-oxobutanoate

gp:CGPAN

X96580

Description

C.glutamicum panB, panC & xylB genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6836013_c2_265	343	5565	443	1332	281	1.1e-21

Protein name

Locus Name

Acc#

sp:NTRY_AZOCA

Q04850

Description

NITROGEN REGULATION PROTEIN NTRY,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7072037_c3_322	344	5566	240	723		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
814126_f2_60	345	5567	84	255		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9766325_f3_148	346	5568	422	1269	1070	3.6e-108

Protein name

Locus Name

Acc#

sp:PUPT_SYNY3

Q55336

Description

2) (FORMATE-DEPENDENT GAR TRANSFORMYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1057762_f2_175	347	5569	214	645	528	9.8e-51

Protein name

Locus Name

Acc#

thio-specific antioxidant (tsa) peroxidase

pir:E72036

E72036

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1173263_c2_422.....	348	5570	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11834382_c2_479.....	349	5571	299	900	79	0.021

Protein name

Locus Name

Acc#

ATP binding protein

gp:BBATPBP

X91965

Description

B.burgdorferi abp gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
118906_c1_393	350	5572	165	498		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12204402_c2_483.....	351	5573	67	204	72	0.020

Protein name

Locus Name

Acc#

pE66L

gp:ASU18466

U18466

Description

African swine fever virus, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12677202_f3_307.....	352	5574	237	714	472	8.5e-45

Protein name

Locus Name

Acc#

hypothetical protein

gp:AHAAMYG

X58627

Description

A.haloplanktis amy gene for alpha-amylase
1,4-alpha-D-glucanglucanohydrolase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13103938_c2_466.....	353	5575	159	480	227	5.6e-22

Protein name

Locus Name

Acc#

single stranded DNA-binding protein

gp:SSU64095

U64095

Description

Shewanella sp. PT99 single stranded DNA-binding protein (ssb) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1367792_f3_258	354	5576	202	609	298	2.3e-26

Protein name

Locus Name

Acc#

sp:YB69_HAEIN

P44118

Description

HYPOTHETICAL PROTEIN HI1169

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1369082_c1_320	355	5577	419	1260	714	3.8e-75

Protein name

Locus Name

Acc#

autoaggregation-mediating protein

gp:AF091502

AF091502

Description

Lactobacillus reuteri autoaggregation-mediating protein (aggH) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13787827_c2_468.....	356	5578	156	471		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13876713_f2_124.....	357	5579	103	312		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13914808_f2_181	358	5580	103	312		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14304550_c2_490.....	359	5581	380	1143		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1441937_c1_386.....	360	5582	322	969		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14494037_c3_524.....	361	5583	262	789	256	1.5e-32

Protein name

Locus Name

Acc#

sp:CCSA_CYACA

P31564

Description

CYTOCHROME C BIOGENESIS PROTEIN CCSA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14660927_c1_394	362	5584	1249	3750	259	7.8e-18

Protein name

Locus Name

Acc#

gp:SCYDL057W

Description

S.cerevisiae chromosome IV reading frame ORF YDL057w.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14665882_c2_461	363	5585	153	462		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14875191_c1_388.....	364	5586	365	1098	116	0.00061

Protein name

Locus Name

Acc#

hypothetical protein

gp:YEN132945

AJ132945

Description

Yersinia enterocolitica WA 314 right arm of the high-pathogenicityisland.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
156325_f2_176.....	365	5587	116	351	211	3.8e-17

Protein name

Locus Name

Acc#

ss-DNA binding protein 12RNP2 precursor

gp:SYO12RNP2

D17359

Description

Synechococcus 6301 gene for ss-DNA binding protein 12RNP2, completecds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15660937_c1_345	366	5588	432	1299	617	3.6e-60

Protein name	Locus Name	Acc#
hypothetical protein	pir:T33724	T33724
Description		

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
162785_c3_565.....	367	5589	322	969	156	7.4e-09

Protein name	Locus Name	Acc#
Mag44	gp:DEPMAG44	D17682
Description		

Dermatophagoides farinae mRNA for Mag44, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16447875_c3_560.....	368	5590	63	192		

Protein name	Locus Name	Acc#
Description		

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16525318_c2_471.....	369	5591	574	1725		

Protein name	Locus Name	Acc#
Description		

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
165882_c1_371	370	5592	1018	3057	179	7.8e-10

Protein name

Locus Name

Acc#

sp:PRIM_CLOAB

P33655

Description

DNA PRIMASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16900087_c2_420	371	5593	279	840	414	1.2e-38

Protein name

Locus Name

Acc#

hypothetical protein yycJ

pir:A70090

A70090

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
17010890_c1_369	372	5594	113	342		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
180302_c3_559	373	5595	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
187930_c3_509	374	5596	359	1080		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19035_f1_47	375	5597	674	2025	1563	2.1e-160

Protein name

Locus Name

Acc#

branching enzyme

gp:AB026630

AB026630

Description

Emericella nidulans gene for branching enzyme, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
197191_f3_291	376	5598	381	1146	129	3.1e-05

Protein name

Locus Name

Acc#

sp:PORP_PSEAE

P05695

Description

PORIN P PRECURSOR (OUTER MEMBRANE PROTEIN D1)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19729591_c1_380	377	5599	171	516		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19734688_c2_423	378	5600	193	582	96	0.021

Protein name	Locus Name	Acc#
two-component sensor histidine kinase homolog ybdK	pir:F69747	F69747

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19740893_c3_542.....	379	5601	408	1227	1169	1.2e-118

Protein name	Locus Name	Acc#
	sp:FSR_ECOLI	P52067

Description

FOSMIDOMYCIN RESISTANCE PROTEIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1988388_f1_44.....	380	5602	64	195		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20314007_c2_407.....	381	5603	827	2484	1786	4.8e-184

Protein name	Locus Name	Acc#
	sp:LON1_MYXXA	P36773

Description

ATP-DEPENDENT PROTEASE LA 1,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20344086_f2_157	382	5604	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20350260_c2_405	383	5605	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
204437_f3_277	384	5606	231	696		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20501551_c1_325	385	5607	183	552		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20980313_c1_392	386	5608	69	210	47	0.034

Protein name

Locus Name

Acc#

sp:YOR5_TTV1

P19280

Description

HYPOTHETICAL 9.5 KD PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2126506_c1_314	387	5609	170	513	93	0.00016

Protein name

Locus Name

Acc#

transcription regulator phage-related homolog ydcN

pir:C69774

C69774

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21485027_c2_481.....	388	5610	192	579		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21490925_c1_365.....	389	5611	110	333		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21664055_c3_585	390	5612	81	246	69	0.042

Protein name

Locus Name

Acc#

ATP synthase gamma chain

gp:AB027877

AB027877

Description

Schizosaccharomyces pombe gene for ATP synthase gamma chain, partial cds, clone:TA25.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21677180_c3_566	391	5613	106	321		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21688925_f1_40.....	392	5614	66	201	56	0.031

Protein name

Locus Name

Acc#

estrogen receptor

pir:S26595

S26595

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21729812_c2_408.....	393	5615	374	1125	236	1.0e-17

Protein name

Locus Name

Acc#

hypothetical protein slr0882

pir:S77272

S77272

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21756268_c2_419	394	5616	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22067162_f1_53	395	5617	506	1521	388	7.9e-41

Protein name

Locus Name

Acc#

sp:GLNA_BACCE

P19064

Description

GLUTAMINE SYNTHETASE, (GLUTAMATE--AMMONIA LIGASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22087762_c3_496	396	5618	189	570		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22132811_f2_180	397	5619	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22459802_f2_159	398	5620	333	1002	759	3.3e-75

Protein name

Locus Name

Acc#

p-aminobenzoate synthase component I homolog

pir:F64187

F64187

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22462807_c2_476	399	5621	178	537	93	0.042

Protein name

Locus Name

Acc#

sp:TGN3_RAT

P19814

Description

TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22656553_f3_296	400	5622	275	828		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23438887_c1_389	401	5623	126	381	87	0.013

Protein name

Locus Name

Acc#

unknown

gp:AF074396

AF074396

Description

Desulfotomaculum thermocisternum
 UDP-acetylglucosamine1-carboxyvinyltransferase (murA) gene, partial cds;
 yydA,ferredoxin (fdx), dissimilatory sulfite reductase subunit A
 (dsrA),dissimilatory sulfite reductase subunit B (dsrB), and dsrD
 genes,complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23472178_f3_271	402	5624	470	1413	1205	1.8e-122
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
Xylose Isomerase	gp:RFL132472				AJ132472	
<u>Description</u>	Ruminococcus flavefaciens xylan utilization operon.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23597202_c3_513	403	5625	198	597	48	0.039
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein F21D9.3	pir:T21205				T21205	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23632132_f1_64.....	404	5626	510	1533	614	7.6e-60
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
xylulose kinase	gp:AF001974				AF001974	
<u>Description</u>						
Thermoanaerobacter ethanolicus putative TrkG gene, partial cds, and putative TrkA, xylose isomerase (xylA) and xylulose kinase (xylB) genes, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23634708_c1_368.....	405	5627	84	255	69	0.042
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:YC13_METJA				Q58610	
<u>Description</u>	HYPOTHETICAL PROTEIN MJ1213					

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23651680_f2_191	406	5628	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23690875_c1_318	407	5629	385	1158	931	1.9e-93

Protein name

Locus Name

Acc#

sp:TGT_BACSU

032053

Description

TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23710926_f2_184	408	5630	355	1068	82	0.013

Protein name

Locus Name

Acc#

M protein precursor

pir:S61081

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23865651_c1_327	409	5631	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23922135_c3_495	410	5632	133	402	73	0.016

Protein name

Locus Name

Acc#

MesF

gp:AF143443

AF143443

Description

Leuconostoc mesenteroides plasmid pHY30 MesG (mesG) gene, partialcds; and mesentericin B105 (mesB), MesH (mesH), and MesF (mesF) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24027213_c2_460	411	5633	206	621		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24241261...f1...77.....	412	5634	229	690		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24265886_c2_469.....	413	5635	158	477		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24305437_c3_556	414	5636	80	243		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24322127_c3_567	415	5637	202	609		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24344641_f3_233	416	5638	120	363		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24397877_c1_374	417	5639	64	195	71	0.0075

Protein name

Locus Name

Acc#

sp:RAFR_ECOLI

P21867

Description

RAFFINOSE OPERON REPRESSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24406557_f2_158	418	5640	252	759	151	4.2e-08

Protein name

Locus Name

Acc#

protein antigen LmSTII

gp:LMU73845

U73845

Description

Leishmania major protein antigen LmSTII mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415912_f3_257	419	5641	122	369	80	0.0029

Protein name

Locus Name

Acc#

putative repressor protein

gp:BA1242593

AJ242593

Description

Bacteriophage A118 complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24484682_c2_492.....	420	5642	359	1077		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24503282_c3_538.....	421	5643	83	252	78	0.017

Protein name

Locus Name

Acc#

hypothetical protein MJ1664

pir:F64507

F64507

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24633387_c1_354	422	5644	331	996	635	4.5e-62
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein T27E13.6			pir:T00580		T00580	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640915_c2_480.....	423	5645	157	474		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644636_c1_372.....	424	5646	111	336		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24645337_f3_295.....	425	5647	439	1320	1245	1.0e-126
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative UDP-glucose dehydrogenase			gp:AF159428		AF159428	
<u>Description</u>						

Burkholderia pseudomallei putative UDP-glucose dehydrogenase (udg), putative ADP-heptose synthase (waaE), and putative ADP-glycero-mannoheptose epimerase (gmhD) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648412_f1_23	426	5648	166	501		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648562_c3_555	427	5649	82	249		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24710926_f3_299	428	5650	174	525	121	1.8e-07

Protein name

Locus Name

Acc#

thiol:disulfide interchange protein homolog
yneN

pir:E69891

E69891

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24782635_f1_93	429	5651	187	564	544	2.0e-52

Protein name

Locus Name

Acc#

dTDP-6-deoxy-D-glucose-3,5 epimerase

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete
sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24798568_f2_219	430	5652	206	621		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24804681_c1_370	431	5653	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24804807_f2_160	432	5654	228	687		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24820925_f1_80	433	5655	113	342		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24882942_c3_544	434	5656	357	1074	666	2.3e-65

Protein name

Locus Name

Acc#

sp:YVAA_BACSU

032223

Description

HYPOTHETICAL OXIDOREDUCTASE IN PHUD-OPUD INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2537802_c2_404	435	5657	181	546	52	0.044

Protein name

Locus Name

Acc#

envelope glycoprotein

gp:AF021739

AF021739

Description

HIV-1 isolate slng clone 45 from the Netherlands, envelope glycoprotein (env) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25428312_f3_285.....	436	5658	174	525		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25556532_c2_402.....	437	5659	145	438		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25572212_c1_315	438	5660	122	369	69	0.042

Protein name	Locus Name	Acc#
hypothetical protein yopO	pir:T12849	

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25664086_c1_390	439	5661	303	912		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2595058_f2_127	440	5662	70	213		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26433216_c3_499	441	5663	81	246		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26517_c1_346	442	5664	69	210		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26601510_c2_448	443	5665	71	216	101	1.7e-05

Protein name	Locus Name	Acc#
hypothetical protein MJ1608	pir:G64500	G64500
<u>Description</u>		

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26601577_c1_359	444	5666	268	807	425	8.1e-40

Protein name	Locus Name	Acc#
conserved hypothetical protein aq_1386	pir:F70420	F70420
<u>Description</u>		

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26692342_c2_446	445	5667	406	1221	856	1.7e-85

Protein name	Locus Name	Acc#
succinate--CoA ligase (ADP-Forming), beta chain	pir:H70439	H70439
<u>Description</u>		

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
273261_c2_477	446	5668	480	1443		

Protein name	Locus Name	Acc#
<u>Description</u>		

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2770305_c3_580	447	5669	214	645		

Protein name	Locus Name	Acc#
<u>Description</u>		

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2822161_c1_395	448	5670	733	2202		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2828211_f1_86	449	5671	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2923187_c2_424	450	5672	149	450	138	2.1e-09

Protein name

Locus Name

Acc#

sp:YG02_HAEIN

P44270

Description

HYPOTHETICAL PROTEIN HI1602

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29339125_f2_122	451	5673	79	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29412901_f1_79	452	5674	221	666	135	7.5e-14

Protein name

Locus Name

Acc#

sp:LSPA_STACA

Q59835

Description

PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29470081_c1_376	453	5675	334	1005	102	0.0029

Protein name

Locus Name

Acc#

hypothetical protein PH0283

pir:D71453

D71453

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30289001_c3_525.....	454	5676	468	1407	1084	1.2e-109

Protein name

Locus Name

Acc#

cytochrome c peroxidase

gp:AF200362

AF200362

Description

Haemophilus ducreyi oxaloacetate decarboxylase gamma chain (oadG) gene, partial cds; oxaloacetate decarboxylase alpha chain (oadA), oxaloacetate decarboxylase beta chain (oadB), and alkylphosphonate uptake protein (phna) genes, complete cds; ccp gene, complete sequence; cytochrome c peroxidase gene, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30588453_f1_1.....	455	5677	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31672502_f1_24	456	5678	262	789	118	0.00032

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
type I restriction enzyme hsdM:hypothetical protein H91_orf543:hypothetical protein H91_orf543	pir:S73820	S73820
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32035967_c3_507	457	5679	121	366	161	7.6e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	gp:SSU18930	Y18930
<u>Description</u>		

Sulfolobus solfataricus 281 Kb genomic DNA fragment, strain P2.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33364762_c1_356.....	458	5680	300	903	890	4.3e-89

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
succinate--CoA ligase (ADP-forming), alpha chain	pir:F69719	F69719
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3385955_c1_360.....	459	5681	586	1761	148	8.5e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein TM1650	pir:G72227	G72227
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34017140_c3_498	460	5682	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34073250_f1_54	461	5683	258	777	234	1.4e-19

Protein name

Locus Name

Acc#

sp:YT29_MYCTU

P71564

Description

PUTATIVE OXIDOREDUCTASE RV0945,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34176462_c2_418	462	5684	472	1419	1369	7.5e-140

Protein name

Locus Name

Acc#

sp:UXAC_ECOLI

Description

ISOMERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34277280_c1_378	463	5685	257	774		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34406502_c2_403	464	5686	130	393		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34407787_f1_55.....	465	5687	198	597	132	7.8e-07

Protein name

Locus Name

Acc#

sp:Y374_METJA

Q57819

Description

HYPOTHETICAL PROTEIN MJ0374

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35634587_f1_74.....	466	5688	532	1599	1249	3.9e-127

Protein name

Locus Name

Acc#

sp:YHCX_BACSU

P54608

Description

HYPOTHETICAL 60.2 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36337562_c3_553.....	467	5689	139	420	91	0.00020

Protein name

Locus Name

Acc#

regulatory protein CsgD

sp:ECOCURL12

AF081826

Description

Escherichia coli csg cluster, partial sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36500003_c1_328	468	5690	430	1293	849	9.5e-85
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
macrolide-efflux determinant			gp:SPU83667		U83667	
<u>Description</u>						
Streptococcus pneumoniae macrolide-efflux determinant (meIE) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3938838_c1_373	469	5691	131	396		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4021882_c3_563.....	470	5692	431	1296		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4062628_c3_577.....	471	5693	115	348		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4065760_f1_63	472	5694	255	768	239	4.1e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:S75926	S75926

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4072687_f1_81.....	473	5695	773	2322	121	1.5e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
outer membrane protein	gp:NGU81959	U81959

Description

Neisseria gonorrhoeae outer membrane protein (omp85) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4157536_c3_576.....	474	5696	88	267	77	0.018

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein ZC47.1	pir:T27592	T27592

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4318885_f2_174.....	475	5697	509	1530	1371	4.6e-140

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
xylose transporter	gp:AB009593	AB009593

Description

Tetragenococcus halophilus rbsC, rbsB, xylR, xylA, xylB and xylE genes, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4345012_f2_166	476	5698	196	591	92	0.028

Protein name

Locus Name

Acc#

sp:CRP_ECOLI

P03020

Description

PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4553288_f1_45	477	5699	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4695285_c2_434.....	478	5700	319	960		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4773400_c3_557.....	479	5701	119	360		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4791400_f2_134	480	5702	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4877135_f3_279.....	481	5703	1149	3450	991	1.7e-211

Protein name

Locus Name

Acc#

isoleucine--tRNA ligase, ileS:isoleucyl-tRNA synthetase:isoleucyl-tRNA synthetase

pir:H70203

H70203

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4883592_c3_574.....	482	5704	181	546		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4978302_c3_504.....	483	5705	424	1275	659	1.3e-64

Protein name

Locus Name

Acc#

probable phosphoserine phosphatase

pir:T36772

T36772

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
564077_c2_447.....	484	5706	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6022037_c1_337	485	5707	353	1062	764	9.6e-76

Protein name

Locus Name

Acc#

sp:YHIM_ECOLI

Description

HYPOTHETICAL 39.2 KD PROTEIN IN RHSB-PIT INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6347188_c3_588	486	5708	1643	4932	161	1.3e-08

Protein name

Locus Name

Acc#

gp:AB008550

AB008550

Description

Pseudomonas aeruginosa phage phi CTX, complete genome sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6834807_f1_78	487	5709	130	393	127	3.1e-08

Protein name

Locus Name

Acc#

probable dnaK suppressor

pir:D71366

D71366

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
817827_c3_515	488	5710	253	762	283	9.0e-25

Protein name

Locus Name

Acc#

rRNA methylase homolog ysgA

pir:G69984

G69984

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
829436_c3_535	489	5711	343	1032	600	2.3e-58

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
protein kinase homolog Thi	gp:AF070520	AF070520

Description

Sinorhizobium meliloti protein kinase homolog Thi (thi) and ExoP-like protein genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
84637_c1_366	490	5712	68	207		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9884427_f3_287	491	5713	66	201		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9957827_c1_326	492	5714	413	1242	110	3.3e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YBGH_ECOLI	P75742

Description

HYPOTHETICAL 54.2 KD PROTEIN IN PHRB-NEI INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10320312_f2_49	493	5715	328	987		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10681577_c3_251	494	5716	103	312	114	7.3e-07

Protein name

Locus Name

Acc#

hypothetical protein APE1165

pir:H72586

H72586

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10828567_f3_89	495	5717	204	615	148	1.8e-10

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:C72361

C72361

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13865887_c2_187	496	5718	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1414187_f3_80	497	5719	316	951	357	1.3e-32

Protein name

Locus Name

Acc#

gp:AB012956

AB012956

Description

Vibrio cholerae genes for O-antigen synthesis, strain MO45, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14485841_f3_95	498	5720	208	627	659	1.3e-64
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
rubrerythrin			gp:AF202316		AF202316	
<u>Description</u>						
Moorella thermoacetica rubrerythrin gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14491537_f1_22	499	5721	682	2049	101	0.012
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
comEA protein-related protein			pir:F72301		F72301	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14569387_f3_81.....	500	5722	158	477		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15105001_c2_156.....	501	5723	119	360	87	0.013
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein M70.1			pir:T33032		T33032	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15751503_c3_228.....	502	5724	219	660		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
158136_f3_76	503	5725	308	927	399	4.6e-37

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:G72409

G72409

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16056463_c3_236.....	504	5726	75	228		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
194025_f1_30.....	505	5727	145	438		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20506875_f3_79.....	506	5728	211	636	202	3.5e-16

Protein name

Locus Name

Acc#

sp:Y516_BORBU

O51468

Description

HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE BB0516,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20509632_f1_31	507	5729	448	1347	829	1.2e-82
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
dihydrolipoamide dehydrogenase, :2-oxoglutarate dehydrogenase complex chain E3:acetoin dehydrogenase complex				pir:I40794		I40794
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20995143_c2_182	508	5730	83	252		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2220010_c1_147.....	509	5731	82	249		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22382311_f1_3.....	510	5732	318	957	287	3.4e-25
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
putative oxidoreductase				gp:SCF76		AL121600
<u>Description</u>						

Streptomyces coelicolor cosmid F76.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22679637_f1_11	511	5733	199	600	366	1.4e-33

Protein name

Locus Name

Acc#

conserved hypothetical protein ysnA

pir:C69986

C69986

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23516942_f1_15.....	512	5734	493	1482	127	8.3e-05

Protein name

Locus Name

Acc#

outer membrane protein tolC precursor (tolC)
RP224

pir:H71733

H71733

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23594000_f1_17.....	513	5735	192	579		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23632911_c2_157.....	514	5736	506	1521	1269	3.0e-129

Protein name

Locus Name

Acc#

sp:YGFH_ECOLI

P52043

Description

HYPOTHETICAL 53.8 KD PROTEIN IN SBM-FBA INTERGENIC REGION (O492)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23986267_f1_19	515	5737	148	447		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24116567_f2_53	516	5738	457	1374	194	2.5e-12

Protein name

Locus Name

Acc#

chromosomal hemolysin D

gp:AF081284

AF081284

Description

Escherichia coli strain CFT073 chromosomal hemolysin D (hlyD) gene, partial cds; and Hp1 (hp1), Hp2 (hp2), Hp3 (hp3), and Hp4 (hp4) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24225302_f1_16	517	5739	607	1824		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24260952_c3_221	518	5740	84	255		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24409662_c2_166	519	5741	104	315	107	6.8e-11

Protein name	Locus Name	Acc#
iron-uptake factor	gp:AF051690	AF051690

Description

Pseudomonas aeruginosa iron-uptake factor (piuC), hydroxamate-typeferrisiderophore receptor (piuA), and iron-uptake factor (piuB)genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24415875_f2_55	520	5742	538	1617	521	7.2e-68

Protein name	Locus Name	Acc#
arylsulfatase	gp:PAATSAGN	Z48540

Description

Pseudomonas aeruginosa atsR, atsB, atsc & atsa genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24495337_c2_190.....	521	5743	338	1017	962	1.0e-96

Protein name	Locus Name	Acc#
	sp:NADA_SYNY3	P74578

Description

QUINOLINATE SYNTHETASE A

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24641537_f3_104.....	522	5744	474	1425	417	5.7e-39

Protein name	Locus Name	Acc#
	sp:FUCO_RAT	P17164

Description

I) (ALPHA-L-FUCOSIDE FUCOHYDROLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24713961_f2_37	523	5745	304	915	376	1.3e-34

Protein name

Locus Name

Acc#

prolipoprotein diacylglyceryl transferase
(lgt) RP046

pir:F71712

F71712

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25505386_f1_4	524	5746	244	735	232	2.3e-19

Protein name

Locus Name

Acc#

chloramphenicol acetyltransferase

gp:AF124757

AF124757

Description

Zymomonas mobilis fosmid clone 43D2, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25579383_f3_82	525	5747	627	1884	81	0.0020

Protein name

Locus Name

Acc#

sp:EREB_ECOLI

P05789

Description

ERYTHROMYCIN ESTERASE TYPE II,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26367135_f3_70	526	5748	374	1125	1148	2.0e-116

Protein name

Locus Name

Acc#

sp:YYAF_BACSU

P37518

Description

REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26757637_f3_88	527	5749	735	2208	867	1.2e-86
Protein name				Locus Name		Acc#
hemolysin secretion protein hlyB:protein sll1180:protein sll1180				pir:S75806		S75806
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2741426_f3_98	528	5750	397	1194	355	2.1e-32
Protein name				Locus Name		Acc#
				sp:PBP_BACSU		P39844
Description						

POTATIVE PENICILLIN BINDING PROTEIN PRECURSOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2928307_c3_215	529	5751	527	1584	1185	2.4e-120
Protein name				Locus Name		Acc#
				sp:NADB_PSEAE		
Description						

L-ASPARTATE OXIDASE, (QUINOLINATE SYNTHETASE B)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33992307_f1_23	530	5752	261	786	257	5.1e-22
Protein name				Locus Name		Acc#
				sp:Y117_HELPY		P56080
Description						

HYPOTHETICAL PROTEIN HP0117

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34376678_c1_141	531	5753	892	2679	1603	1.2e-164
Protein name			Locus Name		Acc#	
			sp:MUTS_HAEIN		P44834	
Description						
DNA MISMATCH REPAIR PROTEIN MUTS						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4094128_f2_51	532	5754	599	1800	83	0.026
Protein name			Locus Name		Acc#	
erythromycin esterase homolog ybfO			pir:A69750		A69750	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
424042_f3_103.....	533	5755	470	1413	557	1.2e-101
Protein name			Locus Name		Acc#	
putative protein			gp:ATAP22		Z99708	
Description						
Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragmentNo. 2.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4332837_f3_86.....	534	5756	228	687		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4422762_f2_52	535	5757	238	717	172	8.4e-12

Protein name Locus Name Acc#
 putative glucosyl transferase gp:AF105116 AF105116

Description
 Streptococcus pneumoniae type 19C Cps19CR (cps19CR) gene, partialcds; putative oligosaccharide repeat unit transporter (cps19CJ), UDP-N-acetyl glucosamine-2-epimerase (cps19CK), and putative glucosyl transferase (cps19CS) genes, complete cds; and glucose-1-phosphate thymidyl transferase (cps19CL) gene, partialcds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4547063_c2_181	536	5758	94	285		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4569126_f2_68	537	5759	88	267	87	0.0057

Protein name Locus Name Acc#
 sp:PBP4_HAEIN P45161

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4901587_c1_114	538	5760	562	1689	1101	1.9e-111

Protein name Locus Name Acc#
 probable sulfate transporter pir:A71463 A71463

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5985875_c3_220	539	5761	810	2433	615	5.9e-60
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ferrichrome-iron receptor 3:protein slr1490:protein slr1490			pir:S74457		S74457	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6767057...f2...34.....	540	5762	372	1119	166	3.7e-09
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein PAB1767			pir:B75136		B75136	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
813302...f1...9.....	541	5763	373	1122		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
970680...f1...10.....	542	5764	965	2898	1588	5.1e-217
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative leucyl tRNA synthetase			gp:AF069441		AF069441	
<u>Description</u>						
Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10158452_c2_398	543	5765	250	753	587	5.5e-57
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative glycosyl transferase			gp:AF048749		AF048749	
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1054637_f3_214	544	5766	211	636	1033	3.0e-104
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
superoxide dismutase			gp:BNRSOD2		D13756	
<u>Description</u>						
Bacteroides fragilis DNA for superoxide dismutase, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10750067_c2_445.....	545	5767	126	381		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10803580_c2_394.....	546	5768	283	852	803	7.1e-80
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
alpha-D-glucose-1-phosphate			gp:YEPASCA		L27130	
<u>Description</u>						
Yersinia pseudotuberculosis alpha-D-glucose-1-phosphatecytidyltransferase (ascA) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10837887_c1_303	547	5769	374	1125	1002	5.8e-101
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
CDP-glucose-4,6-dehydratase	pir:D47070				D47070	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10978425_c3_473.....	548	5770	61	186		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11214032_c2_377.....	549	5771	477	1434	837	1.8e-83
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:ATOC_ECOLI				Q06065	
<u>Description</u>						

DECARBOXYLASE INHIBITOR) (ORNITHINE DECARBOXYLASE ANTIZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11932290_f2_88.....	550	5772	107	324	152	1.2e-10
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:CBIK_SALTY				Q05592	
<u>Description</u>						

CBIK PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
126376_f3_197	551	5773	500	1503		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13785926_c2_372.....	552	5774	172	519		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13834812_c3_485.....	553	5775	347	1044		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14461567_f3_222.....	554	5776	386	1161	890	4.3e-89
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

ThiH gp:AF154064 AF154064

Salmonella typhimurium ThiH (thiH) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14489050_f2_180	555	5777	555	1668	147	4.7e-07
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
aspartate aminotransferase	pir:D75496				D75496	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14642207_f1_18.....	556	5778	595	1788	1878	8.6e-194
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:THIC_BACSU					
<u>Description</u>						

THIAMINE BIOSYNTHESIS PROTEIN THIC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14647206_f3_237.....	557	5779	257	774	96	0.021
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
conserved hypothetical protein MTH469	pir:D69161				D69161	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14729186_f2_148.....	558	5780	155	468	88	0.029
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:GENK_ECOLI				P02988	
<u>Description</u>						

PROTEIN K

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14867327_f3_236	559	5781	408	1227	175	3.0e-10

Protein name

Locus Name

Acc#

sp:YIGN_ECOLI

P27850

Description

HYPOTHETICAL 54.7 KD PROTEIN IN UDP-UBIE INTERGENIC REGION PRECURSOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16064015_c2_385	560	5782	140	423	84	0.0060

Protein name

Locus Name

Acc#

trbA protein

pir:A49852

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
164043_c1_309	561	5783	251	756	493	5.0e-47

Protein name

Locus Name

Acc#

conserved hypothetical protein HP0162

pir:B64540

B64540

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
194086_c3_520	562	5784	790	2373	1337	2.8e-144

Protein name

Locus Name

Acc#

sp:PCRA_BACST

P56255

Description

ATP-DEPENDENT HELICASE PCRA,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1960876_c2_403	563	5785	72	219	81	0.0023
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein MJ1608			pir:G64500		G64500	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19689678_c1_307.....	564	5786	442	1329	128	5.0e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:AF144879		AF144879	
<u>Description</u>						
Leptospira interrogans rfb locus, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19709682_c1_302.....	565	5787	451	1356	1278	3.3e-130
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
CDP-4-keto-6-deoxy-D-glucose-3-dehydratase			gp:YPE251713		AJ251713	
<u>Description</u>						
Yersinia pestis strain EV76 hemH gene (partial) and O-antigen genecluster for ddhD gene, ddhA gene, ddhB pseudogene, ddhC gene, prtgene, wbyH gene, wzx gene, wbyI pseudogene, wbyJ gene, wzy pseudogene, wbyK gene, gmd pseudogene, fcl pseudogene, manC gene, wbyL gene, manB gene, wzz gene and gsk gene (partial).						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19711067_c3_486.....	566	5788	300	903	374	2.1e-34
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein jhp0094			pir:E71975		E71975	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20087751_c3_489	567	5789	318	957	1429	3.3e-146
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative UDP-GlcNAc:undecaprenylphosphate			gp:AF048749		AF048749	
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon,complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20520302_c3_462	568	5790	495	1488	112	9.6e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
immunoreactive 50kD antigen PG53			gp:AF175720		AF175720	
<u>Description</u>						
Porphyromonas gingivalis strain W50 immunoreactive 50kD antigenPG53 gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20596012_f1_1	569	5791	801	2406	181	9.9e-33
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ferrichrome-iron receptor 3:protein slr1490:protein slr1490			pir:S74457		S74457	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21495928_f1_23	570	5792	94	285		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2150305_c1_308	571	5793	299	900	174	1.1e-20

Protein name

Locus Name

Acc#

UDP-glucose-4-epimerase/dTDP-glucose-4,6

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22114755_f1_7	572	5794	478	1437	384	1.8e-35

Protein name

Locus Name

Acc#

precorrin-6Y methylase:protein
sll0099:protein sll0099

pir:S76697

S76697

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22129152_f2_112	573	5795	632	1899		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2349150_c1_344	574	5796	103	312		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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2351432_f2_175	575	5797	68	207		
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Protein name	Locus Name	Acc#
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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23562762_c3_488	576	5798	240	723	366	1.4e-33
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Protein name	Locus Name	Acc#
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putative glycosyl transferase	gp:AF071085	AF071085
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Description

Enterococcus faecalis strain OG1RF polysaccharide biosynthetic genecluster, partial sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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23611383_f1_38	577	5799	68	207		
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Protein name	Locus Name	Acc#
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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23615905_c3_523	578	5800	409	1230	327	6.3e-32
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Protein name	Locus Name	Acc#
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sp:HXX3_HUMAN	P52790
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Description

HEXOKINASE TYPE III, (HK III)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23617802_f2_160	579	5801	82	249	84	0.0054

Protein name	Locus Name	Acc#
PP31_39K_orf36	pir:T41782	T41782

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23704688_c3_459.....	580	5802	439	1320	132	1.8e-11

Protein name	Locus Name	Acc#
conserved hypothetical protein yknZ	pir:E69858	E69858

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23831325_f2_155.....	581	5803	95	288		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23851567_f2_119.....	582	5804	192	579		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23851637_f3_217.....	583	5805	266	801	824	4.2e-82

Protein name	Locus Name	Acc#

sp:THIG_ECOLI

Description

THIG PROTEIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23957812_f3_267	584	5806	109	330	91	0.0011

Protein name

Locus Name

Acc#

chaperone GrpE type 2

gp:AF098636

AF098636

Description

Nicotiana tabacum chaperone GrpE type 2 (GrpE2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24023462_c1_311	585	5807	426	1281	618	2.9e-60

Protein name

Locus Name

Acc#

sp:YDAR_BACSU

P96593

Description

HYPOTHETICAL 45.7 KD PROTEIN IN MUTT-GSIB INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24035952_f2_147	586	5808	95	288	82	0.0018

Protein name

Locus Name

Acc#

unknown protein

gp:SCCXV106K

X95258

Description

S.cerevisiae 10.6kbp fragment from chromosome XV.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24223762_g1_318	587	5809	448	1347	503	1.6e-82

Protein name

Locus Name

Acc#

Na+/H+-exchanging protein:Na+/H+ antiporter

pir:JX0360

JX0360

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24239006_f3_269	588	5810	337	1014	110	0.0058

Protein name

Locus Name

Acc#

gp:ECORHSEX

L19083

Description

Escherichia coli RhsE genetic element; defective RhsE core protein, complete cds; complete ORF-E2; H-rpt subelement; complete ORF-H.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24303127_f2_173	589	5811	142	429		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24407687_c2_400.....	590	5812	827	2484	1188	1.1e-120

Protein name

Locus Name

Acc#

sp:SYFB_ECOLI

Description

TRNA LIGASE BETA CHAIN) (PHERS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24410780_f1_71.....	591	5813	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24412912_f2_94	592	5814	192	579		
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Protein name	Locus Name	Acc#
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24504713_f3_200.....	593	5815	240	723	291	1.3e-25
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Protein name	Locus Name	Acc#
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hypothetical protein MTH671	pir:D69189	D69189
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Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24614415_f1_33.....	594	5816	315	948	337	1.7e-30
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Protein name	Locus Name	Acc#
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sp:YLYB_BACSU

Description

HYPOTHETICAL 33.7 KD PROTEIN IN LSP-PYRR INTERGENIC REGION (ORF-X)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24641937_f1_8.....	595	5817	601	1806	628	2.5e-61
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Protein name	Locus Name	Acc#
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precorrin-3 methylase	pir:A64497	A64497
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642311_c2_392	596	5818	162	489	223	2.1e-18

Protein name

Locus Name

Acc#

unknown

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648563_c1_322	597	5819	136	411		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24694013_f1_3	598	5820	1326	3981	659	1.8e-115

Protein name

Locus Name

Acc#

cobalamin biosynthesis protein N

pir:C69048

C69048

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25906675_c3_492	599	5821	173	522	106	3.1e-05

Protein name

Locus Name

Acc#

hypothetical protein AF0456

pir:H69306

H69306

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25976708_f3_209	600	5822	95	288		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26362791_f3_272	601	5823	603	1812	683	3.7e-67

Protein name

Locus Name

Acc#

probable membrane protein b0847

pir:G64822

G64822

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26604510_c1_314	602	5824	595	1788	1902	2.5e-196

Protein name

Locus Name

Acc#

sp:LEPA_BACSU

P37949

Description

GTP-BINDING PROTEIN LEPA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26835887_f1_20	603	5825	238	717	518	1.1e-49

Protein name

Locus Name

Acc#

MPT-synthase sulfurylase

sp:SYPCCMOEB

Y16560

Description

Synechococcus PCC7942 moeB gene.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2853436_c3_500	604	5826	148	447		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29353952_c1_304.....	605	5827	592	1779	891	3.4e-89
Protein name			Locus Name		Acc#	
			gp:AF025396		AF025396	
Description						

Vibrio anguillarum rfb region, partial sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
30522966_f2_122.....	606	5828	262	789	132	5.9e-07
Protein name			Locus Name		Acc#	
			sp:TENI_BACSU		P25053	
Description						

REGULATORY PROTEIN TENI

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32165905_f1_5.....	607	5829	109	330	82	0.0018
Protein name			Locus Name		Acc#	
hypothetical protein MTH670			pir:C69189		C69189	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33289500_c2_393	608	5830	307	924	1394	1.7e-142

Protein name

Locus Name

Acc#

glucose-1-phosphate thymidyl transferase

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34064010_f3_232	609	5831	478	1437	707	1.1e-69

Protein name

Locus Name

Acc#

RNA methyltransferase homolog yefA

pir:E69793

E69793

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34079635_f1_9	610	5832	168	507		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34173556_c3_482	611	5833	314	945	223	4.7e-18

Protein name

Locus Name

Acc#

ADP-L-glycero-D-manno-heptose-6-epimerase

pir:G70330

G70330

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

34245941_c3_490	612	5834	86	261		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

34384631_f3_216	613	5835	205	618	319	1.4e-28
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Protein name

Locus Name

Acc#

sp:THIE_SYNY3

P72965

Description

PYROPHOSPHORYLASE) (TMP-PPASE) (THIAMINE-PHOSPHATE SYNTHASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

35214385_c2_397	614	5836	297	894	182	6.8e-13
-----------------	-----	------	-----	-----	-----	---------

Protein name

Locus Name

Acc#

glucosyl transferase

gp:SMU52844

U52844

Description

Serratia marcescens putative glycosyltransferase, putative glycosyltransferase, putative heptosyl III transferase (waaQ), 3-deoxy-manno-octulosonic acid transferase (waaA), glucosyltransferase (waaE), and KdtB (kdtB) genes, complete cds; and Fpg (fpg) gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

35348458_c1_327	615	5837	119	360	93	0.00025
-----------------	-----	------	-----	-----	----	---------

Protein name

Locus Name

Acc#

unknown

gp:AF007381

AF007381

Description

Flavobacterium johnsoniae gliding motility protein (gldA) gene, complete cds; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	--------------	--------------	-------	-------------

36330078_c3_518	616	5838	96	291		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	--------------	--------------	-------	-------------

36601442_f3_215.....	617	5839	118	357	118	2.8e-07
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Protein name

Locus Name

Acc#

gp:STYSTMF1

AF170176

Description

Salmonella typhimurium fragment STMF1.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	--------------	--------------	-------	-------------

3939512_c1_326.....	618	5840	909	2730	1830	4.0e-281
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Protein name

Locus Name

Acc#

sp:PODK_CLOSY

P22983

Description

DIKINASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	--------------	--------------	-------	-------------

3940877_f2_96.....	619	5841	472	1419	591	9.3e-60
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Protein name

Locus Name

Acc#

precorrin-3 methylase

gp:BMAJ758

AJ000758

Description

Bacillus megaterium 16kb genomic sequence, cobalamin operon.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
39642_c3_480	620	5842	196	591	841	6.7e-84

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
dTDP-6-deoxy-D-glucose-3,5 epimerase	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
40930_f2_144	621	5843	140	423	391	3.2e-36

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein	pir:C75256	C75256

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4196081_c2_391	622	5844	156	471		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4334455_c3_463	623	5845	436	1311	227	3.5e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:NTRB_RHOCA	P09431

Description

NITROGEN REGULATION PROTEIN NTRB,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4688828_c3_507	624	5846	96	291	87	0.0012

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF007381	AF007381

Description

Flavobacterium johnsoniae gliding motility protein (gldA) gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4881512_f1_72	625	5847	153	462		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4881557_c2_404	626	5848	395	1188	105	0.016

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Na ⁺ /H ⁺ -exchanging protein sll0689:Na ⁺ /H ⁺ antiporter:Na ⁺ /H ⁺ antiporter	pir:S74414	S74414
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4882755_f3_268	627	5849	311	936	103	0.0030

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

growth-associated protein	gp:ZEFGAP	L27645
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Description

Brachydanio rerio growth-associated protein, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4884635_c3_487	628	5850	266	801	403	1.7e-37
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:AF144879		AF144879	
<u>Description</u>						
Leptospira interrogans rfb locus, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4884712_c2_401	629	5851	254	765	636	3.5e-62
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
exodeoxyribonuclease			pir:B69126		B69126	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4957512_c3_506	630	5852	193	582		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
504757_c2_373	631	5853	956	2871	383	3.0e-34
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
RcsC			gp:AF071215		AF071215	
<u>Description</u>						
Proteus mirabilis regulator of swarming behavior precursor (rsbA) and RcsB (rcsB) genes, complete cds; and RcsC (rcsC) gene, partialcds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5110325_c3_521	632	5854	381	1146	1054	1.8e-106
Protein name			Locus Name		Acc#	
carboxynorspermidine decarboxylase:protein sll0873:protein sll0873			pir:S77268		S77268	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5112802_f3_207	633	5855	644	1935	423	2.8e-39
Protein name			Locus Name		Acc#	
CbiD protein			gp:BMAJ758		AJ000758	
Description						
Bacillus megaterium 16kb genomic sequence, cobalamin operon.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6025675_f2_162	634	5856	75	228		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6913875_c1_305	635	5857	450	1353	602	1.4e-58
Protein name			Locus Name		Acc#	
hypothetical protein			pir:S22614		S22614	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7087642_c1_306	636	5858	61	186		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
910262...f3...235.....	637	5859	305	918	670	8.8e-66

Protein name

Locus Name

Acc#

sp:AMP1_SYNY3

P53579

Description

M)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
969165...c1...297.....	638	5860	336	1011	182	1.1e-11

Protein name

Locus Name

Acc#

conserved hypothetical protein MTH1261

pir:F69035

F69035

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9885166...c3...460.....	639	5861	282	849	105	0.014

Protein name

Locus Name

Acc#

sp:YBJZ_ECOLI

P75831

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11757880_c2_81	640	5862	146	441	108	3.2e-06
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein PH1670			pir:F71047			F71047
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14460957_f1_4	641	5863	363	1092		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14728413_f1_8	642	5864	95	288		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15878777_c3_95	643	5865	232	699	178	1.1e-12
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
serine-rich protein			pir:T39903			T39903
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20741053_f2_25	644	5866	240	723	1219	5.9e-124
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
BatC			gp:AF116251			AF116251
<u>Description</u>						
Bacteroides fragilis batI operon, complete sequence.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
209688_f3_38	645	5867	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22027_f3_31	646	5868	355	1068	683	3.7e-67

Protein name

Locus Name

Acc#

sp:GCP_HAEIN

P43764

Description

(GLYCOPROTEASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22039692_f2_24	647	5869	216	651	1014	3.1e-102

Protein name

Locus Name

Acc#

BatB

gp:AF116251

AF116251

Description

Bacteroides fragilis batI operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22297140_f1_3	648	5870	327	984	768	3.6e-76

Protein name

Locus Name

Acc#

sp:FTSY_HAEIN

P44870

Description

CELL DIVISION PROTEIN FTSY

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23649052_f1_9	649	5871	399	1200	166	1.2e-11

Protein name

Locus Name

Acc#

sp:Y531_METJA

Q57951

Description

HYPOTHETICAL PROTEIN MJ0531

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23834376_c2_84	650	5872	122	369	122	1.0e-07

Protein name

Locus Name

Acc#

hypothetical protein APE1982

pir:H72500

H72500

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24259700_f1_6	651	5873	615	1848	3076	0.0

Protein name

Locus Name

Acc#

BatD

gp:AF116251

AF116251

Description

Bacteroides fragilis batI operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24407537_f2_21	652	5874	93	282	177	1.5e-13

Protein name

Locus Name

Acc#

ribosomal protein L28

pir:E64104

E64104

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24415903_fl_7	653	5875	279	840	1381	4.0e-141

Protein name

Locus Name

Acc#

BatE

gp:AF116251

AF116251

Description

Bacteroides fragilis batI operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24823562_fl_2	654	5876	68	207	157	2.0e-11

Protein name

Locus Name

Acc#

sp:RK33_ODOSI

P49565

Description

CHLOROPLAST 50S RIBOSOMAL PROTEIN L33

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25975010_cl_63	655	5877	1129	3390		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
272212_l3_33	656	5878	492	1479	201	1.6e-12

Protein name

Locus Name

Acc#

antigen 332

pir:JN0292

JN0292

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3149069_c1_40	657	5879	847	2544	4304	0.0
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
DNA gyrase A subunit	gp:AB017712				AB017712	
<u>Description</u>						
Bacteroides fragilis gyrA gene for DNA gyrase A subunit, completecds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33397127_f1_5	658	5880	331	996	1656	2.9e-170
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
BatA	gp:AF116251				AF116251	
<u>Description</u>						
Bacteroides fragilis batI operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34101702_f2_23.....	659	5881	289	870	388	6.7e-36
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
conserved hypothetical protein BB0175				pir:G70121		G70121
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34266968_f3_32.....	660	5882	454	1365	942	1.3e-94
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
conserved hypothetical protein aq_849	pir:E70373				E70373	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34564376_f1_1	661	5883	415	1248	603	1.1e-58

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76561

S76561

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3912925_f3_34.....	662	5884	334	1005	821	8.8e-82

Protein name

Locus Name

Acc#

probable moxR protein

pir:B70874

B70874

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4961537_c3_87.....	663	5885	418	1257	164	6.9e-09

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_854

pir:B70374

B70374

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5345637_f2_22.....	664	5886	100	303	154	4.2e-11

Protein name

Locus Name

Acc#

sp:DBH_THEMA

P36206

Description

DNA-BINDING PROTEIN HU

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7072675_f3_36	665	5887	146	441	687	1.4e-67

Protein name

Locus Name

Acc#

BatB

gp:AF116251

AF116251

Description

Bacteroides fragilis batI operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10562517_f3_78	666	5888	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12129682_f2_67	667	5889	516	1551	319	2.6e-26

Protein name

Locus Name

Acc#

lipase-like protein

pir:A64706

A64706

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12679062_f3_97	668	5890	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13834500_c3_196	669	5891	144	435	203	2.7e-16

Protein name

Locus Name

Acc#

hypothetical protein BB0530

pir:A70166

A70166

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
17086686_f3_95	670	5892	268	807		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20585963_f1_19	671	5893	413	1242	226	1.8e-16

Protein name

Locus Name

Acc#

hypothetical protein jhp1380

pir:G71815

G71815

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2151552_c2_146	672	5894	250	753	104	2.7e-05

Protein name

Locus Name

Acc#

cytochrome b

gp:AF017516

AF017516

Description

Bombus pascuorum cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22473516_c3_186	673	5895	500	1503	1054	1.8e-106

Protein name

Locus Name

Acc#

sp:CBIP_SALTY

Q05597

Description

COBYRIC ACID SYNTHASE

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24269180_F2_71	674	5896	400	1203	263	2.9e-21

Protein name

Locus Name

Acc#

hypothetical protein jhp1379

pir:F71815

F71815

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24317806_F2_53.....	675	5897	321	966	436	5.5e-41

Protein name

Locus Name

Acc#

nicotinate-nucleotide--dimethylbenzimidazole
phosphoribosyltransferase

pir:A75577

A75577

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24345167_F1_4.....	676	5898	206	621	310	1.2e-27

Protein name

Locus Name

Acc#

cobinamide kinase / cobinamide phosphate
guanylyltransferase

pir:S52220

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24417212_G3_197.....	677	5899	502	1509	1238	5.7e-126

Protein name

Locus Name

Acc#

proline--tRNA ligase, proS:prolyl-tRNA
synthetase:prolyl-tRNA synthetase

pir:A70150

A70150

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24641903_c2_166	678	5900	168	507		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24666005_c2_156.....	679	5901	114	345		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24822213_f2_68.....	680	5902	333	1002	664	3.8e-65

Protein name

Locus Name

Acc#

immunoreactive 36 kDa antigen PG14

gp:AF145798

AF145798

Description

Porphyromonas gingivalis strain W50 immunoreactive 36 kDa antigenPG14 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24822688_f2_66.....	681	5903	136	411	114	7.3e-07

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76776

S76776

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25401437_c1_115	682	5904	165	498	178	2.0e-13

Protein name

Locus Name

Acc#

sp:YJJP_HAEIN

P44520

Description

HYPOTHETICAL PROTEIN HI0108

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30082887_c2_145	683	5905	279	840	238	5.3e-20

Protein name

Locus Name

Acc#

sp:YJJP_ECOLI

P39402

Description

HYPOTHETICAL 30.5 KD PROTEIN IN DNAT-BGLJ INTERGENIC REGION (F277)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31657080_c2_144	684	5906	580	1743	1106	5.5e-112

Protein name

Locus Name

Acc#

sp:YIDE_ECOLI

Description

HYPOTHETICAL 58.9 KD PROTEIN IN GLVC-IBPB INTERGENIC REGION (ORFA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32228452_c3_172	685	5907	191	576	282	1.2e-24

Protein name

Locus Name

Acc#

conserved hypothetical protein yvqK

pir:D70046

D70046

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33642211_f1_9	686	5908	260	783	156	3.7e-11

Protein name

Locus Name

Acc#

probable phosphoglycerate mutase

pir:B75539

B75539

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34195888_c3_190.....	687	5909	325	978	489	1.3e-46

Protein name

Locus Name

Acc#

sp:COBD_PSEDE

P21634

Description

COBD PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
422125_f1_16.....	688	5910	132	399	93	0.0029

Protein name

Locus Name

Acc#

beta-tropomyosin

pir:S23470

S23470

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4689027_c3_195.....	689	5911	1084	3255	895	1.3e-89

Protein name

Locus Name

Acc#

tricorn protease

gp:TAU72850

U72850

Description

Thermoplasma acidophilum GTP-binding protein and tricorn protease(TRI) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4807062_c1_116	690	5912	448	1347	657	2.1e-64

Protein name

Locus Name

Acc#

cobyrinic acid a,c-diamide synthase

pir:A75619

A75619

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
484451_c2_149	691	5913	821	2466	436	1.3e-37

Protein name

Locus Name

Acc#

two component sensor

gp:AF030352

AF030352

Description

Pseudomonas aeruginosa two component sensor (lemA) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5116586_c1_131	692	5914	289	870	296	3.8e-26

Protein name

Locus Name

Acc#

CobD

gp:STU90625

U90625

Description

Salmonella typhimurium alpha-ribazole-5'-phosphate phosphatase CobC(cobC) gene, partial cds and putative aminotransferase CobD (cobD)gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5172508_f1_34	693	5915	103	312		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5181263_f2_54	694	5916	250	753	268	3.5e-23
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
cobalamin synthase			pir:H75576			H75576
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
812510_c2_164	695	5917	66	201		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10042126_f3_172	696	5918	176	531	135	4.3e-09
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein			gp:SSU18930			Y18930
<u>Description</u>						

Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11799076_c2_266	697	5919	103	312		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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1199075_c2_263	698	5920	64	195		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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1359507_c2_282	699	5921	434	1305	1073	1.7e-108
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Protein name

Locus Name

Acc#

sp:HISX_ECOLI

Description

HISTIDINOL DEHYDROGENASE, (HDH)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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1370937_c3_383	700	5922	119	360		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13756515_f2_119	701	5923	68	207		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13786251_f1_58	702	5924	636	1911	386	1.8e-33
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
histidine kinase	gp:AF114442				AF114442	
<u>Description</u>						
Nostoc punctiforme histidine kinase (hepK) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14630063_c3_356	703	5925	389	1170	880	4.9e-88
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:HIS7_HAEIN				P44327	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15039087_c2_272	704	5926	938	2817	2717	1.1e-282
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
B12-dependent	gp:ECOUW89				U00006	
<u>Description</u>						
E. coli chromosomal region from 89.2 to 92.8 minutes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15085902_c2_125	705	5927	788	2367	1213	2.8e-129
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:RHO_PSEFL				P52155	
<u>Description</u>						
TRANSCRIPTION TERMINATION FACTOR RHO						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15629642_f2_79	706	5928	380	1143	113	0.0067

Protein name

Locus Name

Acc#

gp:PFMAL3P2

Description

Plasmodium falciparum MAL3P2, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1995452_c3_340	707	5929	133	402	88	0.0023

Protein name

Locus Name

Acc#

gp:SYCPURT

L36958

Description

Synechocystis sp. (clone pSYN411) glycineamide ribonucleotidetransformylase (purT), Orf134 and dnaA genes, complete cds, photosystem II reaction center protein D2 (psbD) gene, 5' end.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20119062_f3_159	708	5930	642	1929	1069	1.1e-123

Protein name

Locus Name

Acc#

hypothetical protein Rv2438c

pir:D70680

D70680

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21520006_c2_301	709	5931	289	870	101	0.0091

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF021091

AF021091

Description

Helicobacter pylori hypothetical protein (HP0395), hypothetical protein (HP0394), chemotaxis protein CheV (cheV), bifunctional chemotaxis protein CheF (cheF), chemotaxis protein CheW (cheW), and adhesin-thiol peroxidase TagD (tagD) genes, complete cds; and superoxide dismutase SodB (sodB) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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2161286_f3_160	710	5932	192	579		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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21641562_c2_271	711	5933	198	597		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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222B9781_f3_195	712	5934	676	2031	213	1.5e-13
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:PLEC_CAUCR	P37894
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Description

NON-MOTILE AND PHAGE-RESISTANCE PROTEIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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22902267_c2_318	713	5935	252	759		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23477187_f1_54	714	5936	315	948	398	5.9e-37

Protein name

Locus Name

Acc#

BrkB

pir:I40328

I40328

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23522812_f2_70	715	5937	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23593750_f2_84	716	5938	726	2181		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2381338_c2_316	717	5939	347	1044	87	0.025

Protein name

Locus Name

Acc#

hypothetical protein PH0161

pir:G71237

G71237

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24259427_c3_381	718	5940	265	798		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24335943_c1_236	719	5941	385	1158	190	8.0e-12
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein MTH884			pir:B69218		B69218	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24408517_c3_384	720	5942	93	282		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640677_c2_317	721	5943	290	873		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24641080_c1_214	722	5944	136	411		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24643887_c2_314	723	5945	355	1068		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24648538_c1_233	724	5946	187	564	331	7.4e-30

Protein name

Locus Name

Acc#

sp:Y746_METJA

Q58156

Description

HYPOTHETICAL PROTEIN MJ0746

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24650302_f1_16	725	5947	723	2172		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24650912_c3_349	726	5948	519	1560	1415	1.0e-144

Protein name

Locus Name

Acc#

sodium/proline symporter (proline permease)

pir:C69115

C69115

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24798457_f3_162	727	5949	500	1503		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24806567_c1_221	728	5950	670	2013	233	1.2e-21

Protein name

Locus Name

Acc#

sp:DSBD_HAEIN

P44919

Description

BIOGENESIS PROTEIN CYCZ)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24853385_c2_321	729	5951	343	1032		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2504787_f3_189	730	5952	258	777	89	0.0093

Protein name

Locus Name

Acc#

ORF128 hypothetical protein

gp:AF008210

AF008210

Description

Buchnera aphidicola genomic fragment containing (chaperone Hsp60)groEL, DNA biosynthesis initiating protein (dnaA), ATP operon(atpCDGAHFEB), and putative chromosome replication protein (gidA)genes, complete cds; and termination factor Rho (rho) gene, partialcds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25859425_g3_373	731	5953	64	195	92	0.00016

Protein name

Locus Name

Acc#

hypothetical protein ssr1765

pir:S74779

S74779

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26220277_c1_252	732	5954	193	582		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26367943_f2_120.....	733	5955	341	1026		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26369087_c2_299.....	734	5956	116	351	263	1.2e-22

Protein name

Locus Name

Acc#

sp:YHAI_ECOLI

P42622

Description

HYPOTHETICAL 13.5 KD PROTEIN IN EXUR-TDCC INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26461627_c1_223.....	735	5957	351	1056	500	4.0e-57

Protein name

Locus Name

Acc#

sp:HIS8_CANMA

P56099

Description

PHOSPHATE TRANSAMINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2928387_c1_215	736	5958	197	594		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29314080_c1_231	737	5959	724	2175	1417	6.1e-145

Protein name

Locus Name

Acc#

sp:DCP_ECOLI

Description

PEPTIDYL-DIPEPTIDASE DCP, (DIPEPTIDYL CARBOXYPEPTIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30256552_f1_40	738	5960	245	738	571	2.7e-55

Protein name

Locus Name

Acc#

uridine kinase udk

pir:G69728

G69728

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32228408_f3_176	739	5961	464	1395	473	6.6e-45

Protein name

Locus Name

Acc#

unknown

gp:AF086638

AF086638

Description

Pseudomonas putida CumA precursor (cumA) and CumB (cumB) genes, complete cds; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33235905_c3_385	740	5962	476	1431		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34183438_f1_35	741	5963	239	720	430	2.4e-40

Protein name

Locus Name

Acc#

sp:YHHW_ECOLI

P46852

Description

HYPOTHETICAL 26.3 KD PROTEIN IN GNTR-GGT INTERGENIC REGION (F231)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34625053_f2_129	742	5964	493	1482	352	1.6e-34

Protein name

Locus Name

Acc#

damage-inducible protein PAB0243

pir:A75151

A75151

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36056510_c1_251	743	5965	422	1269		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36132912_c2_281	744	5966	167	504	106	0.00018

Protein name

Locus Name

Acc#

hypothetical protein SC2E9.08 SC2E9.08

pir:T34819

T34819

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3912781_f2_98	745	5967	338	1017	317	1.8e-37

Protein name

Locus Name

Acc#

hypothetical protein F19D11.16:hypothetical
protein F14M4.29:hypothetical protein F14M4.29

pir:T02689

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3928550_f3_161.....	746	5968	1054	3165	325	4.3e-45

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC
protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3938831_f3_147.....	747	5969	416	1251	1961	1.4e-202

Protein name

Locus Name

Acc#

sp:CHUR_BACTN

Q02550

Description

CHONDRO-6-SULFATASE REGULATORY PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3948562_c1_217.....	748	5970	204	615	373	2.6e-34

Protein name

Locus Name

Acc#

sp:Y120_METTH

O26223

Description

PUTATIVE NADH DEHYDROGENASE/NAD(P)H NITROREDUCTASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4022312_c1_209	749	5971	282	849	141	2.7e-09

Protein name

Locus Name

Acc#

ferredoxin (fdx-3) homolog

pir:C69294

C69294

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4069137_c3_387.....	750	5972	301	906	127	1.9e-14

Protein name

Locus Name

Acc#

leader peptidase Lep

gp:AF188620

AF188620

Description

Bordetella pertussis lep operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4117150_c3_197.....	751	5973	426	1278	1151	9.4e-117

Protein name

Locus Name

Acc#

sp:SR54_BACSU

P37105

Description

SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4461562_c3_370.....	752	5974	216	651	216	1.1e-17

Protein name

Locus Name

Acc#

hypothetical protein PAB1763

pir:D75137

D75137

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4689092_c1_232	753	5975	199	600	244	1.2e-20

Protein name

Locus Name

Acc#

ferric uptake regulator homolog

gp:AF095596

AF095596

Description

Staphylococcus aureus strain ISP3 ferric uptake regulator homolog(furB) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4698432_f2_121	754	5976	340	1023	687	1.4e-67

Protein name

Locus Name

Acc#

synthase III

pir:F70394

F70394

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4734638_c3_354.....	755	5977	287	864	639	1.7e-62

Protein name

Locus Name

Acc#

sp:HIS1_SALTY

P00499

Description

ATP PHOSPHORIBOSYLTRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4876563_c1_216.....	756	5978	153	462	361	4.9e-33

Protein name

Locus Name

Acc#

sp:SMPB_BACSU

O32230

Description

SMALL PROTEIN B HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4960812_f3_153	757	5979	158	477	299	1.8e-26

Protein name

Locus Name

Acc#

sp:THIO_BORBU

051088

Description

THIOREDOXIN (TRX)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5175875_c2_320	758	5980	192	579		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5313952_f3_190.....	759	5981	485	1458	1360	6.7e-139

Protein name

Locus Name

Acc#

raw starch digesting amylase precursor

gp:AF067653

AF067653

Description

Cytophaga sp. raw starch digesting amylase precursor, gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
579577_f3_152.....	760	5982	158	477	242	2.0e-20

Protein name

Locus Name

Acc#

thioredoxin-like protein

gp:ATAC010718

AC010718

Description

Arabidopsis thaliana chromosome I BAC F28016 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6056552_c3_386	761	5983	337	1014		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6102312_c1_250	762	5984	349	1050		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6250003_c1_247	763	5985	598	1797	129	4.9e-05

Protein name

Locus Name

Acc#

conserved hypothetical protein BB0195

pir:C70124

C70124

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6442137_c3_352	764	5986	103	312	120	1.7e-07

Protein name

Locus Name

Acc#

sp:YRPX_STRCO

P37977

Description

HYPOTHETICAL 11.1 KD PROTEIN IN RPOX 5'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
829692_c2_303	765	5987	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
906903_c3_346	766	5988	287	864		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
978387_c1_248	767	5989	130	393		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9900327_c3_324	768	5990	237	714	149	1.5e-10

Protein name

Locus Name

Acc#

hypothetical protein PH1670

pir:F71047

F71047

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11721040_f1_42	769	5991	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1256885_f3_133	770	5992	382	1149	510	7.6e-48

Protein name

Locus Name

Acc#

Man26A

gp:AF126471

AF126471

Description

Cellulomonas fimi Man26A (man26A) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12773255_c2_289	771	5993	519	1560	417	5.7e-39

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:B72391

B72391

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13709635_c1_211	772	5994	522	1569	319	6.8e-36

Protein name

Locus Name

Acc#

Arylsulfatase precursor (EC 3.1.6.1)

gp:D90791

Description

E.coli genomic DNA, Kohara clone #280(33.7-34.1 min.).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13711437_c1_215	773	5995	106	321	148	1.4e-09

Protein name

Locus Name

Acc#

TRK system potassium uptake protein (trkA)

gp:U32745

Description

Haemophilus influenzae Rd section 60 of 163 of the complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14651512_f1_5	774	5996	469	1410	782	1.2e-77

Protein name

Locus Name

Acc#

sp:YAGG_ECOLI

Description

HYPOTHETICAL SYMPORTER IN PERR-ARGF INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14726062_c1_203	775	5997	664	1995		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16600327_f3_130.....	776	5998	216	651	442	1.3e-41

Protein name

Locus Name

Acc#

dimethylamine corrinoid protein MtbC

gp:AF102623

AF102623

Description

Methanosarcina barkeri dimethylamine corrinoid protein MtbC (mtbC), trimethylamine methyltransferase MttB (mttB), trimethylaminecorrinoide protein MttC (mttC), putative transmembrane protein MttP (mttP), and dimethylamine methyltransferase MtbB1 (mtbB1) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20525252_c2_307.....	777	5999	637	1914	1050	9.7e-125

Protein name

Locus Name

Acc#

sp:NU5C_SYNP2

P31971

Description

NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2117177_f2_71	778	6000	439	1320	354	1.5e-31

Protein name

Locus Name

Acc#

endo-1,4-beta-mannosidase

pir:D72278

D72278

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21664650_f1_6.....	779	6001	396	1191	239	6.0e-18

Protein name

Locus Name

Acc#

renin-binding protein-related protein:protein
slr1975:protein slr1975

pir:S75649

S75649

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21875377_f1_7.....	780	6002	602	1809		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22270002_f2_70.....	781	6003	258	777	475	4.5e-44

Protein name

Locus Name

Acc#

Man26A

gp:AF126471

AF126471

Description

Cellulomonas fimi Man26A (man26A) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22550917_c2_317	782	6004	398	1197	99	0.036

Protein name

Locus Name

Acc#

endo-beta-1,3-glucanase precursor

gp:AF013169

Description

Pyrococcus furiosus beta-glucosidase (celB) gene, complete cds; adh-lam operon, complete sequence; biotin ligase BirA homolog(birA) gene, complete cds; and 2-phosphoglycerate kinase (pgk)gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23712837_f2_81	783	6005	377	1134	169	4.8e-12

Protein name

Locus Name

Acc#

conserved hypothetical protein SC9C7.14c

pir:T35965

T35965

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24260302_f3_134.....	784	6006	398	1197	283	9.0e-25

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:B72278

B72278

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24409668_f3_124.....	785	6007	140	423		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24415962_c2_304	786	6008	160	483	231	2.9e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NADH dehydrogenase (ubiquinone), I chain I RP795	pir:E71640	E71640

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24492137_f1_2	787	6009	1075	3228	163	1.4e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable secreted glucosidase	pir:T35164	T35164

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24642787_c2_316	788	6010	426	1281		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644052_c1_205	789	6011	405	1218	197	2.4e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

alpha-1,3/4-fucosidase precursor	gp:SSU39394	U39394
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Description

Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24645437_c3_384	790	6012	901	2706	176	3.8e-08

Protein name Locus Name Acc#
 115K outer membrane protein precursor:SusC protein pir:JC6027 JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648388_f3_198.....	791	6013	239	717	518	1.1e-49

Protein name Locus Name Acc#
 probable glycosyl hydrolase pir:T36467 T36467

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25400260_c1_220.....	792	6014	279	840	568	5.7e-55

Protein name Locus Name Acc#
 sp:NUOH_ECOLI

Description

OXIDOREDUCTASE CHAIN 8) (NUO8)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25817656_c3_368.....	793	6015	836	2511	871	4.4e-87

Protein name Locus Name Acc#
 sp:TRKH_ECOLI

Description

TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26230265_f2_67	794	6016	625	1878		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26360717_f3_183.....	795	6017	219	660	346	1.9e-31

Protein name

Locus Name

Acc#

phosphoglycolate phosphatase (gph) homolog

pir:C70184

C70184

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26366542_c2_308.....	796	6018	498	1497	719	1.9e-73

Protein name

Locus Name

Acc#

NADH dehydrogenase (ubiquinone), chain
4.2:protein slr1291:protein slr1291

pir:S74687

S74687

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26384637_c3_372.....	797	6019	531	1596	738	4.7e-85

Protein name

Locus Name

Acc#

NADH dehydrogenase (ubiquinone), I chain
nuoD2

pir:D70413

D70413

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26587708_f2_65	798	6020	536	1611	204	3.8e-13

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26594137_f2_75	799	6021	336	1011	293	7.9e-26

Protein name

Locus Name

Acc#

methylobamide:CoM methyltransferase isozyme A

gp:AF013713

AF013713

Description

Methanosarcina barkeri methylobamide:CoM methyltransferase isozyme A (mtbA), monomethylamine corrinoid protein (mtmC), monomethylaminemethyltransferase (mtmB), putative monomethylamine permease (mtmP), and unknown genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26604712_c2_309.....	800	6022	485	1458	725	1.3e-71

Protein name

Locus Name

Acc#

sp:NU2C_SYNY3

P72714

Description

NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 2,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29457557_c2_300.....	801	6023	126	381	225	1.3e-18

Protein name

Locus Name

Acc#

sp:NU3C_ANTFO

Q31792

Description

NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31776708_c3_371	802	6024	65	198	163	4.7e-12
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
NADH dehydrogenase (ubiquinone), I chain nuoB			pir:C70413			C70413
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32532838_f2_80	803	6025	518	1557		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33835790_f2_74	804	6026	251	756	92	0.045
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein			pir:C72397			C72397
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36132686_c3_364	805	6027	114	345		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36360962_c2_305	806	6028	172	519	204	2.1e-16
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
NADH dehydrogenase (ubiquinone), I chain J			pir:C71839			C71839
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3907132_f2_90	807	6029	932	2799	470	7.6e-41
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
sensory transduction histidine kinase slr2098:protein slr2098:protein slr2098			pir:S75130		S75130	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3995302_c2_301.....	808	6030	185	558	319	1.4e-28
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
NADH dehydrogenase I, subunit nuoB			gp:ECNU00		X68301	
<u>Description</u>						

E.coli DNA sequence of nuo operon.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4146907_c1_202.....	809	6031	1071	3216	714	2.4e-81
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
receptor antigen (RagA)			gp:PGI130872		AJ130872	
<u>Description</u>						

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4553400_c2_287.....	810	6032	694	2085	173	6.3e-18
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
Sip1 protein			pir:S27762		S27762	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4566876_c2_285	811	6033	487	1464	411	2.5e-38

Protein name

Locus Name

Acc#

sp:YIDJ_ECOLI

P31447

Description

HYPOTHETICAL 57.3 KD PROTEIN IN EMRD-GLVG INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4975313_c3_369	812	6034	128	387		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5111038_c2_306.....	813	6035	105	318	231	2.9e-19

Protein name

Locus Name

Acc#

sp:NULC_PLEBO

Q00244

Description

NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4L,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5860027_f3_196.....	814	6036	1380	4143	519	4.9e-46

Protein name

Locus Name

Acc#

utilizing regulatory protein tutC

gp:TTU57900

U57900

Description

Thauera aromatica utilizing regulatory protein tutC (tutC),utilizing regulatory protein tutB (tutB), putative DNA bindingprotein TutB1 (tutB1), and putative protein kinase TutC1 (tutC1)genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6444137_f3_129	815	6037	421	1266	138	2.8e-06

Protein name

Locus Name

Acc#

CmuC protein

gp:MSP011317

AJ011317

Description

Methylobacterium sp. CM4, cobD, metF, cmuB, cmuC, partial cobC andcobQ, genes and genes encoding Orf219 and Orf361.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7074155_f1_1	816	6038	384	1155	211	1.4e-14

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7220153_c2_291.....	817	6039	686	2061	1366	1.6e-139

Protein name

Locus Name

Acc#

sp:DXS_HAEIN

P45205

Description

1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
972167_c1_199.....	818	6040	512	1539	359	3.0e-43

Protein name

Locus Name

Acc#

sp:EXUT_ECOLI

P42609

Description

HEXURONATE TRANSPORTER

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9954806_f1_3	819	6041	820	2463	1419	3.8e-145

Protein name

Locus Name

Acc#

beta-xylo-glucosidase

gp:TBZ56279

Z56279

Description

T.brockii cglF, cglG, xglS and cglT genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33212528_c3_11	820	6042	554	1662		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7119532_f3_6	821	6043	71	216	53	0.017

Protein name

Locus Name

Acc#

sp:GP38_CANFA

Q95152

Description

GLYCOPROTEIN 38 PRECURSOR (GP38) (MUCIN-TYPE MEMBRANE PROTEIN GP40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10007303_f1_21	822	6044	177	534		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10189501_f3_191	823	6045	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10314088_f1_46.....	824	6046	384	1155	631	1.2e-61

Protein name

Locus Name

Acc#

sp:D1NP_ECOLI

Description

DNA-DAMAGE-INDUCIBLE PROTEIN P

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10548816_f1_86.....	825	6047	62	189	102	1.4e-05

Protein name

Locus Name

Acc#

hypothetical protein APE2457

pir:H72476

H72476

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1072177_c2_422.....	826	6048	1110	3333	671	3.2e-184

Protein name

Locus Name

Acc#

sp:SECA_RHOCA

P52966

Description

PREPROTEIN TRANSLOCASE SECA SUBUNIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11147938_f2_90	827	6049	401	1206	295	9.2e-25

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1173557_c1_261.....	828	6050	349	1050	483	5.8e-46

Protein name

Locus Name

Acc#

sp:APBE_HAEIN

P44550

Description

THIAMINE BIOSYNTHESIS LIPOPROTEIN APBE PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1180302_f2_93.....	829	6051	542	1629	256	1.3e-40

Protein name

Locus Name

Acc#

sp:STS_RAT

P15589

Description

SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1208392_c2_362.....	830	6052	541	1626	396	9.6e-37

Protein name

Locus Name

Acc#

sp:RLUA_ECOLI

P39219

Description

(PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
128775_f1_51	831	6053	166	501		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12897563_c3_443.....	832	6054	307	924	488	1.7e-46

Protein name

Locus Name

Acc#

oxidoreductase, short chain
dehydrogenase/reductase family

pir:E72427

E72427

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
130001_c3_460.....	833	6055	540	1623	383	2.1e-72

Protein name

Locus Name

Acc#

sp:YFCC_ECOLI

Description

HYPOTHETICAL 54.8 KD PROTEIN IN PTA-FOLX INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13881262_f2_105.....	834	6056	445	1338		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14331502_f3_177	835	6057	166	501		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14703962_c1_334	836	6058	396	1191		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14723751_c2_360	837	6059	673	2022	778	1.1e-79

Protein name

Locus Name

Acc#

type III DNA modification enzyme
(methyltransferase)

pir:F71810

F71810

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14876578_f1_337	838	6060	296	891	310	1.2e-27

Protein name

Locus Name

Acc#

probable beta-glycosyltransferase trsC

pir:S51262

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15054621_c1_330	839	6061	430	1293		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
156642_c3_469	840	6062	133	402		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15902_f2_153	841	6063	264	795	316	2.9e-28

Protein name

Locus Name

Acc#

sp:YDAO_ECOLI

Description

HYPOTHETICAL 35.6 KD PROTEIN IN DBPA-INTR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
163515_c3_466	842	6064	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16828575_f1_43	843	6065	388	1167	790	1.6e-80

Protein name

Locus Name

Acc#

GTP-binding protein

gp:AF019407

AF019407

Description

Caulobacter crescentus GTP-binding protein (cgtA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16829461_f2_112	844	6066	119	360	108	3.2e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein PH0360			pir:E71143		E71143	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f2_159.....	845	6067	431	1296	1723	2.3e-177
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:JQ1020		JQ1020	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19703461_c1_311.....	846	6068	481	1446	1581	2.6e-162
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:AF048749		AF048749	
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19725250_c2_343.....	847	6069	202	609	327	2.0e-29
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YI12_METTH		O27840	
<u>Description</u>						
HYPOTHETICAL PROTEIN MTH1812						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19797162_f2_119	848	6070	357	1074	1095	8.1e-111

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
nucleotide sugar epimerase	gp:AF059755	AF059755

Description

Vibrio vulnificus nucleotide sugar epimerase gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1992187_f3_212	849	6071	355	1068	193	8.7e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
lumQ protein:protein slr1213:protein slr1213	pir:S77548	S77548

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20050402_f3_253.....	850	6072	163	492	129	1.8e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
phosphopyruvate hydratase	pir:C75251	C75251

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20087751_f3_199.....	851	6073	319	960	1657	2.3e-170

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative UDP-GlcNAc:undecaprenylphosphate	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2037502_f1_17	852	6074	256	771	245	9.6e-21

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:D72320

D72320

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20734625_f3_208.....	853	6075	223	672	225	1.3e-18

Protein name

Locus Name

Acc#

hypothetical protein

gp:SSU18930

Y18930

Description

Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20754427_f3_198.....	854	6076	347	1044	1691	5.7e-174

Protein name

Locus Name

Acc#

UDP-glucose-4-epimerase/dTDP-glucose-4,6

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
211510_f1_57.....	855	6077	342	1029	307	2.6e-27

Protein name

Locus Name

Acc#

activator protein

gp:AF047527

AF047527

Description

Pseudomonas fluorescens activator protein (mtlR) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21640887_f2_117	856	6078	362	1089	157	1.7e-08

Protein name

Locus Name

Acc#

hypothetical protein 7.17

pir:D47677

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21681552_c3_442.....	857	6079	466	1401	793	8.2e-79

Protein name

Locus Name

Acc#

thiophene and furan oxidation protein

pir:C70375

C70375

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22536527_f3_190.....	858	6080	215	648	1136	3.7e-115

Protein name

Locus Name

Acc#

putative methyl transferase

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22540937_f1_4.....	859	6081	522	1569	304	1.1e-45

Protein name

Locus Name

Acc#

sp:STS_HUMAN

P08842

Description

SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f3_255	860	6082	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23472533_f3_254	861	6083	124	375	132	8.7e-08

Protein name

Locus Name

Acc#

phosphopyruvate hydratase

pir:C75251

C75251

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23479066_c3_434.....	862	6084	183	552		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23647758_c2_399.....	863	6085	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23709625_c3_433.....	864	6086	321	966	627	3.2e-61

Protein name

Locus Name

Acc#

dolichol-phosphate mannosyltransferase

pir:G70463

G70463

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24064142_f2_148	865	6087	265	798	362	3.8e-33

Protein name

Locus Name

Acc#

hypothetical protein ywnB

pir:E70063

E70063

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24114142_c2_373.....	866	6088	291	876		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24229677_c2_340.....	867	6089	238	717	280	1.9e-24

Protein name

Locus Name

Acc#

hypothetical protein yisX

pir:G69838

G69838

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24245437_c2_423.....	868	6090	153	462		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24257187_f2_132	869	6091	411	1236	1104	9.0e-112

Protein name	Locus Name	Acc#
putative carboxybiotin decarboxylase subunit of	gp:MRU87980	U87980

Description

Malonomonas rubra putative IS-element gene, partial cds, andmalonate decarboxylase gene cluster (madY, madZ, madG, madB, madA, madE, madC, madD, madH, madK, madF, madL, madM, madN) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24401507_c1_299	870	6092	510	1533	2702	4.2e-281

Protein name	Locus Name	Acc#
unknown	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24473192_c2_372	871	6093	642	1929	110	0.0037

Protein name	Locus Name	Acc#
	sp:Y0BW_MYCLE	Q49757

Description

HYPOTHETICAL 31.1 KD PROTEIN B1937_F2_39

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24473817_f2_106	872	6094	431	1296	457	3.3e-43

Protein name

Locus Name

Acc#

putative hemolysin

gp:AF051356

AF051356

Description

Streptococcus mutans YtqB (ytqB) gene, partial cds; ABC transporter(abcX), putative permease (perM), putative hemolysin (hlyX), pyruvate-formate lyase activating enzyme (pflC), D-alanine-D-alanyl carrier protein ligase (dltA), integral membrane protein (dltB), D-alanyl carrier protein (dltC), extramembranal protein (dltD), and putative exopolyphosphatase (ppx1) genes,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24495337_c2_345	873	6095	499	1500	119	0.00014

Protein name

Locus Name

Acc#

immunogenic 75 kDa protein PG4

gp:AF145800

AF145800

Description

Porphyromonas gingivalis strain W50 immunogenic 75 kDa protein PG4 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24631305_f2_116	874	6096	183	552	575	1.0e-55

Protein name

Locus Name

Acc#

unknown

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24647763_c1_275	875	6097	498	1497	685	2.3e-67

Protein name

Locus Name

Acc#

sp:RIBB_ECOLI

P24199

Description

3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE (DHBP SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24651515_f2_91	876	6098	108	327		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24666000_c3_437.....	877	6099	306	921	150	4.1e-16

Protein name

Locus Name

Acc#

probable uridine phosphorylase APE2105

pir:D72516

D72516

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24804663_f3_195.....	878	6100	386	1161		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25972937_c3_459.....	879	6101	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26212777_c3_450.....	880	6102	300	903	215	1.4e-17

Protein name

Locus Name

Acc#

hypothetical protein sll1671

pir:S74655

S74655

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26261313_f1_58	881	6103	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26444687_c2_341.....	882	6104	434	1305	1588	4.6e-163

Protein name

Locus Name

Acc#

sp:ENO_STAAU

069174

Description

GLYCERATE HYDRO-LYASE) (LAMININ BINDING PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26594206_f1_42.....	883	6105	180	543	896	9.9e-90

Protein name

Locus Name

Acc#

putative hypoxanthine guanine

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26594686_c2_346.....	884	6106	158	477		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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26595337_f3_180	885	6107	175	528		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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26564012_c2_404	886	6108	355	1068	112	0.0032
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Protein name

Locus Name

Acc#

gamma response I protein

gp:ATH131708

AJ131708

Description

Arabidopsis thaliana gr I gene, exons 1-3.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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26761057_c2_361	887	6109	1017	3054	627	1.0e-119
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Protein name

Locus Name

Acc#

restriction endonuclease

gp:AF060119

AF060119

Description

Pasteurella haemolytica methyltransferase (mod) and restrictionendonuclease (res) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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26836680_f2_109	888	6110	416	1251	1189	8.9e-121
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Protein name

Locus Name

Acc#

immunoreactive 47 kD antigen PG120

gp:AF144640

AF144640

Description

Porphyromonas gingivalis strain W50 immunoreactive 47 kD antigenPG120 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
275125_f2_111	889	6111	469	1410	111	2.7e-06
Protein name			Locus Name		Acc#	
hypothetical protein Rv2333c			pir:F70705		F70705	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2812827_f3_207	890	6112	270	813	298	2.3e-26
Protein name			Locus Name		Acc#	
			sp:YFIH_HAEIN		P44552	
Description						
HYPOTHETICAL PROTEIN HI0175						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29336040_f1_36	891	6113	420	1263	144	7.9e-07
Protein name			Locus Name		Acc#	
NADH dehydrogenase (ubiquinone), chain 2			pir:T11319		T11319	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29703165_f2_118	892	6114	396	1191	369	6.9e-34
Protein name			Locus Name		Acc#	
			sp:CAPA_BACAN		P19579	
Description						
CAPA PROTEIN						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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30084688_f2_127	893	6115	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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3023452_c3_522	894	6116	524	1575	572	2.1e-55
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Protein name

Locus Name

Acc#

alkaline phosphatase

gp:SSPPHOA2

Z48801

Description

Synechococcus PCC7942 phoV gene for alkaline phosphatase.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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31330037_c2_347	895	6117	182	549	204	6.9e-15
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Protein name

Locus Name

Acc#

DNA polymerase III, alpha subunit

pir:C72360

C72360

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

3240675_f3_182	896	6118	135	408	115	7.2e-07
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Protein name

Locus Name

Acc#

protein-export membrane protein

pir:E71837

E71837

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

33301250_c2_380	897	6119	421	1266		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33397811_f1_45	898	6120	898	2697	115	0.00042

Protein name Locus Name Acc#
histidine kinase sensor protein pir:D70328 D70328

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33489041_f2_110	899	6121	260	783	94	0.045

Protein name Locus Name Acc#
sp:TPMN_XENLA Q01174

Description

TROPOMYOSIN ALPHA CHAIN, NON MUSCLE

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33881887_f3_192	900	6122	83	252	69	0.042

Protein name Locus Name Acc#
sp:YA49_HAEIN

Description

HYPOTHETICAL PROTEIN HI1049

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34189385_f1_38	901	6123	311	936	514	3.0e-49

Protein name Locus Name Acc#
gp:BCY11138 Y11138

Description

B.cereus DNA for ORF1, ORF2 and ORF3 (2402 bp).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34407193_f1_47	902	6124	144	435		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34412513_f3_194	903	6125	303	912	193	1.4e-14

Protein name

Locus Name

Acc#

glycosyl transferase PAB0772

pir:B75096

B75096

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34640915_f1_53	904	6126	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34650341_f3_230	905	6127	79	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34652167_f2_108	906	6128	375	1128	530	6.0e-51

Protein name

Locus Name

Acc#

pyridoxal phosphate biosynthetic protein PdxA

pir:H70373

H70373

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34666452_f3_224	907	6129	172	519		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36134637_f3_249	908	6130	123	372	221	3.3e-18

Protein name

Locus Name

Acc#

hypothetical protein

pir:H75473

H75473

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3944005_f1_39	909	6131	440	1323	1205	1.8e-122

Protein name

Locus Name

Acc#

putative UDP-glucose dehydrogenase

gp:AF159428

AF159428

Description

Burkholderia pseudomallei putative UDP-glucose dehydrogenase (udg), putative ADP-heptose synthase (waaE), and putative ADP-glycero-mannoheptose epimerase (gmhD) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3988318_c2_384	910	6132	699	2100	3614	0.0

Protein name

Locus Name

Acc#

putative TonB-dependent outer membrane receptor

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3990900_f3_193	911	6133	392	1179	272	1.3e-31
Protein name			Locus Name		Acc#	
probable galactosyltransferase trsD			pir:S51263			
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4065757_c1_259.....	912	6134	262	789		
Protein name			Locus Name		Acc#	
Description			NO-HIT			

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4094512_c3_436.....	913	6135	344	1035	1054	1.8e-106
Protein name			Locus Name		Acc#	
Description			sp:YQFA_BACSU		P54466	
HYPOTHETICAL 35.6 KD PROTEIN IN RPSU-PHOH INTERGENIC REGION						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4116680_f3_175.....	914	6136	245	738		
Protein name			Locus Name		Acc#	
Description			NO-HIT			

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4119677_f2_125.....	915	6137	248	747	198	1.2e-15
Protein name			Locus Name		Acc#	
hypothetical protein jhp1456			pir:C71806		C71806	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4147280_c2_374	916	6138	67	204		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

425010_f3_196	917	6139	385	1158	642	8.2e-63
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Protein name

Locus Name

Acc#

WbpU

gp:AF035937

AF035937

Description

Pseudomonas aeruginosa strain IAT5 O6 RpsA (rpsA) gene, partialcds; Ihf-Beta, Wzz (wzz), and Wzx (wzx) genes, complete cds; andwbp gene cluster for O-antigen biosynthesis, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

427215_f3_162	918	6140	473	1422	143	1.6e-06
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Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

4323262_c1_273	919	6141	955	2868		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4331300_c2_390	920	6142	82	249	103	1.1e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			gp:SSU18930		Y18930	
<u>Description</u>						
Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4409462_c2_403	921	6143	506	1521	631	1.2e-61
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein aq_1365			pir:F70418		F70418	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4694152_f2_107.....	922	6144	717	2154	122	0.00078
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative peptidyl-prolyl cis-trans isomerase			gp:ASAJ2316		AJ002316	
<u>Description</u>						
Acinetobacter sp. ADP1 alKR & alKM genes, ORF1 & ORF4.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4725257_f2_104.....	923	6145	427	1284	89	0.011
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
membrane protein			gp:PPUY18245		Y18245	
<u>Description</u>						
Pseudomonas putida todX, todF, todC1, todC2, todB, todA, todD, todE, todG, todI, todH, todS, todT genes.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4804632_c3_476	924	6146	218	657	1119	2.3e-113

Protein name

Locus Name

Acc#

unknown

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5110700_f1_35	925	6147	485	1458	780	1.9e-77

Protein name

Locus Name

Acc#

O-antigen repeat unit transporter Wzx

gp:AF172324

AF172324

Description

Escherichia coli GalF (galF) gene, partial cds; O-antigen repeat unit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy (wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase Gale (gale), 6-phosphogluconate dehydrogenase Gnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF) genes, complete cds; and chain length determinant

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5270252_f2_124	926	6148	192	579	335	3.4e-40

Protein name

Locus Name

Acc#

gp:AB017508

AB017508

Description

Bacillus halodurans C-125 genomic DNA, 32 kb fragment, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5313775_f1_34	927	6149	157	474	614	7.6e-60

Protein name

Locus Name

Acc#

unknown

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
553212_f3_241	928	6150	654	1965	485	6.4e-45
Protein name			Locus Name		Acc#	
sensory transduction histidine kinase slr2098:protein slr2098:protein slr2098			pir:S75130		S75130	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
657956_c1_258.....	929	6151	210	633		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6671887_f3_238.....	930	6152	1294	3885	384	6.5e-33
Protein name			Locus Name		Acc#	
putative alpha-glucosidase			gp:AAC252161		AJ252161	
Description						

Alicyclobacillus acidocaldarius maltose/maltodextrine transportgene region (maleFGR genes, cdaA gene and glcA gene).

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6687552_f1_19.....	931	6153	349	1050	602	1.4e-58
Protein name			Locus Name		Acc#	
			sp:YFGB_ECOLI		P36979	
Description						

HYPOTHETICAL 43.1 KD PROTEIN IN NDK-GCPE INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6767537_f1_13	932	6154	75	228		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6854762_c3_470	933	6155	68	207		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7225916_f1_83	934	6156	65	198		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
796875_f2_158	935	6157	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
961067_c3_479	936	6158	63	192		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9813_c3_473	937	6159	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9921927_c1_288.....	938	6160	419	1260	568	5.7e-55

Protein name

Locus Name

Acc#

conserved hypothetical protein ykgB

pir:D69856

D69856

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10009632_c1_84.....	939	6161	598	1797	75	0.032

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10753760_f2_32.....	940	6162	131	396	224	1.6e-18

Protein name

Locus Name

Acc#

IgA Fc receptor-like protein A428L

pir:T17931

T17931

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12787768_f3_65	941	6163	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13953388_c1_94	942	6164	296	891	133	2.2e-06

Protein name

Locus Name

Acc#

sp:VIRF_YEREN

P13225

Description

VIRULENCE REGULON TRANSCRIPTIONAL ACTIVATOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14511086_c1_86	943	6165	330	993	212	1.5e-18

Protein name

Locus Name

Acc#

hypothetical protein F14F9.5

pir:T33774

T33774

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16832885_f3_68	944	6166	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22860128_f1_11	945	6167	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23469691_c3_111	946	6168	179	540		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23515762_f2_52	947	6169	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23984402_c1_82	948	6170	711	2136	488	8.9e-44

Protein name

Locus Name

Acc#

receptor antigen (RagA)

sp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640675_c2_99	949	6171	511	1536		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24806300_f2_40	950	6172	267	804		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25706687_c1_83	951	6173	415	1248	162	2.3e-17

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26360636_f1_5	952	6174	201	606	208	8.0e-17

Protein name

Locus Name

Acc#

gp:AHU56832

U56832

Description

Aeromonas hydrophila FK506 binding protein (fkpA) gene, complete cds in 3.9 kb fragment.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2813912_c3_110	953	6175	460	1383	508	1.3e-48

Protein name

Locus Name

Acc#

sp:YHAM_ECOLI

P42626

Description

HYPOTHETICAL 19.4 KD PROTEIN IN EXUR-TDCC INTERGENIC REGION (F188)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3417677_c1_85	954	6176	354	1065	171	3.3e-12

Protein name

Locus Name

Acc#

KIAA0879 protein

gp:AB020686

AB020686

Description

Homo sapiens mRNA for KIAA0879 protein, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
37925_f1_10	955	6177	63	192	54	0.020

Protein name

Locus Name

Acc#

gp:AFSCR

X70080

Description

A.franciscana Scr gene (homologue of Drosophila Sex combs reduced).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
474167_c3_105	956	6178	559	1680		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4742812_f3_64	957	6179	378	1137	388	7.2e-50

Protein name

Locus Name

Acc#

hypothetical protein

gp:ATH132745

AJ132745

Description

Arabidopsis thaliana hypothetical protein, clone EMG9a29.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4804562_c2_103	958	6180	452	1359	156	2.6e-11

Protein name

Locus Name

Acc#

putative outer membrane porin

gp:AF030977

Description

Vibrio cholerae glutamyl tRNA synthetase (gltX) gene, partial cds; putative outer membrane porin (ompA), unknown protein, vibriobactin receptor precursor (viuA), and ViuB protein (viuB) genes, complete cds; and VibF (vibF) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4875035_c1_80	959	6181	193	582	180	7.4e-14

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4882012_c1_95	960	6182	377	1131	253	1.4e-19

Protein name

Locus Name

Acc#

gp:AF083424

AF083424

Description

Ateline herpesvirus 3 complete genome.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5351507_f2_39	961	6183	378	1137		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5881877_c3_107	962	6184	352	1059	147	1.3e-07

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
970385_c3_108	963	6185	824	2475	209	1.2e-13

Protein name

Locus Name

Acc#

serine/threonine protein kinase related protein

pir:H69064

H69064

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1064063_c2_139	964	6186	297	894	126	0.00030

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10742332_c1_106	965	6187	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11836662_f2_46.....	966	6188	659	1980	1330	1.0e-135

Protein name

Locus Name

Acc#

sp:YFIC_BACSU

P54719

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN GLVBC 3' REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16284692_c2_135.....	967	6189	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20507827_f3_79.....	968	6190	574	1725	1246	8.1e-127

Protein name

Locus Name

Acc#

ABC transporter, ATP-binding protein

pir:E72396

E72396

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23562802_c3_144	969	6191	421	1266	575	1.0e-55

Protein name

Locus Name

Acc#

sp:SBCE_RHOCA

068033

Description

EXONUCLEASE SBCE HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24651557_c2_138	970	6192	380	1143	78	0.038

Protein name

Locus Name

Acc#

fibronectin type III

gp:HUMFN3A

M12549

Description

Human fibronectin gene type III homology unit corresponding to the cell-binding domain, exons 6 and 7.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24666005_c3_145	971	6193	996	2991	464	1.5e-84

Protein name

Locus Name

Acc#

probable exonuclease,

pir:T03465

T03465

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25978516_c2_119	972	6194	98	297		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
273442_c2_117	973	6195	363	1092	180	2.7e-11
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
cation efflux system (czcB-like)			pir:C70415		C70415	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2947138_f1_6	974	6196	195	588		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29940912_f3_90	975	6197	345	1038	279	2.4e-24
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein TM1693			pir:G72223		G72223	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3157813_f1_7	976	6198	390	1173	305	4.2e-27
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable phosphoesterase, ykuE			pir:B69865		B69865	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34173431_f1_5	977	6199	180	543	183	3.6e-14

Protein name

Locus Name

Acc#

SigX

gp:AF115334

Description

Pseudomonas fluorescens PpsA (ppsA) gene, partial cds; EstX (estX), MenG (menG), CmaX (cmaX), CrfX (crfX), CmpX (cmpX), SigX (sigX), OprF (oprF), and CobA (cobA) genes, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34661301_c1_102	978	6200	1083	3252	394	6.3e-53

Protein name

Locus Name

Acc#

acriflavine resistance protein (acrB) homolog

pir:D70117

D70117

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3938215_c2_118.....	979	6201	550	1653	384	7.4e-33

Protein name

Locus Name

Acc#

cation efflux (AcrB/AcrD/AcrF family)

pir:F70368

F70368

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4394642_f3_71.....	980	6202	152	459		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4805286_c1_99	981	6203	486	1461	533	2.7e-50

Protein name Locus Name Acc#
 acriflavine resistance protein (acrB) homolog pir:D70117 D70117

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5195317_c1_101.....	982	6204	430	1293	110	0.0047

Protein name Locus Name Acc#
 sp:YD40_HAEIN P44165

Description

HYPOTHETICAL PROTEIN H11340

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6853436_c1_115.....	983	6205	161	486		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10235877_c2_250.....	984	6206	389	1170	2007	1.8e-207

Protein name Locus Name Acc#
 putative epimerase/dehydratase gp:AF125164 AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10585817_f3_105	985	6207	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1064005_f1_40.....	986	6208	632	1899	291	5.0e-23

Protein name

Locus Name

Acc#

hypothetical protein Rv2731

pir:B70506

B70506

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10667943_f2_70.....	987	6209	113	342	125	5.0e-08

Protein name

Locus Name

Acc#

HipA protein.

gp:D90794

Description

E.coli genomic DNA, Kohara clone #303(34.3-34.6 min.).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10969017_c3_293.....	988	6210	343	1032	1742	2.2e-179

Protein name

Locus Name

Acc#

putative epimerase/dehydratase

gp:AF125164

AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11023432_c1_205	989	6211	414	1245	2081	2.7e-215

Protein name	Locus Name	Acc#
putative glycosyltransferase	gp:AF125164	AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1188951_f2_61	990	6212	60	183		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12187817_f3_117.....	991	6213	162	489	93	0.031

Protein name	Locus Name	Acc#
cell cycle progression restoration 8 protein	gp:AF011794	AF011794

Description

Homo sapiens cell cycle progression restoration 8 protein (CPR8)mRNA, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12520688_c3_280.....	992	6214	61	186		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13804187_f1_47	993	6215	98	297	84	0.0018

Protein name

Locus Name

Acc#

hypothetical protein

gp:MTH243656

AJ243656

Description

Methanobacterium thermoautotrophicum ehbA, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, & ORFS 1,2 & 3.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14250637_f3_147	994	6216	387	1164		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14258450_f3_118	995	6217	121	366	100	2.2e-05

Protein name

Locus Name

Acc#

hypothetical protein TM1330

pir:F72267

F72267

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14275252_f3_162	996	6218	681	2046	1133	7.6e-115

Protein name

Locus Name

Acc#

(p)ppGpp synthetase

gp:BSU86377

U86377

Description

Bacillus subtilis (p)ppGpp synthetase (relA) and adeninephosphoribosyltransferase (apt) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14648380_f1_18	997	6219	295	888		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14650882_f3_114.....	998	6220	121	366	96	0.00067

Protein name

Locus Name

Acc#

hypothetical protein PFB0225c

pir:E71620

E71620

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14660952_f3_150.....	999	6221	119	360	220	4.3e-18

Protein name

Locus Name

Acc#

ybeB protein homolog iojap:protein
slr1886:protein slr1886

pir:S77145

S77145

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14925162_f3_119.....	1000	6222	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15709675_c1_193	1001	6223	367	1104	798	2.4e-79

Protein name

Locus Name

Acc#

sp:YS18_MYCTU

P71777

Description

HYPOTHETICAL 36.3 KD PROTEIN CY277.18

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15790675_c1_199	1002	6224	401	1206	862	4.0e-86

Protein name

Locus Name

Acc#

phosphonopyruvate decarboxylase, fom2

pir:S60212

S60212

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19533462_c3_278.....	1003	6225	419	1260	869	7.2e-87

Protein name

Locus Name

Acc#

sp:YBDG_ECOLI

Description

HYPOTHETICAL 46.6 KD PROTEIN IN PHEP-NFNB INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1964058_f2_92.....	1004	6226	279	840	716	1.2e-70

Protein name

Locus Name

Acc#

sp:SOJ_BACSU

P37522

Description

SOJ PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20736678_c3_296	1005	6227	204	615	1056	1.1e-106
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative undecaprenyl-phosphate			gp:AF125164		AF125164	
<u>Description</u>						
Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22689642_c2_249	1006	6228	355	1068	465	4.7e-44
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative glycosyltransferase			gp:AF125164		AF125164	
<u>Description</u>						
Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23490876_c3_289.....	1007	6229	508	1527	195	3.4e-12
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative flippase	gp:AF125164				AF125164	
<u>Description</u>	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23553136_c2_238.....	1008	6230	345	1038		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23554555_f3_142	1009	6231	254	765		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23595137_f3_115.....	1010	6232	119	360		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23635952_c1_182.....	1011	6233	333	1002	123	6.7e-11

Protein name

Locus Name

Acc#

dolichol-P-glucose synthetase homolog

pir:E69322

E69322

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23678252_c2_247.....	1012	6234	444	1335	1376	1.4e-140

Protein name

Locus Name

Acc#

phosphoenolpyruvate phosphomutase FOM1

pir:S60206

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2382882_c2_216.....	1013	6235	383	1152	403	1.7e-37

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76344

S76344

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24017687_f3_152	1014	6236	284	855	304	5.4e-27

Protein name

Locus Name

Acc#

sp:CDSA_HAEIN

Description

SYNTHASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24226587_c2_241	1015	6237	314	945	301	1.1e-26

Protein name

Locus Name

Acc#

activator protein

gp:AF047527

AF047527

Description

Pseudomonas fluorescens activator protein (mtlR) gene, completecds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24398376_f3_148	1016	6238	107	324		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24413577_f1_44	1017	6239	288	867		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24641925_c1_203	1018	6240	401	1206	136	3.8e-06
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
galactosyltransferase homolog					pir:G69465	G69465
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24806538_c3_292.....	1019	6241	342	1029	179	2.0e-11
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
capsular polysaccharide biosynthesis protein					pir:F70441	F70441
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2537575_c2_234.....	1020	6242	124	375	87	0.011
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
probable membrane protein YOL019w:hypothetical protein O2313					pir:S66701	S66701
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26204682_f3_128.....	1021	6243	326	981	221	3.3e-18
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					sp:Y266_ARCFU	O29973
<u>Description</u>						
HYPOTHETICAL PROTEIN AF0266						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26367176_c2_217	1022	6244	251	756		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26379677_f1_43	1023	6245	300	903	539	6.7e-52

Protein name

Locus Name

Acc#

sp:YGI2_PSEPU

P31857

Description

HYPOTHETICAL 32.4 KD PROTEIN IN GIDB-UNCI INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29850282_f1_19	1024	6246	269	810	216	1.7e-17

Protein name

Locus Name

Acc#

sp:Y665_HAEIN

P44033

Description

HYPOTHETICAL PROTEIN HI0665

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32636311_f2_83	1025	6247	480	1443		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33376906_c3_290	1026	6248	316	951	351	5.6e-32

Protein name

Locus Name

Acc#

LicD1

gp:AF106539

AF106539

Description

Streptococcus pneumoniae LicD1 (licD1) and LicD2 (licD2) genes, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33406567_f2_82	1027	6249	925	2778	129	6.1e-05

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33839461_c1_200.....	1028	6250	338	1017	348	1.2e-31

Protein name

Locus Name

Acc#

putative alcohol dehydrogenase

gp:CZA382

AL078635

Description

Amycolatopsis orientalis cosmid pCZA382.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35396876_c3_295.....	1029	6251	418	1257	2046	1.4e-211

Protein name

Locus Name

Acc#

putative epimerase

gp:AF125164

AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35401627_c3_288	1030	6252	141	426	431	1.9e-40
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
WcgF	gp:AF125164				AF125164	
<u>Description</u>						
Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>						
36362675_c1_207	1031	6253	197	594	317	2.2e-28						
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>							
			gp:AB008550		AB008550							
<u>Description</u>												
Pseudomonas aeruginosa phage phi CTX, complete genome sequence.												

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3914025_c3_287.....	1032	6254	166	501	181	5.8e-14
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
unknown	gp:AF125164				AF125164	
<u>Description</u>						
Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3943753_c2_245.....	1033	6255	296	891	1278	3.3e-130
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
glucose-1-phosphate thymidyltransferase			gp:AF125164		AF125164	
<u>Description</u>						
Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3955062_c3_299	1034	6256	265	798	918	4.6e-92

Protein name unknown Locus Name gp:AF125164 Acc# AF125164

Description
Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3991300_c3_258	1035	6257	295	888	405	1.1e-37

Protein name stationary phase survival protein Sure Locus Name pir:A70372 Acc# A70372

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4157762_c2_244	1036	6258	182	549	95	0.00012

Protein name unknown Locus Name gp:AF048749 Acc# AF048749

Description
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4175255_f3_151	1037	6259	680	2043	1389	4.3e-148

Protein name FtsH2 Locus Name gp:AB023310 Acc# AB023310

Description
Cyanidioschyzon merolae gene for FtsH2, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4304812_c2_246	1038	6260	140	423	532	3.7e-51
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
WcgG	gp:AF125164				AF125164	
<u>Description</u>						
Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4803555_c3_297	1039	6261	198	597	996	2.5e-100
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative acetyltransferase	gp:AF125164				AF125164	
<u>Description</u>						
Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>						
4878277_c1_192.....	1040	6262	205	618	95	0.0062						
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>							
			gp:YP102KB		AL031866							
<u>Description</u>												
Yersinia pestis 102 kbases unstable region: from 1 to 119443.												

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4897128_c1_201.....	1041	6263	298	897	299	1.8e-26
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
N-acetylglucosaminyltransferase	gp:AB017355				AB017355	
<u>Description</u>	Streptococcus agalactiae DNA, cps (capsular polysaccharide) genes,partial and complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4897256_c1_183	1042	6264	498	1497	1152	7.4e-117

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
X-His dipeptidase,:aminoacylhistidine dipeptidase:aminopeptidase D:beta-alanyl-histidine	pir:JU0300	
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4962760_c2_233	1043	6265	1927	5784	167	6.8e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:E72310	E72310
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5136411_c1_202.....	1044	6266	362	1089	178	5.4e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
capsular polysaccharide biosynthesis homolog yveQ	pir:F70036	F70036
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5213541_c3_263.....	1045	6267	281	846	297	3.0e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein APE2014	pir:H72504	H72504
<u>Description</u>		

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5275281_f1_45	1046	6268	440	1323	375	1.3e-38
Protein name			Locus Name		Acc#	
probable membrane-bound lytic murein transglycosylase D (dniR)			pir:H71301		H71301	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6037801_c3_276	1047	6269	379	1140		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6648452_f2_87	1048	6270	272	819	396	9.6e-37
Protein name			Locus Name		Acc#	
Description			sp:KSGA_MYCCA		P43038	

DIMETHYLTRANSFERASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6832757_f3_149	1049	6271	471	1416	665	3.0e-65
Protein name			Locus Name		Acc#	
Ykok			gp:AB013374		AB013374	
Description						

Bacillus halodurans C-125 mamX, yjdA, ykok and yvfK genes, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6853387_c1_198	1050	6272	367	1104	1050	4.8e-106

Protein name

Locus Name

Acc#

PCZA361.5

gp:AOPCZA361

AJ223998

Description

Amycolatopsis orientalis cosmid PCZA361.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
800812_c2_235	1051	6273	379	1140		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
824051_c1_206.....	1052	6274	402	1209	1943	1.1e-200

Protein name

Locus Name

Acc#

putative aminotransferase

gp:AF125164

AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
882702_c2_237.....	1053	6275	279	840	114	1.3e-06

Protein name

Locus Name

Acc#

unknown

gp:AF068902

AF068902

Description

Streptococcus pneumoniae D-glutamic acid adding enzyme MurD (murD), undecaprenyl-PP-MurNac-pentapeptide-UDPGlcNAc GlcNAc transferase (murG), cell division protein DivIB (divIB), orotidine-5'-decarboxylase PyrF (pyrF), and orotate phosphoribosyltransferase PyrE (pyrE) genes, complete cds; and unknown

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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9944428_f3_97	1054	6276	100	303		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24864688_c1_7	1055	6277	77	234		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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29317557_c2_9	1056	6278	519	1560	142	6.3e-06
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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receptor antigen (RagA)	gp:PGI130872	AJ130872
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Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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1038461_f3_25	1057	6279	274	825		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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16211377_f3_28	1058	6280	158	477		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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16486287_f1_6	1059	6281	151	456		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24647938_f1_5	1060	6282	133	402	110	2.2e-06
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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muramoyl-pentapeptide carboxypeptidase	pir:T34747	T34747
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24666313_f3_31	1061	6283	948	2847	218	6.3e-14
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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slow myosin heavy chain 2	gp:GGU85023	U85023
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Description

Gallus gallus slow myosin heavy chain 2 (SM2) mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4100885_f3_26	1062	6284	316	951		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4119637_f1_8	1063	6285	215	648	115	0.00017
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Protein name

Locus Name

Acc#

hypothetical protein jhp0052

pir:F71980

F71980

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4900252_f1_1	1064	6286	264	795		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5946032_f2_16	1065	6287	285	858		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10755437_f1_11	1066	6288	168	507	280	1.9e-24

Protein name

Locus Name

Acc#

sp:BKDR_PSEPU

P42179

Description

BKD OPERON TRANSCRIPTIONAL REGULATOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1175211_f3_35	1067	6289	215	648	550	4.6e-53

Protein name

Locus Name

Acc#

inner membrane ABC transporter

gp:AF213822

AF213822

Description

Zymomonas mobilis strain ZM4 fosmid clone 42B3, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12272127_f3_40	1068	6290	140	423		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1423427_f1_4	1069	6291	608	1827	871	4.4e-87

Protein name

Locus Name

Acc#

gp:YP102KB

AL031866

Description

Yersinia pestis 102 kbases unstable region: from 1 to 119443.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15657687_f1_13	1070	6292	185	558	373	2.6e-34

Protein name

Locus Name

Acc#

sp:YBDM_ECOLI

P77174

Description

HYPOTHETICAL 23.9 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15900317_f1_5	1071	6293	337	1014	315	1.6e-27

Protein name

Locus Name

Acc#

NrpB

gp:PMU46488

U46488

Description

Proteus mirabilis NrpS (nrpS) gene, partial cds, NrpU (nrpU), NrpT (nrpT), NrpA (nrpA), NrpB (nrpB), NrpG (nrpG) and IrpP (irpP) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20980080_f1_15	1072	6294	117	354	135	4.0e-08

Protein name

Locus Name

Acc#

60kDa protein

gp:AB004560

AB004560

Description

Porphyromonas gingivalis DNA for 60kDa protein, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22657052_c1_54	1073	6295	156	471		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22928450_f1_16	1074	6296	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23556577_f2_25	1075	6297	434	1305	537	1.2e-59

Protein name Locus Name Acc#

sp:YBDN_ECOLI P77216

Description

HYPOTHETICAL 47.8 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23867917_c2_88	1076	6298	96	291	84	0.0043

Protein name Locus Name Acc#

MHC class II alpha chain gp:AF091557 AF091557

Description

Aulonocara hansbaenschii MHC class II alpha chain MHC-Auha-DAA1 mRNA (MHC-Auha-DAA1*01 allele), complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24431537_c2_75	1077	6299	108	327		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24492078_f1_1	1078	6300	307	924		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29580387_f3_38	1079	6301	317	954	142	1.7e-07

Protein name

Locus Name

Acc#

pobR regulator

gp:PSEY18527

Y18527

Description

Pseudomonas sp. pobA, pobR, pcaQ, pcaH and pcaG genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31691875_f2_19	1080	6302	214	645	166	4.7e-12

Protein name

Locus Name

Acc#

gp:LIINLC

Y07639

Description

L.ivanovii 23S rRNA, 5S rRNA, tRNA-Asn, tRNA-Thr, ORF Z, inID, and inIC genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33399057_c1_52	1081	6303	288	867	159	1.5e-09

Protein name

Locus Name

Acc#

sp:LCRF_YERPE

P28808

Description

THERMOREGULATORY PROTEIN LCRF

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35650462_f3_43	1082	6304	200	603	272	4.8e-23
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
60kDa protein	gp:AB004560				AB004560	
<u>Description</u>	Porphyromonas gingivalis DNA for 60kDa protein, complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4069180_f1_14	1083	6305	197	594		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4953586_c2_89.....	1084	6306	119	360	92	0.0026
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
lipase precursor	gp:AF053006				AF053006	
<u>Description</u>						
Staphylococcus epidermidis lipase precursor (geh1) gene, completecds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4954462_f1_3.....	1085	6307	275	828	265	7.3e-23
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:TCMP_STRGA				P39887	
<u>Description</u>						
(EC 2.1.1.-)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5260317_c2_80	1086	6308	61	186	54	0.042
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
pqqG protein				pir:B55527		B55527
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7065802_f3_28.....	1087	6309	238	717	81	0.0088
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein MTH1102				pir:F69013		F69013
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9963202_c3_101.....	1088	6310	511	1536	373	1.2e-32
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
sensory transduction histidine kinase sll0474:protein sll0474:protein sll0474				pir:S76650		S76650
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11723417_c2_40.....	1089	6311	484	1455	121	2.8e-06
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
unknown				gp:U96771		U96771
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16601526_c1_38	1090	6312	1089	3270	801	7.4e-91
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
receptor antigen (RagA)			gp:PGI130872		AJ130872	
<u>Description</u>						
Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20507937_c2_42	1091	6313	542	1629	138	3.6e-07
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
unknown	gp:U96771				U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase,B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21678137_f3_27	1092	6314	420	1263	101	0.024
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein ytaP	pir:B69988				B69988	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24491512_c3_49.....	1093	6315	543	1632	147	5.0e-07
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
unknown	gp:U96771				U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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35351583_f3_34	1094	6316	71	216		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4120307_f3_26	1095	6317	443	1332	520	6.9e-50
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Protein name

Locus Name

Acc#

hypothetical protein PAB1371

pir:C75064

C75064

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4144515_f2_17	1096	6318	70	213		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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781932_c1_35	1097	6319	1100	3303	543	2.7e-85
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Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22697711_c3_9	1098	6320	329	990	614	9.2e-68

Protein name

Locus Name

Acc#

neuraminidase precursor

gp:BNRNANASE

D28493

Description

Bacteroides fragilis nanH gene for neuraminidase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11182950_c2_139	1099	6321	248	747	619	2.2e-60

Protein name

Locus Name

Acc#

TruB

gp:AF169967

AF169967

Description

Flavobacterium johnsoniae LeuS (leuS) gene, partial cds; and Fjoi2 (fjoi2), FtsX (ftsX), Fjoi3 (fjoi3), BacA (bacA), and TruB (truB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11956503_c1_120	1100	6322	142	429	110	1.9e-06

Protein name

Locus Name

Acc#

sp:RNPA_BORBU

P50069

Description

RIBONUCLEASE P PROTEIN COMPONENT, (PROTEIN C5) (RNASE P)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13864002_f1_26	1101	6323	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14882902_c1_108	1102	6324	381	1146	117	0.00018
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
sensory transduction system regulatory protein slr1837:protein slr1837:protein slr1837				pir:S77341	S77341	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15109377_c1_119	1103	6325	254	765	108	0.0011
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
				sp:HEM4_SCHPO	P87214	
<u>Description</u>						

(UROI11S)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20176878_c3_156	1104	6326	280	843	106	0.00063
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
ATPase subunit 6				gp:TCU40265	U40265	
<u>Description</u>						

Trypanosoma cruzi ATPase subunit 6 mRNA, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
204775_c3_153	1105	6327	304	915	466	3.7e-44
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
FtsX				gp:AF169967	AF169967	
<u>Description</u>						

Flavobacterium johnsoniae LeuS (leuS) gene, partial cds; and Fjo12(fjo12), FtsX (ftsX), Fjo13 (fjo13), BacA (bacA), and TruB (truB) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2116037_c1_107	1106	6328	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21522150_c2_141	1107	6329	437	1314	597	1.4e-110

Protein name

Locus Name

Acc#

sp:METK_HAEIN

P43762

Description

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23442175_c1_122	1108	6330	439	1320	1071	2.8e-108

Protein name

Locus Name

Acc#

sp:SYT_BACST

P00952

Description

TYROSYL-TRNA SYNTHETASE, (TYROSINE--TRNA LIGASE) (TYRRS)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23447031_c1_109	1109	6331	298	897		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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23453160_f1_10	1110	6332	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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23712752_c3_149	1111	6333	89	270		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24256300_c2_138	1112	6334	676	2031		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24406253_c3_163	1113	6335	93	279	142	1.5e-09
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Protein name

Locus Name

Acc#

oxidoreductase, short chain
dehydrogenase/reductase family

pir:A72395

A72395

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26605287_c1_114	1114	6336	268	807	400	3.6e-37

Protein name

Locus Name

Acc#

sp:BACA_ECOLI

Description

(EC 2.7.1.66)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29303427_f1_14	1115	6337	81	246	70	0.033

Protein name

Locus Name

Acc#

hypothetical protein A635R

pir:T18137

T18137

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29932918_c3_151.....	1116	6338	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32228430_c3_161.....	1117	6339	527	1584	447	3.8e-42

Protein name

Locus Name

Acc#

choline sulfatase

gp:RMU39940

U39940

Description

Sinorhizobium meliloti bet operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34251637_f2_70	1118	6340	90	273		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35791416_c1_105.....	1119	6341	692	2079	449	2.4e-39

Protein name

Locus Name

Acc#

putative secreted beta-galactosidase

gp:SCF81

AL133171

Description

Streptomyces coelicolor cosmid F81.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36366552_c1_113.....	1120	6342	79	240	175	2.5e-13

Protein name

Locus Name

Acc#

Fjo13

gp:AF169967

AF169967

Description

Flavobacterium johnsoniae LeuS (leuS) gene, partial cds; and Fjo12(fjo12), FtsX (ftsX), Fjo13 (fjo13), BacA (bacA), and TruB (truB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36437893_c3_148.....	1121	6343	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3937750_c1_110	1122	6344	354	1065		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3942082_c2_140.....	1123	6345	357	1074	753	1.4e-74

Protein name

Locus Name

Acc#

S-adenosylmethionine tRNA ribosyltransferase

pir:A72360

A72360

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4102177_c3_162.....	1124	6346	283	852	735	1.1e-72

Protein name

Locus Name

Acc#

sp:KDUI_ERWCH

Q05529

Description

(5-KETO-4-DEOXYURONATE ISOMERASE) (DKI ISOMERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4119005_c3_158.....	1125	6347	212	639	159	1.6e-11

Protein name

Locus Name

Acc#

HI0454

gp:AF174390

AF174390

Description

Haemophilus influenzae strain Rd KW20 HI0454 gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4188438_c3_157	1126	6348	76	231	226	9.9e-19

Protein name	Locus Name	Acc#
conserved hypothetical protein	pir:G72251	G72251

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4398382_c1_118	1127	6349	201	606	374	2.1e-34

Protein name	Locus Name	Acc#
conserved hypothetical protein yvdD	pir:D70033	D70033

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4757_c3_152	1128	6350	375	1128		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4867142_f3_74	1129	6351	1098	3297	302	1.1e-38

Protein name	Locus Name	Acc#
hypothetical protein c0624	pir:S73091	S73091

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4876438_f3_102	1130	6352	590	1773	162	1.7e-09

Protein name	Locus Name	Acc#
response regulator	gp:SPAJ6398	AJ006398

Description

Streptococcus pneumoniae rr09 and hk09 genes; two component system09.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4876515_c2_134	1131	6353	376	1131		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4954376_c2_137	1132	6354	355	1068		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5273377_c2_132	1133	6355	359	1080		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
553161_c2_133	1134	6356	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
553161_c2_135	1135	6357	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5892138_c1_106	1136	6358	409	1230	133	4.7e-06

Protein name

Locus Name

Acc#

hypothetical protein PH0283

pir:D71453

D71453

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6829630_c2_136.....	1137	6359	376	1131		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6835381_f3_93.....	1138	6360	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6837828_c1_117.....	1139	6361	154	465	326	2.5e-29

Protein name

Locus Name

Acc#

sp:HPPK_PORGI

083019

Description

(HPPK) (6-HYDROXYMETHYL-7,8-DIHYDROPTERIN PYROPHOSPHOKINASE) (PPPK)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7315641_c1_111	1140	6362	311	936	140	2.7e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ubiquinone/menaquinone biosynthesis methyltransferase-related protein	pir:F72262	F72262

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10978590_F3_64.....	1141	6363	77	234		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14257762_F3_66.....	1142	6364	110	333		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16453180_F3_65.....	1143	6365	150	453	50	0.020

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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WW domain binding protein 5	gp:MMU92454	U92454
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Description

Mus musculus WW domain binding protein 5 mRNA, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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2084768_f3_57	1144	6366	149	450		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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23.705002_f1_10	1145	6367	746	2241	243	1.2e-29
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Protein name

Locus Name

Acc#

conserved hypothetical protein ylbK

pir:H69874

H69874

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24422676_f1_15	1146	6368	1023	3072		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

24492125_c1_105	1147	6369	1025	3075	2141	1.2e-221
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Protein name

Locus Name

Acc#

hypothetical protein mexF

pir:T30830

T30830

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

24643800_f2_37	1148	6370	258	777	572	2.1e-55
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Protein name

Locus Name

Acc#

sp:YAFV_ECOLI

Q47679

Description

HYPOTHETICAL 28.9 KD PROTEIN IN DNAQ-GMHA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25975307_f1_27	1149	6371	112	339		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26680340_f1_16	1150	6372	125	378		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26756551_c1_104	1151	6373	409	1230	485	3.5e-46

Protein name

Locus Name

Acc#

sp:ACRE_ECOLI

P24180

Description

ACRIFLAVIN RESISTANCE PROTEIN E PRECURSOR (ENVC PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30583162_c2_108	1152	6374	981	2946	1508	2.3e-166

Protein name

Locus Name

Acc#

transcription-repair coupling factor

sp:AF023181

AF023181

Description

Listeria monocytogenes transcription-repair coupling factor (mfdL), low temperature requirement B protein (ltrB), and DivIC homolog(divL) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31375817_f2_44	1153	6375	113	342	69	0.042
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein AF0188			pir:D69273		D69273	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32147151_f1_12.....	1154	6376	392	1179	444	7.8e-42
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:NAGA_VIBCH		O32445	
<u>Description</u>						
DEACETYLASE)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32282637_f2_36.....	1155	6377	196	591	310	1.2e-27
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:G75263		G75263	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34181513_f1_26.....	1156	6378	460	1383	293	4.1e-42
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
dihydroorotase (pyrc) PAB1149			pir:C75027		C75027	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34430317_f2_38	1157	6379	262	789	304	5.4e-27

Protein name

Locus Name

Acc#

protein-tyrosine phosphatase

gp:AB028630

AB028630

Description

Clostridium perfringens hyp27, bacH, ptp, cpd genes forhypothetical protein, bacterial hemoglobin, protein-tyrosinephosphatase, 2', 3'-cuclic nucleotide 2'-phosphodiesterase,partial and complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4554753_f2_45	1158	6380	161	486	211	3.8e-17

Protein name

Locus Name

Acc#

sp:YQGC_BACSU

P54486

Description

HYPOTHETICAL 17.3 KD PROTEIN IN CCCA-SODA INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4570341_f1_25	1159	6381	263	792	531	4.7e-51

Protein name

Locus Name

Acc#

putative glycosyl transferase.

gp:SC6D7

AL133213

Description

Streptomyces coelicolor cosmid 6D7.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
47200_f1_13	1160	6382	689	2070	439	7.4e-41

Protein name

Locus Name

Acc#

sp:NAGB_BACSU

O35000

Description

PHOSPHATE DEAMINASE) (GNPDA) (GLCN6P DEAMINASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4876090_c1_82	1161	6383	204	615	122	0.00012

Protein name

Locus Name

Acc#

sp:MFD_BACSU

P37474

Description

TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4876300_c1_88	1162	6384	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
7157576...F3...67.....	1163	6385	642	1929	886	1.1e-88

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:C72391

C72391

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
835175...F1...28.....	1164	6386	226	678	237	1.9e-18

Protein name

Locus Name

Acc#

sp:METH_HUMAN

Description

(METHIONINE SYNTHASE, VITAMIN-B12 DEPENDENT) (MS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10437958_c3_133	1165	6387	135	408		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10647055_f2_17	1166	6388	263	792	124	5.7e-06

Protein name

Locus Name

Acc#

transcription regulator, crp family

pir:F72285

F72285

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1406526_c2_128	1167	6389	417	1254	876	1.3e-87

Protein name

Locus Name

Acc#

sp:PATB_BACSU

Q08432

Description

PUTATIVE AMINOTRANSFERASE B,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14494530_f1_6	1168	6390	862	2589	169	1.2e-08

Protein name

Locus Name

Acc#

outer membrane assembly protein (asmA) RP347

pir:E71691

E71691

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14648577_c1_93	1169	6391	368	1107	174	1.1e-10

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14875635_c3_139	1170	6392	313	942	602	1.4e-58

Protein name

Locus Name

Acc#

conserved hypothetical protein ytqA

pir:D69999

D69999

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20088937_f1_11.....	1171	6393	292	879	717	9.2e-71

Protein name

Locus Name

Acc#

lipoic acid synthase

pir:A75480

A75480

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22478311_c3_145.....	1172	6394	149	450		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22708153_c3_132	1173	6395	364	1095	317	2.2e-28

Protein name Locus Name Acc#

GldB gp:AF158372 AF158372

Description

Flavobacterium johnsoniae hypothetical protein gene, partial cds;GldB (gldB), GldC (gldC), and hypothetical protein genes, completedcds; and hypothetical protein gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23620910_c2_111	1174	6396	85	258		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24337765_f3_68	1175	6397	904	2712	432	9.6e-68

Protein name Locus Name Acc#

115K outer membrane protein precursor:SusC protein pir:JC6027 JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24431510_c3_137	1176	6398	243	732	108	0.00085

Protein name Locus Name Acc#

hypothetical protein yvqF pir:G70045 G70045

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24695187_c2_110	1177	6399	274	825	998	1.5e-100

Protein name

Locus Name

Acc#

sp:NAGB_BORBU

030564

Description

PHOSPHATE DEAMINASE) (GNPDA) (GLCN6P DEAMINASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2814055_c2_99	1178	6400	320	963	304	5.4e-27

Protein name

Locus Name

Acc#

enoyl-acyl carrier protein reductase

pir:H75330

H75330

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2869825_c2_103	1179	6401	157	474	143	6.2e-10

Protein name

Locus Name

Acc#

hypothetical protein APE2345

pir:F72462

F72462

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
30470261_c3_143	1180	6402	369	1110	562	2.5e-54

Protein name

Locus Name

Acc#

O-acetylhomoserine sulfhydrylase

pir:D72324

D72324

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3256642_c2_97	1181	6403	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36360812_f2_36	1182	6404	374	1125		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36406537_f1_5	1183	6405	673	2022	344	2.8e-40

Protein name

Locus Name

Acc#

gp:SC9745

Description

S.cerevisiae chromosome XIII cosmid 9745.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3944711_f3_52	1184	6406	207	624	399	4.6e-37

Protein name

Locus Name

Acc#

probable translation factor yciO

pir:F64874

F64874

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3946886_f3_53	1185	6407	144	435	114	7.3e-07

Protein name

Locus Name

Acc#

maturation protein pPM32

gp:AF166485

AF166485

Description

Glycine max maturation protein pPM32 (PM32) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4007687_f1_10	1186	6408	745	2238	1937	4.8e-200
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
DPP IV			gp:AB008194			AB008194
<u>Description</u>						
Porphyromonas gingivalis gene for DPP IV, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4119037_c3_138	1187	6409	281	846	134	9.7e-07
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
two-component response regulator lytT-involved			pir:B69655			B69655
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4960937_c2_109.....	1188	6410	402	1209	524	2.6e-50
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein b2710			pir:B65051			B65051
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6772836_f3_47.....	1189	6411	292	879	376	1.3e-34
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
conserved hypothetical protein ykrA			pir:C69862			C69862
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
969812_c3_144	1190	6412	204	615	164	3.7e-12
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
RNA polymerase ECF-type sigma factor homolog yhdM			pir:C69826		C69826	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
975405_c2_100.....	1191	6413	245	738	339	1.0e-30
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
sam-dependent methyltransferase			pir:C72086		C72086	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10011662_c1_209.....	1192	6414	458	1374	922	1.7e-92
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:PRIA_BACSU			
<u>Description</u>						
PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10350927_f3_138.....	1193	6415	510	1533	172	5.8e-16
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein MJ0749			pir:E64393		E64393	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11767812_f1_20	1194	6416	265	798	281	1.5e-24
Protein name			Locus Name			Acc#
two-component response regulator lytT-involved			pir:B69655			B69655
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1204052_f1_26	1195	6417	280	843	131	3.5e-08
Protein name			Locus Name			Acc#
			sp:YGEK_ECOLI			Q46791
Description						

HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN KDUI-LYSS INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13729582_f1_24	1196	6418	195	588	128	2.4e-08
Protein name			Locus Name			Acc#
hypothetical protein			pir:C72325			C72325
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13773262_f1_41	1197	6419	87	264		
Protein name			Locus Name			Acc#
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14252182_f1_45	1198	6420	212	639	222	2.6e-18
Protein name			Locus Name			Acc#
resolvase			pir:S38652			S38652
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14354025_f1_1	1199	6421	447	1344		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14570301_f2_66	1200	6422	65	198		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14928462_c3_289	1201	6423	63	192		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16673406_f2_95	1202	6424	419	1260		
Protein name			Locus Name			Acc#
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c1_170	1203	6425	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19614050_c1_162.....	1204	6426	165	498		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19735306_f2_97.....	1205	6427	65	198	63	0.045

Protein name

Locus Name

Acc#

sp:SRD2_CAEEL

Q21767

Description

SRD-2 PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19773437_f3_126.....	1206	6428	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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20328267_c1_164	1207	6429	66	201		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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20390875_f3_151.....	1208	6430	192	579	193	3.1e-15
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Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:E72312

E72312

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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20437675_c2_241.....	1209	6431	235	708		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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20703426_f2_94.....	1210	6432	67	204		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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20723160_c2_218.....	1211	6433	240	723	138	3.3e-09
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Protein name

Locus Name

Acc#

conserved hypothetical protein HP0713

pir:A64609

A64609

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20976426_f3_114	1212	6434	91	276	124	3.9e-07

Protein name

Locus Name

Acc#

asparaginase homolog yccc

pir:F69754

F69754

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21647925_f1_7	1213	6435	459	1380	1231	3.1e-125

Protein name

Locus Name

Acc#

sp:DCUB_HAEIN

P44855

Description

ANAEROBIC C4-DICARBOXYLATE TRANSPORTER DCUB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21992175_f3_117	1214	6436	327	984	84	0.0070

Protein name

Locus Name

Acc#

putative transmembrane efflux protein.

gp:SCF91

AL132973

Description

Streptomyces coelicolor cosmid F91.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c2_219	1215	6437	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23617137_c3_268	1216	6438	224	675	267	4.5e-23

Protein name

Locus Name

Acc#

sp:YJV7_YEAST

P40893

Description

HYPOTHETICAL 22.0 KD PROTEIN IN HXT11-HXT8 INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23631252_c2_239	1217	6439	229	690		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23631550_c1_174.....	1218	6440	123	372	125	5.0e-08

Protein name

Locus Name

Acc#

hypothetical protein MJ1618

pir:A64502

A64502

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23632787_c1_193.....	1219	6441	314	945	110	3.6e-05

Protein name

Locus Name

Acc#

probable integrase/recombinase

pir:B71194

B71194

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24009637_c3_256	1220	6442	76	231	67	0.025

Protein name

Locus Name

Acc#

sp:VE2_HP38

Q80910

Description

REGULATORY PROTEIN E2

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24066056_f3_155	1221	6443	91	276	134	5.5e-09

Protein name

Locus Name

Acc#

sp:CEBA_BACAM

P23939

Description

BAMHI CONTROL ELEMENT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24236057_f2_73	1222	6444	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24353391_f1_40	1223	6445	153	462		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24394017_f3_153	1224	6446	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24485932_c3_279.....	1225	6447	848	2547	106	0.0070

Protein name

Locus Name

Acc#

arylesterase

gp:AF044683

AF044683

Description

Agrobacterium radiobacter putative dihydrolipoamideS-acetyltransferase (dla) gene, partial cds; arylesterase (ada)gene, complete cds; and putative dihydrolipoamide dehydrogenase(dlh) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2461567_c3_281.....	1226	6448	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24640807_f2_53.....	1227	6449	397	1194		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24882203_f1_29	1228	6450	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24882932_c1_175.....	1229	6451	178	537	348	1.2e-31

Protein name

Locus Name

Acc#

adaptive response regulatory protein

gp:AF047839

AF047839

Description

Pseudoalteromonas sp. S9 putative glucosyl hydrolase precursor and adaptive response regulatory protein (ada) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2531640_c2_242.....	1230	6452	200	603	352	4.4e-32

Protein name

Locus Name

Acc#

unknown

gp:AF006034

AF006034

Description

Clostridium pasteurianum 1,3-propanediol dehydrogenase (dhaT) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25578438_f2_86.....	1231	6453	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25914666_f3_147	1232	6454	92	279	86	0.010

Protein name

Locus Name

Acc#

probable serine-threonine-protein kinase

pir:T41341

T41341

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26178177_c2_221.....	1233	6455	172	519	126	3.9e-08

Protein name

Locus Name

Acc#

hypothetical protein MTH847

pir:A69213

A69213

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26306637_c3_297.....	1234	6456	448	1347	303	3.0e-24

Protein name

Locus Name

Acc#

sp:PRIA_BACSU

Description

PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26360312_c3_290.....	1235	6457	328	987		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26369028_f1_8	1236	6458	323	972	912	2.0e-91

Protein name

Locus Name

Acc#

sp:ASG2_ECOLI

P00805

Description

AMIDOHYDROLASE II) (L-ASNASE II) (COLASPASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26460937_f2_102	1237	6459	392	1179	590	2.6e-57

Protein name

Locus Name

Acc#

mannose-1-phosphate guanylyltransferase

pir:H72303

H72303

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26593800_c3_267.....	1238	6460	197	594	580	3.0e-56

Protein name

Locus Name

Acc#

sp:YJV8_YEAST

P40892

Description

(EC 2.3.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26595192_f1_22.....	1239	6461	462	1389	534	2.3e-51

Protein name

Locus Name

Acc#

oxidoreductase, aldo/keto reductase family

pir:E72284

E72284

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26601062_c3_259	1240	6462	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29328501_f3_131	1241	6463	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31723562_c2_248	1242	6464	385	1158		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3320802_c3_294	1243	6465	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33245255_c1_188	1244	6466	261	786	103	0.014

Protein name

Locus Name

Acc#

hypothetical protein 2

pir:S49113

S49113

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34078300_f3_152	1245	6467	284	855	182	6.3e-12

Protein name

Locus Name

Acc#

integrase

gp:BFU75371

U75371

Description

Bacteroides fragilis transposon Tn4555 TnpA (tnpA), integrase(int), TnpC (tnpC), excisionase (xis), mobilization protein (mobA), and beta-lactamase (cfxA) genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34104127_f3_141	1246	6468	808	2427	274	3.0e-20

Protein name

Locus Name

Acc#

sp:IRGA_VIBCH

P27772

Description

IRON-REGULATED OUTER MEMBRANE VIRULENCE PROTEIN PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34260911_f3_150.....	1247	6469	166	501		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35314080_f2_65.....	1248	6470	716	2151		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35704786_f2_92	1249	6471	92	279	326	2.5e-29

Protein name

Locus Name

Acc#

integrase IntN1

gp:BUU51917

U51917

Description

Bacteroides uniformis insertion element NB01 fragment, integraseIntN1 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3938817_c2_247	1250	6472	480	1443	1319	1.5e-134

Protein name

Locus Name

Acc#

aspartate ammonia-lyase

gp:WSAJ2933

AJ002933

Description

Wolinella succinogenes aspA, dcuA genes and partial ansA gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3940943_f2_74	1251	6473	355	1068	180	2.8e-11

Protein name

Locus Name

Acc#

AlgZ

gp:PAU52431

U52431

Description

Pseudomonas aeruginosa AlgR-cognate sensor AlgZ (algZ) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4000953_f2_87	1252	6474	301	906	147	3.1e-08

Protein name

Locus Name

Acc#

transcription regulator

gp:AF008220

AF008220

Description

Bacillus subtilis rrnB-dnaB genomic region.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4072187_c1_172	1253	6475	587	1764	483	9.3e-95

Protein name

Locus Name

Acc#

sp:DXS_BACSU

P54523

Description

PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
423162_c1_207	1254	6476	221	666		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4345337...f3...110.....	1255	6477	401	1206	143	3.8e-09

Protein name

Locus Name

Acc#

gp:ECASPA

X02307

Description

E. coli aspA gene for aspartase (L-aspartate ammonia-lyase) (EC4.3.1.1).

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4454000_c2_238.....	1256	6478	806	2421	171	1.0e-08

Protein name

Locus Name

Acc#

R27-2 protein

pir:T30296

T30296

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4960312_f1_46	1257	6479	523	1572	227	7.2e-16
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative integrase			gp:BA1242593		AJ242593	
<u>Description</u>						
Bacteriophage A118 complete genome.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
579712_f1_42	1258	6480	339	1020		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6728452_c3_293.....	1259	6481	87	264		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
867688_f3_136.....	1260	6482	206	621	243	1.6e-20
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein sir2078			pir:S77566		S77566	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9800466_c1_192	1261	6483	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
994002_f2_99.....	1262	6484	197	594	92	0.00034

Protein name

Locus Name

Acc#

probable prefoldin subunit APE1440

pir:G72622

G72622

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10647550_f2_40.....	1263	6485	812	2439	498	2.7e-45

Protein name

Locus Name

Acc#

putative transmembrane protein Wzc

gp:AF104912

AF104912

Description

Escherichia coli K30 capsule biosynthesis cluster, partial sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10985663_f1_25.....	1264	6486	101	306	75	0.034

Protein name

Locus Name

Acc#

nuclear factor kappa-B2

gp:HSU20816

U20816

Description

Human nuclear factor kappa-B2 (NF-KB2) gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
133301_f2_28	1265	6487	588	1767	1406	9.0e-144

Protein name

Locus Name

Acc#

sp:SYQ_ECOLI

Description

(GLNRS)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1350033_f1_11	1266	6488	224	675		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1381287_c2_91	1267	6489	172	519	470	1.4e-44

Protein name

Locus Name

Acc#

sp:TPX_MYCTU

P95282

Description

PROBABLE THIOL PEROXIDASE,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13859702_f3_54	1268	6490	379	1140	181	3.8e-11

Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13945437_c3_98	1269	6491	155	468	86	0.00077

Protein name

Locus Name

Acc#

sp:DBH_THEMA

P36206

Description

DNA-BINDING PROTEIN HU

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15738937_f1_24	1270	6492	104	315		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15909682...f3...52.....	1271	6493	212	639	137	1.9e-08

Protein name

Locus Name

Acc#

hypothetical protein Rv1624c

pir:F70558

F70558

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23475200...f1...8.....	1272	6494	482	1449	179	1.1e-10

Protein name

Locus Name

Acc#

conserved hypothetical protein MTH72

pir:B69196

B69196

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24070786_c2_97	1273	6495	254	762	356	1.7e-32

Protein name

Locus Name

Acc#

sp:YQGH_BACSU

P46339

Description

REGION (ORF72)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26438887_c3_100	1274	6496	424	1275		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29947188...f1...15.....	1275	6497	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30563966...f1...20.....	1276	6498	153	462	121	1.3e-07

Protein name

Locus Name

Acc#

hypothetical protein

pir:T28682

T28682

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34179077_f1_16	1277	6499	262	789	170	1.2e-10

Protein name

Locus Name

Acc#

sp:EPSA_BURSO

Q45407

Description

EPS I POLYSACCHARIDE EXPORT OUTER MEMBRANE PROTEIN EPSA PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36131937_c1_78	1278	6500	149	450	123	2.5e-07

Protein name

Locus Name

Acc#

phosphate-binding protein PstS

pir:H69097

H69097

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4176337_f3_55	1279	6501	470	1413	656	2.7e-64

Protein name

Locus Name

Acc#

GumD protein

pir:S67820

S67820

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4744002_c2_89	1280	6502	198	597	249	3.6e-21

Protein name

Locus Name

Acc#

hypothetical protein (repA 5' region)

pir:S30120

S30120

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4867127_f2_31	1281	6503	216	651	308	2.0e-27

Protein name

Locus Name

Acc#

DedA family protein

pir:B75253

B75253

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6721890_c3_99	1282	6504	163	492	270	2.1e-23

Protein name

Locus Name

Acc#

N-acetylmuramoyl-L-alanine amidase homolog

pir:G64126

G64126

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7313162_f1_4	1283	6505	285	858	410	3.1e-38

Protein name

Locus Name

Acc#

phosphate-binding protein PstS

pir:H69097

H69097

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1212751_c1_87	1284	6506	147	444		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14103176_c3_114	1285	6507	681	2046	246	2.5e-34

Protein name

Locus Name

Acc#

gp:PGU60208

U60208

Description

Porphyromonas gingivalis orf1, orf2 and orf3 genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
179762_c2_94	1286	6508	399	1200	465	9.2e-62

Protein name

Locus Name

Acc#

sp:YBDG_ECOLI

Description

HYPOTHETICAL 46.6 KD PROTEIN IN PHEP-NFNB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22063387_c2_92	1287	6509	620	1863	378	9.5e-67

Protein name

Locus Name

Acc#

alpha-1,3/4-fucosidase precursor

gp:SSU39394

U39394

Description

Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
238255_c3_113.....	1288	6510	322	969	106	0.0027

Protein name

Locus Name

Acc#

sp:YEHT_ECOLI

Description

HYPOTHETICAL 27.9 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24397305_c2_98.....	1289	6511	91	276		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24406550_c2_99	1290	6512	209	630	106	1.0e-05

Protein name

Locus Name

Acc#

gp:GGU25741

U25741

Description

Group G streptococcus strain g6 emmL gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25428436_c2_105	1291	6513	288	864		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25897507_f1_15.....	1292	6514	356	1071	105	0.038

Protein name

Locus Name

Acc#

probable extracellular nuclease

pir:D75625

D75625

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26210912_c3_117.....	1293	6515	408	1227	109	0.0058

Protein name

Locus Name

Acc#

silent surface layer protein

gp:AF079365

AF079365

Description

Lactobacillus crispatus silent surface layer protein (cbsB) gene,partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
265878_f3_62	1294	6516	114	345	80	0.043

Protein name

Locus Name

Acc#

MAR binding filament-like protein 1:MFP1
protein

pir:T07111

T07111

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2845427_c1_89.....	1295	6517	939	2820	132	0.00012

Protein name

Locus Name

Acc#

sp:PFEA_PSEAE

Q05098

Description

FERRIC ENTEROBACTIN RECEPTOR PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30192086_c1_76.....	1296	6518	566	1701	831	7.7e-83

Protein name

Locus Name

Acc#

sp:BGAL_THEMA

Description

BETA-GALACTOSIDASE, (LACTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31256287_c3_116.....	1297	6519	641	1926	730	3.9e-72

Protein name

Locus Name

Acc#

DNA-directed DNA polymerase, III chain
dnaX:DNA polymerase III (gamma and tau
subunits) dnaX

pir:S13786

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34570437_f2_47	1298	6520	492	1479	1142	8.5e-116

Protein name

Locus Name

Acc#

sp:PEPD_ECOLI

P15288

Description

(PEPTIDASE D)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35990807_c1_79	1299	6521	222	669	611	1.6e-59

Protein name

Locus Name

Acc#

transaldolase-related protein

pir:G72394

G72394

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4101555_c2_102.....	1300	6522	332	999	144	2.0e-09

Protein name

Locus Name

Acc#

gp:APU72238

U72238

Description

Anabaena PCC7120 ORFR1, ORFR2, ORFR3, ORFR4, and ORFR5 genes, complete sequences.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
447825_c3_106.....	1301	6523	502	1509	977	2.6e-98

Protein name

Locus Name

Acc#

sp:BGAL_BACME

O52847

Description

BETA-GALACTOSIDASE, (LACTASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4961691_f2_39	1302	6524	117	354		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15112533_f3_19	1303	6525	355	1068	210	5.1e-15

Protein name

Locus Name

Acc#

probable proteinase PAB1960

pir:A75179

A75179

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15820341_f2_14	1304	6526	157	474		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
204811_f2_16	1305	6527	274	825	105	0.012

Protein name

Locus Name

Acc#

gp:ATAC012563

AC012563

Description

Arabidopsis thaliana chromosome I BAC T23K23 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21664062_f1_5	1306	6528	168	507		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26604687_f2_12	1307	6529	205	618		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33456962_f1_2	1308	6530	293	882		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4098437_f1_1	1309	6531	268	807	115	0.00062

Protein name

Locus Name

Acc#

sp:Y066_METJA

Q60377

Description

HYPOTHETICAL PROTEIN MJ0066

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6837782_f1_4	1310	6532	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9939142_f1_3	1311	6533	115	348		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10041563_c1_120	1312	6534	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10726552_c3_185	1313	6535	80	243		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12500086_c1_119	1314	6536	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13860653_c3_194	1315	6537	488	1467	1040	5.5e-105

Protein name	Locus Name	Acc#
cell division protein	gp:PAL249201	AJ249201

Description

Prevotella albensis ftsQ (partial), ftsA and ftsZ genes and ORF-fts (partial).

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14298312_c1_131	1316	6538	489	1470	1275	6.8e-130

Protein name	Locus Name	Acc#
	sp:MURC_PORGI	Q51831

Description

ACETYLMURANOYL-L-ALANINE SYNTHETASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14644152_c2_164	1317	6539	254	765	341	6.4e-31

Protein name	Locus Name	Acc#
FtsQ	gp:AB004555	AB004555

Description

Porphyromonas gingivalis genes for FtsQ, FtsA, FtsZ, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
164651_c2_169	1318	6540	669	2010	3334	0.0

Protein name	Locus Name	Acc#
DNA gyrase B subunit	gp:AB017713	AB017713

Description

Bacteroides fragilis gyrB gene for DNA gyrase B subunit, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16593937_c1_127	1319	6541	435	1308	388	6.7e-36

Protein name

Locus Name

Acc#

sp:YLAO_BACSU

007639

Description

HYPOTHETICAL 43.7 KD PROTEIN IN NPPE-PYCA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16808437_c3_192	1320	6542	135	408	223	6.9e-18

Protein name

Locus Name

Acc#

UDP-N-acetylmuramoylalanine-D-glutamate
ligase

pir:H70477

H70477

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
177253_c1_137	1321	6543	66	201	62	0.047

Protein name

Locus Name

Acc#

Orf10c

gp:SCU42227

U42227

Description

Saccharomyces cerevisiae replicative mitochondrial DNA polymerase catalytic subunit (MIP1) gene, nuclear gene encoding mitochondrial protein, partial cds, and putative 10-formyl-tetrahydrofolate binding protein (FTB1) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19808211_c1_135	1322	6544	181	546	289	2.1e-25

Protein name

Locus Name

Acc#

hypothetical protein 1

pir:S70830

S70830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20010316_f2_72	1323	6545	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2149013_c3_187.....	1324	6546	343	1032	614	7.6e-60

Protein name

Locus Name

Acc#

unknown

gp:EFU94707

U94707

Description

Enterococcus faecalis strain A24836 cell wall/cell division genecluster, yllB, yllC, yllD, pbpC, mraY, murD, murG, divlB, ftsA andftsZ genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2151417_f3_78.....	1325	6547	180	543	186	2.5e-13

Protein name

Locus Name

Acc#

sp:YGY4_HALSQ

P21562

Description

HYPOTHETICAL 80.2 KD PROTEIN IN THE 5' REGION OF GYRA AND GYRB (ORF 4)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22303400_c2_166.....	1326	6548	442	1329	1291	1.4e-131

Protein name

Locus Name

Acc#

cell division protein

gp:PAL249201

AJ249201

Description

Prevotella albensis ftsQ (partial), ftsA and ftsZ genes and ORF-fts (partial).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23468837_f3_100	1327	6549	171	516		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23646942_c1_126.....	1328	6550	328	987	368	8.9e-34

Protein name

Locus Name

Acc#

sp:MURD_BACSU

Description

ADDING ENZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24072177_c3_175.....	1329	6551	452	1359	730	3.9e-72

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76527

S76527

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24413875_c2_167.....	1330	6552	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24414077_f1_33	1331	6553	208	627		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
245643_f3_75	1332	6554	140	423	146	4.8e-09

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:H75460

H75460

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24658577_f2_68	1333	6555	113	342		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25832161_f2_41	1334	6556	880	2643		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2620187_f3_96	1335	6557	217	654		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26750336_f1_37	1336	6558	347	1044	1218	7.5e-124

Protein name

Locus Name

Acc#

hemolysin A

gp:PMU27587

U27587

Description

Prevotella melaninogenica hemolysin A (phyA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2931518_c3_189	1337	6559	486	1461	892	2.6e-89

Protein name

Locus Name

Acc#

UDP-MurNac-tripeptide synthetase

pir:E70450

E70450

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30166437_c3_191	1338	6560	82	249	75	1.5e-06

Protein name

Locus Name

Acc#

phospho-n-acetylmuramoyl-pentapeptide-transferase (mraY1) RP595

pir:E71664

E71664

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31534452_f1_40	1339	6561	595	1788	342	1.6e-28

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_854

pir:B70374

B70374

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3166057_c2_163	1340	6562	389	1170	641	1.0e-62

Protein name

Locus Name

Acc#

sp:MURG_BACSU

Description

(EC 2.4.1.-)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33398557_f3_102	1341	6563	206	621		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33787927_f1_39.....	1342	6564	150	453	419	3.5e-39

Protein name

Locus Name

Acc#

sp:DUT_AQUAE

066592

Description

(DUTPASE) (DUTP PYROPHOSPHATASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33986038_f1_35.....	1343	6565	723	2172	164	9.8e-15

Protein name

Locus Name

Acc#

putative TonB-dependent outer membrane
receptor

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete
sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34260912_c1_122	1344	6566	118	357	75	0.0099

Protein name

Locus Name

Acc#

hypothetical protein 2

pir:140759

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
37542_c2_153.....	1345	6567	198	597	229	4.8e-19

Protein name

Locus Name

Acc#

probable RNA polymerase sigma factor

pir:T42015

T42015

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
390927_f1_11.....	1346	6568	168	507	190	2.7e-14

Protein name

Locus Name

Acc#

gp:AB028868

AB028868

Description

Mus musculus P4(21)n mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3992135_f3_95.....	1347	6569	122	369		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4079668_f2_66	1348	6570	414	1245	105	0.032

Protein name

Locus Name

Acc#

RING finger protein

gp:AF036255

AF036255

Description

Rattus norvegicus RING finger protein mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4174013_f1_7	1349	6571	265	798	101	6.7e-05

Protein name

Locus Name

Acc#

RecO

gp:HIU17037

U17037

Description

Haemophilus influenzae opacity associated proteins OapA and OapB (oapA and oapB) genes, complete cds, and DNA recombination and repair protein (recO) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4875812_c3_186	1350	6572	171	516	84	0.0019

Protein name

Locus Name

Acc#

DNA-binding protein HB:DNA-binding protein HU:DNA-binding protein II

pir:S00015

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4957837_f2_65	1351	6573	352	1059		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5117268_c1_121	1352	6574	160	483	177	1.5e-13

Protein name

Locus Name

Acc#

sp:YABB_ECOLI

P22186

Description

HYPOTHETICAL 17.4 KD PROTEIN IN FRUR-FTSL INTERGENIC REGION (ORF)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5994087_c1_123	1353	6575	708	2127	337	2.1e-34

Protein name

Locus Name

Acc#

sp:SP5D_BACSU

Q03524

Description

BINDING PROTEIN)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6072683_c1_125	1354	6576	376	1131	344	8.1e-51

Protein name

Locus Name

Acc#

sp:MRAY_BORBU

Q44776

Description

(UDP-MURNAC-PENTAPEPTIDE PHOSPHOTRANSFERASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6649037_c2_168	1355	6577	89	270	153	5.4e-11

Protein name

Locus Name

Acc#

probable ribosomal protein S20 rpS1

pir:G70684

G70684

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6758437_f1_36	1356	6578	286	861	186	7.0e-13
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
probable sulfolipid biosynthesis protein SqdA			pir:A42380			A42380
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10328140_f1_3	1357	6579	71	216		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10442793_f3_46	1358	6580	115	348		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10744192_c1_95	1359	6581	281	846	153	8.1e-08
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
potassium channel alpha subunit Kv2.2			gp:XLU20342			U20342
<u>Description</u>						

Xenopus laevis potassium channel alpha subunit Kv2.2 (XShab12)mRNA, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12518961_c2_100	1360	6582	325	978	241	5.2e-28
Protein name			Locus Name			Acc#
probable protoporphyrinogen oxidase (hemK) RP847			pir:G71646			G71646
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14256430_f2_37.....	1361	6583	191	576	445	6.1e-42
Protein name			Locus Name			Acc#
conserved hypothetical protein MTH700			pir:E69193			E69193
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14508510_f3_76.....	1362	6584	62	186		
Protein name			Locus Name			Acc#
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15835436_c3_152.....	1363	6585	308	927	228	6.1e-19
Protein name			Locus Name			Acc#
hypothetical protein yitL			pir:E69840			E69840
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16892517_c3_134.....	1364	6586	70	213		
Protein name			Locus Name			Acc#
Description						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19953510_c2_102	1365	6587	457	1374	626	4.1e-61

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
argininosuccinate lyase	pir:D70419	D70419

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23673455_c1_80.....	1366	6588	161	486	126	3.9e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RECX_PSEAE	P37860

Description

REGULATORY PROTEIN RECX

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24026562_f3_59.....	1367	6589	415	1248	567	7.2e-55

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ASSY_METJA	Q60174

Description

LIGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24300018_c3_133.....	1368	6590	166	501		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24353376_f1_6	1369	6591	533	1602	1279	2.6e-130

Protein name

Locus Name

Acc#

gp:AB024946

AB024946

Description

Escherichia coli plasmid pB171 DNA, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25663952_f1_2	1370	6592	188	567	280	1.9e-24

Protein name

Locus Name

Acc#

sp:MTGA_ACICA

O24849

Description

(EC 2.4.2.-) (MONOFUNCTIONAL TGASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25975187_c3_153	1371	6593	221	666		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26369087_f2_44	1372	6594	347	1044	554	1.7e-53

Protein name

Locus Name

Acc#

riboflavin-specific deaminase

pir:G72207

G72207

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32228388_c2_122	1373	6595	252	759	113	0.0016

Protein name

Locus Name

Acc#

sp:HEXA_BLADI

Q17127

Description

HEXAMERIN PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33367175_c3_131	1374	6596	163	492		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36211443_f2_35	1375	6597	326	981	548	7.5e-53

Protein name

Locus Name

Acc#

N-acetyl-gamma-glutamyl-phosphate reductase,

pir:F69508

F69508

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4007801_c2_121	1376	6598	228	687		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4095050_f3_61	1377	6599	260	783	375	1.6e-34
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
pyrroline-5-carboxylate reductase			gp:CSAJ10739		AJ010739	
<u>Description</u>						
Clostridium sticklandii proC gene and 5' flanking region.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4377005_c3_130	1378	6600	230	693	541	4.1e-52
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:PYRE_BACSU		P25972	
<u>Description</u>						
OROTATE PHOSPHORIBOSYLTRANSFERASE, (OPRT) (OPRTASE)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4801552_f2_45	1379	6601	458	1377		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4804051_f2_34	1380	6602	203	612		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4804813_f2_36	1381	6603	377	1134	670	8.8e-66

Protein name

Locus Name

Acc#

sp:ARGD_BACSU

P36839

Description

ACETYLORNITHINE AMINOTRANSFERASE, (ACOAT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5110712_c2_114	1382	6604	413	1242	398	1.3e-37

Protein name

Locus Name

Acc#

sensory transduction histidine kinase
slr2104:protein slr2104:protein slr2104

pir:S75136

S75136

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5131925_c1_81	1383	6605	659	1980	108	0.033

Protein name

Locus Name

Acc#

hypothetical protein F10M10.30

pir:T04772

T04772

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5270050_f2_33	1384	6606	160	483	254	1.1e-21

Protein name

Locus Name

Acc#

arginine repressor

gp:BSAJ10954

AJ010954

Description

Bacillus stearothermophilus argR gene and partial recN gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5270302_f1_11	1385	6607	554	1665	1248	5.0e-127
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
acetyl-CoA synthetase related protein			pir:F69193		F69193	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
994002_f3_53	1386	6608	334	1005	273	1.0e-23
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable malate dehydrogenase, :2-ketoacid dehydrogenase:protein sll0891:2-ketoacid dehydrogenase:protein sll0891			pir:S75735		S75735	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10345327_f2_103	1387	6609	760	2283	410	7.8e-40
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10580052_f3_183	1388	6610	114	345		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10662877_c1_202	1389	6611	321	966	224	1.6e-18

Protein name

Locus Name

Acc#

putative transposase

gp:AF007429

AF007429

Description

Haemophilus paragallinarum IS-like putative transposase gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10725942_c3_342	1390	6612	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10819681_c2_294.....	1391	6613	138	417	170	8.5e-13

Protein name

Locus Name

Acc#

sp:MTGA_HAEIN

P44890

Description

(EC 2.4.2.-) (MONOFUNCTIONAL TGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11035088_c2_306.....	1392	6614	333	1002	1634	6.2e-168

Protein name

Locus Name

Acc#

mobilization protein B

gp:AF118242

AF118242

Description

Bacteroides fragilis mobilization protein B (mobB) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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11832332_f1_34	1393	6615	322	969		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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11881313_c3_349	1394	6616	288	867	113	0.00062
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Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF060193

AF060193

Description

Pseudomonas aeruginosa pigACDE operon, complete sequence;hypothetical PigB (pigB) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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12109558_c2_272	1395	6617	148	447	156	5.1e-11
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Protein name

Locus Name

Acc#

collagen-like protein

gp:BTU67921

U67921

Description

Bacillus thuringiensis plasmid pTX14-1, MOB, REP, and collagen-likeprotein genes, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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1271010_c3_387	1396	6618	96	291		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13071943_c1_216	1397	6619	466	1401	397	7.5e-37
Protein name			Locus Name		Acc#	
conserved hypothetical protein			pir:H72331		H72331	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13750800_c1_207	1398	6620	78	237		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13806517_t2_85	1399	6621	401	1206	169	1.0e-09
Protein name			Locus Name		Acc#	
transposase			gp:AF038866		AF038866	
Description						

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14469691_c1_213	1400	6622	193	582	199	7.2e-16
Protein name			Locus Name		Acc#	
RNA polymerase sigma factor SigZ-like protein			gp:AF137263		AF137263	
Description						

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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14589067_f3_150	1401	6623	93	282		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

14663552_f2_77	1402	6624	296	891	116	0.00021
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Protein name

Locus Name

Acc#

sp:LCRF_YERPE

P28808

Description

THERMOREGULATORY PROTEIN LCRF

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

14723156_f2_132	1403	6625	123	372	83	0.029
-----------------	------	------	-----	-----	----	-------

Protein name

Locus Name

Acc#

hypothetical protein aq_2087

pir:H70478

H70478

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

14875302_c1_267	1404	6626	162	489		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

15659758_f1_51	1405	6627	63	192		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

15671890_g3_394	1406	6628	428	1287	191	3.9e-12
-----------------	------	------	-----	------	-----	---------

Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

15736057_f1_29	1407	6629	523	1572	2044	2.2e-211
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Protein name

Locus Name

Acc#

sp:TRA2_BACFR

Q45119

Description

TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS21-LIKE

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

15829061_g1_200	1408	6630	478	1437	468	2.2e-44
-----------------	------	------	-----	------	-----	---------

Protein name

Locus Name

Acc#

sp:PPOX_MYXXA

P56601

Description

PROTOPORPHYRINOGEN OXIDASE, (PPO)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
-----------------	-------------	-------------	------------------	------------------	--------------	--------------------

16491593_c2_279	1409	6631	157	474		
-----------------	------	------	-----	-----	--	--

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
-----------------	-------------	-------------	------------------	------------------	--------------	--------------------

19531438_f1_49	1410	6632	88	267		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
-----------------	-------------	-------------	------------------	------------------	--------------	--------------------

19937637_f2_111	1411	6633	62	189		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
-----------------	-------------	-------------	------------------	------------------	--------------	--------------------

2145012_f3_156	1412	6634	67	204	95	0.00024
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Protein name

Locus Name

Acc#

hypothetical 26.8K protein

pir:JC2322

JC2322

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
-----------------	-------------	-------------	------------------	------------------	--------------	--------------------

21683280_c3_350	1413	6635	527	1584		
-----------------	------	------	-----	------	--	--

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

22459687_c3_347	1414	6636	187	564		
-----------------	------	------	-----	-----	--	--

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

22691552_c1_262	1415	6637	434	1305	140	2.7e-06
-----------------	------	------	-----	------	-----	---------

Protein name

Locus Name

Acc#

immunoreactive 53 kD antigen PG123

gp:AF144641

AF144641

Description

Porphyromonas gingivalis strain W50 immunoreactive 53 kD antigenPG123 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

22692067_c1_233	1416	6638	324	975	445	6.1e-42
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Protein name

Locus Name

Acc#

sp:HTPX_STRGC

O30795

Description

PUTATIVE HEAT SHOCK PROTEIN HTPX

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

22836061_f2_82	1417	6639	133	402	97	0.00018
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Protein name

Locus Name

Acc#

MbpB

gp:BFU25716

U25716

Description

Bacteroides fragilis mobilization protein MbpA (mbpA), MbpB (mbpB) and MbpC (mbpC) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22933438_c3_397	1418	6640	322	969		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22933438_f1_21	1419	6641	242	729		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23495700_f2_138	1420	6642	67	204		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23531265_f3_149	1421	6643	216	651		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23648392_f2_86	1422	6644	431	1296	141	2.1e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 53 kD antigen PG123	gp:AF144641	AF144641

Description

Porphyromonas gingivalis strain W50 immunoreactive 53 kD antigenPG123 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23679510_c3_345	1423	6645	197	594	345	2.4e-31

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative acetyltransferase	gp:SCF1	AL117322

Description

Streptomyces coelicolor cosmid F1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24026502_f1_27	1424	6646	88	267		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24259637_c3_336	1425	6647	690	2073	253	3.1e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF079317	AF079317

Description

Sphingomonas aromaticivorans plasmid pNL1, complete plasmidsequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24332035_c1_197	1426	6648	83	252		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24407551_c2_293.....	1427	6649	231	696	427	5.0e-40

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

immunogenic 23 kDa lipoprotein PG3	gp:AF145799	AF145799
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Description

Porphyromonas gingivalis strain W50 immunogenic 23 kDa lipoproteinPG3 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415757_c3_348.....	1428	6650	424	1275		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24641061_f2_96.....	1429	6651	316	951	147	9.5e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

vr1E protein	pir:T17384	T17384
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Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24642137_f1_62	1430	6652	401	1206	176	2.9e-11

Protein name

Locus Name

Acc#

putative outer membrane porin

gp:AF030977

Description

Vibrio cholerae glutamyl tRNA synthetase (gltX) gene, partial cds; putative outer membrane porin (ompA), unknown protein, vibriobactin receptor precursor (viuA), and ViuB protein (viuB) genes, complete cds; and VibF (vibF) gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24642212_f2_110	1431	6653	301	906	631	1.2e-61

Protein name

Locus Name

Acc#

sp:YBFH_BACSU

031448

Description

HYPOTHETICAL 33.8 KD PROTEIN IN GLPT-PUT INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24647826_f1_28	1432	6654	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24725380_c1_245	1433	6655	186	561	593	1.3e-57

Protein name

Locus Name

Acc#

mobilization protein A

gp:AF118241

AF118241

Description

Bacteroides fragilis mobilization protein A (mobA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24726592_c3_355	1434	6656	152	459	339	1.0e-30

Protein name

Locus Name

Acc#

sp:MTGA_ECOLI

P46022

Description

(EC 2.4.2.-) (MONOFUNCTIONAL TGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24803426_c1_210	1435	6657	204	615	120	1.9e-06

Protein name

Locus Name

Acc#

hypothetical protein MTH847

pir:A69213

A69213

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24847551_c2_302.....	1436	6658	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2538277_c2_282.....	1437	6659	105	318	120	1.7e-07

Protein name

Locus Name

Acc#

hypothetical protein ydaT

pir:C69770

C69770

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25511052_c1_232	1438	6660	206	621	401	2.8e-37

Protein name

Locus Name

Acc#

LemA

gp:LMU66186

U66186

Description

Listeria monocytogenes LemA (lemA) gene, complete cds, and LemB(lemB) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25527053_f1_22	1439	6661	436	1311		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26354518_f2_95	1440	6662	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2767137_c1_266	1441	6663	887	2664	128	0.00031

Protein name

Locus Name

Acc#

hypothetical protein H02F09.3

pir:T33369

T33369

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2792942_f2_70	1442	6664	87	264		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29713458_f2_83.....	1443	6665	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31923438_g2_291.....	1444	6666	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32213312_f3_163.....	1445	6667	171	516	237	6.8e-20

Protein name

Locus Name

Acc#

putative ECF sigma factor RpoE1

gp:AF049107

AF049107

Description

Myxococcus xanthus response regulator FrzZ (frzZ) gene, partialcds; alanine dehydrogenase (aldA), putative ECF sigma factor RpoE1(rpoE1), and response regulator homolog (frzS) genes, complete cds;and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33214538_f3_155	1446	6668	744	2235		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33486716_c2_276.....	1447	6669	497	1494	793	8.2e-79

Protein name

Locus Name

Acc#

sp:HEMN_AQUAE

067886

Description

OXYGEN-INDEPENDENT COPROPORPHYRINOGEN II

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33632692_c1_229.....	1448	6670	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34181502_f2_122.....	1449	6671	426	1281	134	6.9e-06

Protein name

Locus Name

Acc#

probable carboxy-terminal proteinase, D1

pir:T05975

T05975

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35302_f1_52	1450	6672	203	612		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3.942130...c1...264.....	1451	6673	388	1167	86	0.0055

Protein name

Locus Name

Acc#

integrase

gp:HIVU69223

U69223

Description

HIV-1 strain CMR273 from Cameroon integrase (pol) gene, partialcds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3.954762...f3...187.....	1452	6674	291	876	111	6.4e-06

Protein name

Locus Name

Acc#

transcription regulator homolog: hypothetical
137 protein

pir:PC4110

PC4110

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4.114055...c3...337.....	1453	6675	415	1248	288	5.0e-24

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF149851

AF149851

Description

Pseudomonas sp. KC hypothetical proteins, methallothionein-likeprotein, MoeB-like protein, putative proteins, hypotheticalprotein, putative oxidoreductase, and putative AMP ligase (entE)genes, complete cds; and putative receptor gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4720187_f2_99	1454	6676	283	852	954	7.1e-96

Protein name

Locus Name

Acc#

sp:ISTB_BACFR

Q45120

Description

INSERTION SEQUENCE IS21-LIKE PUTATIVE ATP-BINDING PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4822751_f2_101	1455	6677	594	1785	370	1.8e-48

Protein name

Locus Name

Acc#

oxaloacetate decarboxylase, subunit alpha
(oadA) homolog

pir:C69406

C69406

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4864702_f2_124	1456	6678	152	459		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4879635_f1_61	1457	6679	772	2319	214	4.6e-14

Protein name

Locus Name

Acc#

collagen

gp:AB008933

AB008933

Description

Hydra vulgaris HT2 mRNA for collagen, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5177157_f2_88	1458	6680	182	549		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5285692_c2_281	1459	6681	86	261		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5321932_f1_53	1460	6682	234	705		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
564037_c3_346	1461	6683	282	849	229	4.8e-19
Protein name			Locus Name		Acc#	
hypothetical protein			pir:B72308		B72308	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5970252_c2_316	1462	6684	61	186		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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6025010_c3_333	1463	6685	74	225		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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6046907_f1_35	1464	6686	636	1911		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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6775438_c3_401	1465	6687	124	375		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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785322_f1_64	1466	6688	584	1752	220	2.7e-20
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Protein name

Locus Name

Acc#

sp:FECA_ECOLI

P13036

Description

IRON(III) DICITRATE TRANSPORT PROTEIN FECA PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15808290_c1_33	1467	6689	61	186	99	2.8e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glycine-rich protein (clone w10-1)	pir:S14982	S14982

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19659503_c1_32	1468	6690	383	1152		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26367141_c1_30	1469	6691	292	879	130	3.5e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

membrane glycoprotein	gp:D88733	D88733
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Description

Equine herpesvirus 1 DNA for membrane glycoprotein, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26425336_c2_38	1470	6692	250	753		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34666302_c3_43	1471	6693	495	1488	213	1.3e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 53 kD antigen PG123	gp:AF144641	AF144641

Description

Porphyromonas gingivalis strain W50 immunoreactive 53 kD antigenPG123 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
807033_c1_29	1472	6694	112	339		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11063391_c2_40.....	1473	6695	344	1035	452	1.1e-42

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YF23_HAEIN	P44243

Description

HYPOTHETICAL PROTEIN HI1523

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14348958_f2_14.....	1474	6696	87	264		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14650012_f3_26	1475	6697	145	435	73	0.022

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glucosidase II beta-subunit	gp:AF066061	AF066061

Description

Mus musculus glucosidase II beta-subunit gene, alternatively spliced products, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15835261_c1_28	1476	6698	116	351		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23472832_c1_31	1477	6699	366	1101	454	6.8e-43

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:CBH_CLOPE	P54965

Description

HYDROLASE) (CBAH) (BILE SALT HYDROLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24337962_f1_6	1478	6700	62	189		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24798401_f1_2	1479	6701	141	426		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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30355305_f3_24	1480	6702	271	816	409	4.0e-38
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Protein name

Locus Name

Acc#

sp:SOJ_BACSU

P37522

Description

SOJ PROTEIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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33882837_f3_25	1481	6703	97	294	80	0.024
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Protein name

Locus Name

Acc#

hypothetical protein F20D10.230

pir:T05638

T05638

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4407575_f2_12	1482	6704	522	1569	115	2.8e-10
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Protein name

Locus Name

Acc#

endo-xylanase homolog PCZA361.14

pir:T17480

T17480

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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5869167_f1_7	1483	6705	73	222		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6838437_f1_1	1484	6706	422	1269	100	0.0024

Protein name

Locus Name

Acc#

outer membrane protein

gp:BNROMPB

L77614

Description

Bacteroides thetaiotaomicron outer membrane protein (susD) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10547256_f2_6	1485	6707	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11126552_c2_14	1486	6708	152	459	95	7.5e-05

Protein name

Locus Name

Acc#

hypothetical protein aq_1018

pir:H70387

H70387

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2117841_f1_1	1487	6709	749	2250		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26682828_c3_19	1488	6710	136	411	93	0.023
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
surface exclusion protein sepl precursor			pir:S72375		S72375	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31417187_c1_10	1489	6711	261	786		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6035687_c2_18	1490	6712	265	795	1378	8.3e-141
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
fructanase			pir:A36915		A36915	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
85912_c1_11	1491	6713	790	2373	2229	5.5e-231
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:BNRSCRL		M83774	
<u>Description</u>						

Bacteroides fragilis levanase (scrL) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14333277_c1_10	1492	6714	127	384		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15735882_f3_5	1493	6715	400	1203	696	1.5e-68

Protein name	Locus Name	Acc#
renin-binding protein-related protein:protein slr1975:protein slr1975	pir:S75649	S75649

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26819566_f3_4	1494	6716	73	222		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31381_f3_6	1495	6717	417	1254	280	8.7e-23

Protein name	Locus Name	Acc#
hexuronate transporter homolog yjmg	pir:A69853	A69853

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3956707_f1_1	1496	6718	149	450	126	1.4e-07

Protein name	Locus Name	Acc#
N-acetylneuraminate lyase	gp:CPNANA	Y12876

Description

C.perfringens gene encoding N-acetylneuraminate lyase and twopartial open reading frames.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5117337_f2_3	1497	6719	150	453	201	4.4e-16

Protein name

Locus Name

Acc#

sp:YHCH_HAEIN

P44583

Description

HYPOTHETICAL PROTEIN HI0227

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781932_f3_7	1498	6720	698	2094	543	3.1e-53

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC
protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11209542_c3_31.....	1499	6721	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24023442_c3_32.....	1500	6722	329	990	630	1.5e-61

Protein name

Locus Name

Acc#

metabolite transporter homolog yfnA

pir:D69814

D69814

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25433212_f1_2	1501	6723	116	351	193	5.1e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
alpha-N-acetylglucosaminidase	gp:NTA18209	Y18209

Description

Nicotiana tabacum mRNA for alpha-N-acetylglucosaminidase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26681533_c2_26	1502	6724	202	609	327	3.5e-29

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable cationic amino acid transporter	pir:T34694	T34694

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29931309_c1_18	1503	6725	432	1299	195	1.9e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 52kD antigen PG41	gp:AF175716	AF175716

Description

Porphyromonas gingivalis strain W50 immunoreactive 52kD antigenPG41 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30516442_f1_1	1504	6726	446	1341	618	2.9e-60

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ANAG_HUMAN	P54802

Description

GLUCOSAMINIDASE) (NAG)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10580062_c2_93	1505	6727	301	903	279	8.0e-24

Protein name

Locus Name

Acc#

60kDa protein

gp:AB004560

AB004560

Description

Porphyromonas gingivalis DNA for 60kDa protein, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13175950_c2_91	1506	6728	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13869000_c2_78.....	1507	6729	999	3000	886	1.6e-109

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14347666_f2_26.....	1508	6730	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14647808_f2_20	1509	6731	287	864	126	4.3e-06

Protein name

Locus Name

Acc#

sp:YDIP_ECOLI

P77402

Description

HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AROD-PPS INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14660892_c1_74	1510	6732	207	624		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15835062_f1_18	1511	6733	96	291	78	0.0048

Protein name

Locus Name

Acc#

hypothetical protein c04005

pir:S75372

S75372

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20007812_c3_102	1512	6734	467	1404	195	1.7e-12

Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22683287_f3_56	1513	6735	486	1461		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24492177_c2_88	1514	6736	342	1029		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24895165_f1_13	1515	6737	65	198	47	0.029

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein T11B7.2	pir:T24826	T24826
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26771041_c3_94	1516	6738	260	783	417	5.7e-39

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein C33G8.2	pir:T34137	T34137
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33772811_f3_47	1517	6739	109	330		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34510418_c1_63	1518	6740	259	780	424	1.0e-39
Protein name			Locus Name		Acc#	
hypothetical protein F36H12.3			pir:T33457		T33457	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35734500_c2_79	1519	6741	512	1539	202	7.9e-13
Protein name			Locus Name		Acc#	
unknown			gp:U96771		U96771	
Description						

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36198958_c2_76	1520	6742	278	837	430	2.4e-40
Protein name			Locus Name		Acc#	
hypothetical protein C33G8.2			pir:T34137		T34137	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36574092_c2_80	1521	6743	430	1293	545	3.1e-59
Protein name			Locus Name		Acc#	
			sp:YBDN_ECOLI		P77216	
Description						

HYPOTHETICAL 47.8 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
397175_c2_77	1522	6744	176	531		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4062906_c3_101	1523	6745	785	2358	130	1.3e-08

Protein name

Locus Name

Acc#

sp:FYUA_YEREN

P46360

Description

PESTICIN RECEPTOR PRECURSOR (IRPC) (IPR65)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4969091_c3_97	1524	6746	138	417		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5900377_c1_66	1525	6747	177	534	351	5.6e-32

Protein name

Locus Name

Acc#

sp:YBDM_ECOLI

P77174

Description

HYPOTHETICAL 23.9 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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6485055_c2_89	1526	6748	92	279		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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103287_f3_99	1527	6749	501	1506	479	1.5e-45
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Protein name

Locus Name

Acc#

immunoreactive 51kD antigen PG52

gp:AF175719

AF175719

Description

Porphyromonas gingivalis strain W50 immunoreactive 51kD antigenPG52 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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11976562_c3_189	1528	6750	61	186		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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12304718_f1_2	1529	6751	518	1557	139	3.1e-13
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Protein name

Locus Name

Acc#

sp:BGAL_THEET

P77989

Description

BETA-GALACTOSIDASE, (LACTASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13704552_c1_129	1530	6752	496	1491	1403	1.9e-143

Protein name	Locus Name	Acc#
	sp:6PGD_TREPA	083351

Description

6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13758530_c3_190	1531	6753	136	411		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13907312_c3_186.....	1532	6754	74	225	77	0.0096

Protein name	Locus Name	Acc#
putative signal transduction protein GarA	gp:AF173844	AF173844

Description

Mycobacterium smegmatis garA-containing gene cluster, partial sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13962757_c2_175.....	1533	6755	383	1152	350	7.2e-32

Protein name	Locus Name	Acc#
cytochrome d oxidase subunit II	gp:AF001503	AF001503

Description

Salmonella typhimurium cytochrome d oxidase subunit I (cydA) and cytochrome d oxidase subunit II (cydB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1444627_c1_132	1534	6756	62	189	58	0.039
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ribosomal protein S5			gp:U87145		U87145	
<u>Description</u>						
Toxoplasma gondii chloroplast, complete genome.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16441305_f3_103	1535	6757	236	711	244	1.2e-20
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein b2381			pir:B65012		B65012	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16517156_f3_101.....	1536	6758	450	1353	717	9.2e-71
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:S76946		S76946	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
194128_c1_130.....	1537	6759	84	255	63	0.0078
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
p20-CGGBP			gp:HSCGGBP		AJ000258	
<u>Description</u>						
Homo sapiens trinucleotide repeat 5-d(CGG)n-3ds binding proteinp20-CGGBP.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19687836_f3_87	1538	6760	429	1290	945	6.4e-95

Protein name

Locus Name

Acc#

sp:YCAJ_HAEIN

P45262

Description

HYPOTHETICAL PROTEIN HI1590

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2068766_c1_143	1539	6761	525	1578	1098	3.9e-111

Protein name

Locus Name

Acc#

sp:CYDA_AZ0VI

Q09049

Description

CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20735878_c2_163	1540	6762	142	429		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2204377_f2_70	1541	6763	446	1341	911	2.6e-91

Protein name

Locus Name

Acc#

RumB(R391)

gp:XXU13633

U13633

Description

IncJ plasmid R391 rumA(R391) and rumB(R391) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22273312_c1_131	1542	6764	287	864	271	1.7e-23

Protein name

Locus Name

Acc#

urea transport protein

gp:AF167577

AF167577

Description

Actinobacillus pleuropneumoniae transcriptional regulator (apuR) gene, partial cds; and putative periplasmic binding protein (cbiK), putative cytoplasmic membrane protein (cbiL), cobalt membranetransport protein homolog (cbiM), cobalt membrane transport proteinhomolog (cbiQ), cobalt transport ATP-binding protein homolog(cbiO), and urea transport protein

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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22535925_c2_176	1543	6765	359	1080	184	2.2e-12
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Protein name

Locus Name

Acc#

molybdate metabolism regulator

pir:B64979

B64979

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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22941306_f2_62	1544	6766	258	777	651	9.1e-64
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Protein name

Locus Name

Acc#

ABC transporter, ATP-binding protein

pir:H72385

H72385

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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23985880_f1_26	1545	6767	105	318		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24100265_c3_188	1546	6768	505	1518	1300	1.5e-132

Protein name

Locus Name

Acc#

sp:G6PD_ACTAC

P77809

Description

GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, (G6PD)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24229800_f3_98	1547	6769	79	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24647180_c3_191	1548	6770	690	2073	101	0.0017

Protein name

Locus Name

Acc#

hypothetical protein MTH357

pir:A69146

A69146

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25517013_f1_1	1549	6771	297	894	392	3.8e-35

Protein name

Locus Name

Acc#

putative secreted beta-galactosidase

gp:SCF81

AL133171

Description

Streptomyces coelicolor cosmid F81.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25667675_c3_205	1550	6772	341	1026		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25970016_f3_100.....	1551	6773	411	1236	326	2.5e-29

Protein name

Locus Name

Acc#

probable membrane protein b0878

pir:F64826

F64826

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31769537_f1_24.....	1552	6774	206	621	222	2.0e-17

Protein name

Locus Name

Acc#

sp:YEHU_ECOLI

Description

HYPOTHETICAL 62.1 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION PRECURSOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31886308_c2_159.....	1553	6775	259	780	387	8.6e-36

Protein name

Locus Name

Acc#

probable glucose-6-phosphate 1-dehydrogenase

pir:C71319

C71319

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3257635_c1_134.....	1554	6776	426	1281		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34382687_c3_193	1555	6777	419	1260		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3945257_f3_102	1556	6778	158	477		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4103890_c1_147	1557	6779	515	1548	145	9.4e-08
Protein name			Locus Name		Acc#	
conserved hypothetical protein AF0444			pir:D69305		D69305	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4737662_f1_39	1558	6780	395	1188	578	4.9e-56
Protein name			Locus Name		Acc#	
probable glutamate/ aspartate transporter			pir:G71309		G71309	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5117762_f3_106	1559	6781	149	450	304	5.4e-27
Protein name			Locus Name		Acc#	
RumA(R391)			gp:XXU13633		U13633	
Description						

IncJ plasmid R391 rumA(R391) and rumB(R391) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5275250_f2_47	1560	6782	319	960	554	1.7e-53

Protein name

Locus Name

Acc#

sp:DHGY_METEX

Q59516

Description

REDUCTASE) (HPR-A)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
7287787_c1_133	1561	6783	267	804		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9.7.7.0.13.7_c1_145.....	1562	6784	287	864	109	5.1e-09

Protein name

Locus Name

Acc#

gp:AB016260

Description

Agrobacterium tumefaciens plasmid pTi-SAKURA, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9922057_c3_206.....	1563	6785	432	1299	293	8.0e-26

Protein name

Locus Name

Acc#

coproporphyrinogen oxidase, III,
oxygen-independent hemN

pir:B69640

B69640

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13869003_f3_21	1564	6786	535	1608	123	0.0010

Protein name Locus Name Acc#
 glycoprotein Vp260-like protein A18L pir:T17508 T17508

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23864381_c2_38	1565	6787	474	1425	747	6.1e-74

Protein name Locus Name Acc#
 metabolite transport protein homolog ywtG pir:E70070 E70070

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25632943_c1_29	1566	6788	184	555		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26364040_f1_6	1567	6789	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33400260_f3_23	1568	6790	503	1512	124	0.00028

Protein name Locus Name Acc#
 STARP antigen gp:PFSTARP Z26314

Description

P.falciparum gene for STARP antigen.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
791406_c3_44	1569	6791	70	213	77	0.026

Protein name

Locus Name

Acc#

sp:ATP6_ACACA

Q37385

Description

ATP SYNTHASE A CHAIN, (PROTEIN 6)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9862501_c3_41	1570	6792	109	330		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14664052_f3_7	1571	6793	205	618	545	1.6e-52

Protein name

Locus Name

Acc#

gp:PGPGAAGEN

X95938

Description

P.gingivalis rnhB & pgaA genes & orfs 150, 197, 202 & 199.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34406512_f1_4	1572	6794	311	936	663	4.9e-65

Protein name

Locus Name

Acc#

2,3-bisphosphoglycerate-independent

gp:AF120090

AF120090

Description

Bacillus megaterium 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (pgm) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36135311_c1_9	1573	6795	315	948	444	7.8e-42
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
probable transport protein			pir:A75272			A75272
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36330175_f1_5	1574	6796	62	186		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15039156_f3_6	1575	6797	192	579	398	4.7e-36
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
putative large secreted protein			gp:SCF12			AL117669
<u>Description</u>						

Streptomyces coelicolor cosmid F12.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15117192_f2_5	1576	6798	89	270	79	0.042
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			gp:PFMAL3P7			
<u>Description</u>						

Plasmodium falciparum MAL3P7, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24343756_c1_7	1577	6799	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4860650_f1_3	1578	6800	95	288	75	0.0099

Protein name

Locus Name

Acc#

ct602 hypothetical protein

pir:F72036

F72036

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10660763_c3_339	1579	6801	387	1164		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1176302_f1_16	1580	6802	799	2400	150	3.0e-14

Protein name

Locus Name

Acc#

putative TonB-dependent outer membrane receptor

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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12117076_c1_211	1581	6803	67	204		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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12506402_f1_15	1582	6804	954	2865	249	4.1e-17
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Protein name

Locus Name

Acc#

putative histidine protein kinase

gp:REU82564

U82564

Description

hydrogenase-like protein small subunit(hoxB) gene, hydrogenase-like protein large subunit (hoxC) gene,and putative histidine protein kinase (hoxJ) gene, complete cds,and nickel permease (hoxN) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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12540880_c3_343	1583	6805	343	1032	361	4.9e-33
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Protein name

Locus Name

Acc#

capsular polysaccharide biosynthesis homolog yveT

pir:A70037

A70037

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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12714062_c3_354	1584	6806	76	231		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1290933_f3_136	1585	6807	143	432	165	2.9e-12
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein slr1861			pir:S77097		S77097	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12923260_c2_271	1586	6808	516	1551	207	1.6e-13
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative flippase			gp:AF125164		AF125164	
<u>Description</u>						

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14070180_c1_202	1587	6809	150	453	175	2.5e-13
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein 1			pir:S28678		S28678	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1448442_c1_203	1588	6810	354	1065	599	2.9e-58
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
mannose-1-phosphate guanylyltransferase			pir:H72303		H72303	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14567135_c1_201	1589	6811	369	1110	118	0.00040

Protein name

Locus Name

Acc#

immunoreactive 43kD antigen PG32

gp:AF175714

AF175714

Description

Porphyromonas gingivalis strain W50 immunoreactive 43kD antigenPG32 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14658342_f2_65	1590	6812	583	1752	139	2.5e-06

Protein name

Locus Name

Acc#

hypothetical protein SPAC17G6.19c

pir:T37851

T37851

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14726512_f1_11.....	1591	6813	105	318	161	7.6e-12

Protein name

Locus Name

Acc#

hypothetical protein slr1856

pir:S77093

S77093

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15628390_f1_9.....	1592	6814	647	1944	979	1.6e-98

Protein name

Locus Name

Acc#

sp:CAPD_STAAU

P39853

Description

CAPD PROTEIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15797007_c2_274	1593	6815	383	1152	322	6.6e-29

Protein name

Locus Name

Acc#

Cps1K

gp:AF155804

AF155804

Description

Streptococcus suis strain 6555 Cps1E (cps1E) gene, partial cds; Cps2F (cps2F), Cps1G (cps1G), Cps1H (cps1H), Cps1I (cps1I), and Cps1J (cps1J) genes, complete cds; and Cps1K (cps1K) gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15822807_f1_2	1594	6816	549	1650		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
171902_f1_31	1595	6817	67	204	49	0.037

Protein name

Locus Name

Acc#

probable RNA-directed DNA polymerase, :reverse transcriptase

pir:S20016

S20016

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19710937_f2_123	1596	6818	490	1473		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19728412_c3_391	1597	6819	459	1380	472	9.2e-54
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
folypolyglutamate synthase/dihydrofolate synthase			pir:D72411		D72411	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2032137_c1_213	1598	6820	88	267		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21651557_c3_338	1599	6821	354	1065	128	2.2e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein RP338			pir:D71690		D71690	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23455077_c3_348	1600	6822	421	1266		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23594641_c1_195	1601	6823	250	753	316	2.9e-28

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative UDP-N-acetyl-D-mannosamine transferase	gp:SPU09239	U09239

Description

Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cps19fABCDEFGHIJKLMNO) genes, complete cds, and aliA gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23632802_f3_146	1602	6824	270	813	412	1.9e-38

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:AB008550	AB008550

Description

Pseudomonas aeruginosa phage phi CTX, complete genome sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2377092_f3_153	1603	6825	64	195	219	1.3e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative aminotransferase	gp:AF125164	AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24038512_f3_134	1604	6826	251	756	375	1.6e-34

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YACO_BACSU	Q06753

Description

HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE YACO,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24412537_f1_20	1605	6827	276	831		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24413887_c1_200	1606	6828	178	537	72	0.048
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Protein name

Locus Name

Acc#

sp:Y235_METJA

Q57687

Description

HYPOTHETICAL PROTEIN MJ0235

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24417550_f2_120	1607	6829	63	192	71	0.026
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Protein name

Locus Name

Acc#

sp:FLIT_BACSU

P39740

Description

FLAGELLAR PROTEIN FLIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24475937_c3_328	1608	6830	80	243		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24506692_c1_243	1609	6831	201	606		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642837...f3...145.....	1610	6832	114	345		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24647535...f1...59.....	1611	6833	323	972		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24651502_c1_218.....	1612	6834	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24694187_c1_198	1613	6835	449	1350	128	0.00060

Protein name

Locus Name

Acc#

lacunin

gp:AF078161

AF078161

Description

Manduca sexta lacunin mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24864003_f3_131	1614	6836	403	1212	842	5.2e-84

Protein name

Locus Name

Acc#

pantothenate metabolism flavoprotein dfp
homolog yloI:probable aspartate
1-decarboxylase activase

pir:D69878

D69878

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25517305_c3_352.....	1615	6837	455	1368		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25578390_f1_30.....	1616	6838	418	1257	862	4.0e-86

Protein name

Locus Name

Acc#

methylmalonyl-CoA decarboxylase, beta-subunit

gp:PMAJ2015

AJ002015

Description

Propionigenium modestum mmdD, mmdC, mmdB genes and partial mmdA gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25625438_c1_190	1617	6839	398	1197	109	0.0069

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transmembrane protein	gp:YSCPTM	L11895

Description

Saccharomyces cerevisiae putative transmembrane protein (PTM1) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26210302_f1_10	1618	6840	393	1182	252	3.3e-36

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sensory transduction system regulatory protein slr1983:protein slr1983:protein slr1983	pir:S75664	S75664

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26366312_c2_287	1619	6841	159	480		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26369000_f2_81	1620	6842	134	405	91	0.0067

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
positive regulator for virulence factors	gp:CLOORF1	D14877

Description

Clostridium perfringens virR gene for positive regulator for virulence factors, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26595260_f2_82	1621	6843	206	621	120	5.9e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein AF0417	pir:A69302	A69302

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26687791_f3_144.....	1622	6844	193	582		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26815891_c1_187.....	1623	6845	190	573	213	2.4e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

unknown	gp:AF048749	AF048749
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Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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2767217_f2_89.....	1624	6846	549	1650	428	3.3e-39
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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2', 3'-cyclic nucleotide 2'-phosphodiesterase	gp:AB028630	AB028630
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Description

Clostridium perfringens hyp27, bacH, ptp, cpd genes for hypothetical protein, bacterial hemoglobin, protein-tyrosine phosphatase, 2', 3'-cyclic nucleotide 2'-phosphodiesterase, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2848255_f2_124	1625	6847	75	228	106	1.1e-05

Protein name

Locus Name

Acc#

GlyA

gp:AF136495

AF136495

Description

Campylobacter lari GlyA (glyA) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2931557_f1_4	1626	6848	258	777	217	8.9e-18

Protein name

Locus Name

Acc#

probable DNA pol III epsilon chain

pir:B71536

B71536

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29563916_c3_345.....	1627	6849	368	1107	366	1.4e-33

Protein name

Locus Name

Acc#

galactosyl transferase

gp:SPN239004

AJ239004

Description

Streptococcus pneumoniae type 8 capsular gene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31423265_c2_276.....	1628	6850	378	1137		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31849128_f3_133	1629	6851	298	897	420	2.7e-39

Protein name

Locus Name

Acc#

DNA repair protein

pir:A75391

A75391

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32040875_f3_132	1630	6852	263	792	394	1.6e-36

Protein name

Locus Name

Acc#

sp:REC_N_ECOLI

Description

DNA REPAIR PROTEIN REC_N (RECOMBINATION PROTEIN N)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32681627_f1_3	1631	6853	151	456	128	2.4e-08

Protein name

Locus Name

Acc#

sp:DP3B_VIBHA

P52620

Description

DNA POLYMERASE III, BETA CHAIN, (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3322152_c1_199	1632	6854	192	579		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33788882_c1_212	1633	6855	228	687	395	1.2e-36

Protein name	Locus Name	Acc#
conserved hypothetical protein aq_274	pir:C70325	C70325

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34070311_c1_191	1634	6856	347	1044	132	7.0e-06

Protein name	Locus Name	Acc#
transmembrane protein	gp:SPAJ6986	AJ006986

Description

Streptococcus pneumoniae type 33F DNA, capsular gene cluster.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35784765_f2_61	1635	6857	316	951	593	1.3e-57

Protein name	Locus Name	Acc#
UDP-N-acetylenolpyruvoylglucosamine reductase	gp:BPE238308	AJ238308

Description

Bordetella pertussis partial gene for putative thioesterase, tRNA-Gly, murB, dapB, omlA genes and partial fur gene.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3914642_f2_80	1636	6858	300	903		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3943802_f2_66	1637	6859	133	402	343	4.0e-31
Protein name			Locus Name		Acc#	
YjgF			gp:AF095578		AF095578	
Description						
Salmonella typhimurium YjgF (yjgF) gene, complete cds; and unknowngene.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3944687_f3_143	1638	6860	294	885	221	3.3e-18
Protein name			Locus Name		Acc#	
hypothetical protein AF0417			pir:A69302		A69302	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4064000_f1_29	1639	6861	88	267	83	0.0014
Protein name			Locus Name		Acc#	
probable integral membrane protein			pir:T37050		T37050	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4101561_c2_277	1640	6862	392	1179		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4104636_c1_192	1641	6863	191	576	199	7.2e-16
Protein name			Locus Name		Acc#	
serine acetyltransferase			pir:G72349		G72349	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4149067_c3_341	1642	6864	194	585	230	3.7e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
serine acetyltransferase	pir:G72349	G72349

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4330032_f2_73	1643	6865	536	1611	135	4.6e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:Y143_SYNY3	P74442

Description

HYPOTHETICAL WD-REPEAT PROTEIN SLR0143

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4690675_f3_152	1644	6866	225	678		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4710902_f1_17	1645	6867	813	2442	756	5.2e-74

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:BACA_BACLI	O68006

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4773261_c1_196	1646	6868	237	714	103	0.017

Protein name

Locus Name

Acc#

sp:YJBH_ECOLI

P32689

Description

PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4802168_c3_406	1647	6869	206	621		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4882192_c1_194	1648	6870	409	1230	162	1.4e-09

Protein name

Locus Name

Acc#

probable lipopolysaccharide
N-acetylglucosaminyltransferase, rfbU

pir:F64500

F64500

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4898450_f2_62	1649	6871	255	768	458	2.6e-43

Protein name

Locus Name

Acc#

phnP protein (phnP) homolog

pir:D70166

D70166

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4954380_f2_90	1650	6872	620	1863	357	4.4e-47

Protein name

Locus Name

Acc#

oxaloacetate decarboxylase, subunit alpha
(oadA) homolog

pir:C69406

C69406

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4957965_f3_130	1651	6873	265	798	300	1.4e-26

Protein name

Locus Name

Acc#

sp:DP3B_PSEPU

P13455

Description

DNA POLYMERASE III, BETA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5086537_f2_76	1652	6874	282	849	251	8.3e-21

Protein name

Locus Name

Acc#

putative histidine protein kinase

gp:REU82564

U82564

Description

hydrogenase-like protein small subunit (hoxB) gene, hydrogenase-like protein large subunit (hoxC) gene, and putative histidine protein kinase (hoxJ) gene, complete cds, and nickel permease (hoxN) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5260957_c1_193	1653	6875	440	1323	108	2.8e-05

Protein name

Locus Name

Acc#

sp:FER_METBA

P00202

Description

FERREDOXIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5272656_c2_275	1654	6876	332	999	443	1.0e-41

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ss-1,4-galactosyltransferase	gp:SPCPS14E	X85787

Description

S.pneumoniae cps14 locus.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6048452_f1_21	1655	6877	78	237		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6414677_c1_188	1656	6878	405	1218	149	1.5e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NADH dehydrogenase (ubiquinone), , 39 kDa subunit homolog	pir:H69478	H69478

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6694425_c3_365	1657	6879	307	924	420	2.7e-39

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein sll0744	pir:S77079	S77079

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6742762_f1_28	1658	6880	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6834387_f1_19	1659	6881	120	363		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6845277_c2_288	1660	6882	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
819433_c3_340	1661	6883	371	1116	339	1.0e-30

Protein name

Locus Name

Acc#

capsular polysaccharide biosynthesis homolog
yveT

pir:A70037

A70037

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
960825_f2_69	1662	6884	465	1398	771	1.7e-76
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
phosphate starvation inducible protein homolog ylaK			pir:A69873		A69873	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9773281_f2_125.....	1663	6885	70	210		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10573830_c1_296.....	1664	6886	168	507		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10664128_c3_491.....	1665	6887	214	645	125	1.8e-11
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ribonuclease H, 1			pir:JC5787		JC5787	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10720337_f1_75	1666	6888	211	636	258	4.0e-22

Protein name

Locus Name

Acc#

sp:YC08_YEAST

P37261

Description

HYPOTHETICAL 21.1 KD PROTEIN IN FUS1-AGP1 INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10986288_f3_169	1667	6889	406	1221	149	2.2e-07

Protein name

Locus Name

Acc#

hypothetical protein BBI16

pir:G70241

G70241

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10988261_f1_7	1668	6890	714	2145	1016	1.9e-102

Protein name

Locus Name

Acc#

DNA topoisomerase III topB

pir:H69724

H69724

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11910250_f2_102	1669	6891	159	480		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11924205_g3_539	1670	6892	110	333		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1212762_c2_390	1671	6893	300	903	354	2.7e-32

Protein name

Locus Name

Acc#

gp:AB012957

AB012957

Description

Vibrio cholerae genes for o-antigen synthesis, strain O22, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12298425_c2_391	1672	6894	300	903	219	5.5e-18

Protein name

Locus Name

Acc#

putative glycosyl transferase

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12501087_t2_116.....	1673	6895	168	507		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12691280_c3_510.....	1674	6896	1022	3069	726	1.3e-81

Protein name

Locus Name

Acc#

probable swf/snf helicase

pir:E71481

E71481

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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13885212_f3_220	1675	6897	388	1167		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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14116635_f2_158.....	1676	6898	416	1251		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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14736262_c3_545.....	1677	6899	427	1284	241	7.6e-20
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Protein name

Locus Name

Acc#

MocB (Tn4399)

pir:B48487

B48487

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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15017287_f3_252.....	1678	6900	837	2514	391	2.2e-32
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Protein name

Locus Name

Acc#

enhanced entry protein EnhC

gp:AF057704

AF057704

Description

Legionella pneumophila EnhA (enhA), EnhB (enhB), and enhanced entryprotein EnhC (enhC) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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16135886_f3_193	1679	6901	103	312		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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16229025_f2_124	1680	6902	280	843	105	0.00081
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Protein name

Locus Name

Acc#

sp:YS21_BORBU

Description

HYPOTHETICAL PROTEIN BBD21

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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16829717_f3_188	1681	6903	1951	5856	1011	1.5e-118
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Protein name

Locus Name

Acc#

gp:AB016260

Description

Agrobacterium tumefaciens plasmid pTi-SAKURA, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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16832885_f2_168	1682	6904	450	1353	1713	2.6e-176
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Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19562660_f2_134	1683	6905	478	1437	113	0.0074
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ES/130			gp:AF006751		AF006751	
<u>Description</u>						
Homo sapiens ES/130 mRNA, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
197131_f1_35	1684	6906	335	1008		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19945402_f1_57	1685	6907	375	1128		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1995941_f2_89	1686	6908	427	1284	1049	6.1e-106
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
transposase			gp:AF038866		AF038866	
<u>Description</u>						
Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20213132_c2_406	1687	6909	61	186		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2036268_c3_584	1688	6910	84	255		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2053887_f2_143	1689	6911	114	345		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
214526_c3_517	1690	6912	66	201		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21484662_f1_6	1691	6913	532	1599	144	9.4e-07

Protein name

Locus Name

Acc#

sp:M49_STRPY

P16947

Description

M PROTEIN, SEROTYPE 49 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21515632_f1_17	1692	6914	785	2358	3809	0.0

Protein name

Locus Name

Acc#

tetracycline resistance element regulator
RteA

pir:A41860

A41860

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21526437_f2_130.....	1693	6915	138	417		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21601625_c1_295.....	1694	6916	133	402		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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21679626_f1_45	1695	6917	174	525		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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22459443_c3_486.....	1696	6918	150	453	130	1.5e-08
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Protein name

Locus Name

Acc#

gp:APU72238

U72238

Description

Anabaena PCC7120 ORFR1, ORFR2, ORFR3, ORFR4, and ORFR5 genes, complete sequences.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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22687625_c3_523.....	1697	6919	433	1302	95	4.3e-05
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Protein name

Locus Name

Acc#

phage abortive infection protein

pir:T30326

T30326

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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22689031_c2_386.....	1698	6920	386	1161	1201	4.7e-122
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Protein name

Locus Name

Acc#

UDP-galactopyranose mutase

gp:SPAJ6986

AJ006986

Description

Streptococcus pneumoniae type 33F DNA, capsular gene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22774087_f2_126	1699	6921	246	741	85	0.0034

Protein name non-structural 5a protein Locus Name gp:HCU56570 Acc# U56570

Description
Hepatitis C virus isolate 925821 non-structural 5a (NS5a) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f3_258	1700	6922	83	252	64	0.031

Protein name Locus Name sp:SPRC_XENLA Acc# P36378

Description
(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22892905_f2_115.....	1701	6923	452	1359	2093	1.4e-216

Protein name Locus Name gp:BNRRTEAB Acc#

Description
Bacteroides thetaiotaomicron rteA and rteB genes involved in production of plasmid-like forms, complete cds, and tetQ gene, 3'end.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23443750_f2_148.....	1702	6924	433	1302	160	2.4e-08

Protein name Locus Name gp:AF059569 Acc# AF059569

Description
Homo sapiens actin binding protein MAYVEN mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23492786_f2_162	1703	6925	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23596911_f2_139	1704	6926	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23644552_f1_31	1705	6927	941	2826	537	8.3e-85

Protein name

Locus Name

Acc#

gp:BFU63096

U63096

Description

Bacteroides fragilis (bctA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23710777_c1_327	1706	6928	146	441	81	0.029

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF036485

Description

Plasmid pNZ4000, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24251937_f1_1	1707	6929	94	285		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24259442_f3_246.....	1708	6930	313	942	370	5.4e-34
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Protein name

Locus Name

Acc#

sp:GSPA_BACSU

P25148

Description

GENERAL STRESS PROTEIN A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24347090_f1_34.....	1709	6931	198	597		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24410812_f1_58.....	1710	6932	269	810		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24415885_f3_171	1711	6933	80	243		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24491255_c3_506.....	1712	6934	299	900	283	9.0e-25
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

ribonuclease III (rnc) homolog

pir:H70187

H70187

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24609762_c3_576.....	1713	6935	101	306	82	0.0018
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

vrII protein

pir:T17388

T17388

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24632687_f3_256.....	1714	6936	637	1914	1505	2.9e-154
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

arginine decarboxylase, 2:protein
slr0662:protein slr0662

pir:S76771

S76771

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640876_f3_248.....	1715	6937	488	1467	125	0.00018
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

complement C9 precursor

pir:C9HU

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24644056_c2_395	1716	6938	350	1053	698	9.5e-69
Protein name			Locus Name		Acc#	
			sp:PDXB_ECOLI		P05459	
Description						
ERYTHRONATE-4-PHOSPHATE DEHYDROGENASE,						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24645461_f1_19	1717	6939	207	624	889	5.5e-89
Protein name			Locus Name		Acc#	
tetracycline resistance element mobilization regulatory protein rteC			pir:A36927		A36927	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24647250_f1_84	1718	6940	263	792	377	9.9e-35
Protein name			Locus Name		Acc#	
acetylglutamate kinase			pir:F69111		F69111	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24647942_c1_284	1719	6941	505	1518	198	6.1e-22
Protein name			Locus Name		Acc#	
auxin-responsive GH3-like protein			gp:ATAC005396		AC005396	
Description						
Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24650067_f3_257	1720	6942	173	522		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24695282_f3_176	1721	6943	136	411		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24782036_f3_198	1722	6944	599	1800	161	2.2e-15
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Protein name

Locus Name

Acc#

sp:REP_BUCAP

051889

Description

ATP-DEPENDENT DNA HELICASE REP,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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25398427_f1_68	1723	6945	489	1470	416	7.3e-39
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Protein name

Locus Name

Acc#

unknown

gp:AF144879

AF144879

Description

Leptospira interrogans rfb locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25578201_f1_70	1724	6946	343	1032	537	1.1e-51

Protein name

Locus Name

Acc#

sp:LPSA_BACNO

P39907

Description

LPSA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
259837_f2_111	1725	6947	658	1977	3380	0.0

Protein name

Locus Name

Acc#

tetracycline resistance protein tetQ:tetA(Q)2

pir:I40188

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2617942_c2_450.....	1726	6948	703	2112	309	1.6e-24

Protein name

Locus Name

Acc#

mobilization protein C

gp:AF118243

AF118243

Description

Bacteroides fragilis mobilization protein C (mobC) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26462933_f3_255.....	1727	6949	249	750		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26571900_f3_173	1728	6950	233	702		
Protein name			Locus Name			Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26584437_f1_81	1729	6951	599	1800	216	3.4e-25
Protein name			Locus Name			Acc#

sp:HS90_PODAN 043109

Description

INCOMPATIBILITY MOD-E)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26600927_f2_132	1730	6952	209	630		
Protein name			Locus Name			Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26759678_f3_249	1731	6953	612	1839	872	4.6e-91
Protein name			Locus Name			Acc#

ABC transporter (ATP-binding protein) homolog
ygaD

pir:G69815 G69815

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26818752_c2_422	1732	6954	135	408		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2923125_f3_254	1733	6955	119	360		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29344216_c1_317	1734	6956	474	1425	80	0.032

Protein name

Locus Name

Acc#

M protein precursor

pir:S60858

S60858

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2947141_f2_94	1735	6957	117	354		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29573763_f3_197	1736	6958	409	1230	252	2.4e-19

Protein name

Locus Name

Acc#

hypothetical protein Rv0597c

pir:H70908

H70908

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29869676_f1_44	1737	6959	296	891	149	2.7e-09

Protein name

Locus Name

Acc#

sp:PRIM_LISMO

P47762

Description

DNA PRIMASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31736291_f2_93	1738	6960	177	534		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31814442_c3_526.....	1739	6961	266	801		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31885192_f3_195.....	1740	6962	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31892650_c1_351	1741	6963	807	2424		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33245255_c2_378.....	1742	6964	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33399058_f2_118.....	1743	6965	653	1962	172	1.5e-10

Protein name

Locus Name

Acc#

sp:VOLD_BPP2

P13520

Description

OVERCOMING LYSOGENIZATION DEFECT PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33706251_f2_167.....	1744	6966	180	543	185	2.2e-14

Protein name

Locus Name

Acc#

putative RNA polymerase sigma factor (ECF

gp:SCE46

AL133252

Description

Streptomyces coelicolor cosmid E46.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34037503_f3_170	1745	6967	99	300		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34063441_f2_138	1746	6968	198	597		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34178438_f3_244	1747	6969	272	819		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34183402_f1_28	1748	6970	116	351		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34199183_f3_212	1749	6971	627	1884	1219	5.9e-124
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						
maturase-related protein (intL intron)				pir:S77648		S77648

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34268878_f1_27	1750	6972	160	483	81	0.0034

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glucosidase II beta-subunit	gp:AF066061	AF066061

Description

Mus musculus glucosidase II beta-subunit gene, alternatively spliced products, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35171937_c1_350	1751	6973	439	1320		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35352031_c2_420.....	1752	6974	179	540		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35725786_c1_300.....	1753	6975	152	459		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3933375_c3_520	1754	6976	430	1293	82	0.017
Protein name			Locus Name			Acc#
hypothetical protein			pir:B72242			B72242
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4007635_c3_521	1755	6977	93	282		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
414687_f1_55	1756	6978	232	699	479	1.5e-45
Protein name			Locus Name			Acc#
			sp:YLCA_ECOLI			P77380
Description						

PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN YLCA

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4192500_f2_150	1757	6979	367	1104	510	7.9e-49
Protein name			Locus Name			Acc#
conserved hypothetical protein aq_1224			pir:G70405			G70405
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
422552_f1_76	1758	6980	190	573	259	3.1e-22
Protein name			Locus Name			Acc#
shikimate kinase			pir:A70487			A70487
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4298525_c2_397	1759	6981	425	1278	1152	7.4e-117
Protein name			Locus Name			Acc#
synthase,			pir:G69842			G69842
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4307136_f3_231	1760	6982	89	270		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4707750_f1_72	1761	6983	311	936	288	2.9e-37
Protein name			Locus Name			Acc#
hypothetical protein PH0424			pir:A71153			A71153
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
475002_f3_189	1762	6984	63	192		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4876592_f1_85	1763	6985	162	489		
Protein name			Locus Name			Acc#
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4884628_f3_232	1764	6986	456	1371	334	4.2e-30
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
copper resistance sensor kinase pcoS:copper sensor			pir:S52258			
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5272917_f3_233	1765	6987	887	2664	2321	9.8e-241
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:ATMA_ECOLI		P39168	
<u>Description</u>						
MG(2+) TRANSPORT ATPASE, P-TYPE 1,						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6429200_f2_147	1766	6988	62	189		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6500_c1_275	1767	6989	64	195	73	0.031
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YGEG_ECOLI		Q46787	
<u>Description</u>						
HYPOTHETICAL 19.1 KD PROTEIN IN KDUI-LYSS INTERGENIC REGION						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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6532501_c2_461	1768	6990	438	1317		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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6814017_f1_30.....	1769	6991	126	381	70	0.033
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Protein name

Locus Name

Acc#

41kd antigen

gp:A13461

A13461

Description

P.falciparum gene for 41kd antigen, clone 41-7.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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6828312_c2_396.....	1770	6992	82	249	266	5.7e-23
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Protein name

Locus Name

Acc#

acyl carrier protein (ACP)

gp:ABACPF

X82399

Description

A.brasilense acpF gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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78126_f2_152.....	1771	6993	351	1056	710	5.1e-70
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Protein name

Locus Name

Acc#

sp:K6PF_SYNY3

P72830

Description

(PHOSPHOHEXOKINASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
783410_f3_172	1772	6994	391	1176		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
85827...F2...155.....	1773	6995	207	624	371	4.3e-34
Protein name			Locus Name		Acc#	
phosphoribosylglycinamide formyltransferase			gp:ATPUR3		X74767	
Description						

Arabidopsis thaliana mRNA for phosphoribosylglycinamideformyltransferase encoded by PUR3 gene.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9787906...F2...121.....	1774	6996	80	243		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9923130...c3...577.....	1775	6997	111	336	85	0.00086
Protein name			Locus Name		Acc#	
hypothetical protein SCE68.26c			pir:T36276		T36276	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14176629_c2_6	1776	6998	68	207	113	9.3e-07
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein Rv3069			pir:F70650			F70650
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4978886_t3_2	1777	6999	217	654	628	2.5e-61
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein			pir:JQ1020			JQ1020
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12697201_c2_20	1778	7000	599	1797	340	2.0e-27
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
115K outer membrane protein precursor:SusC protein			pir:JC6027			JC6027
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19532637_c3_23	1779	7001	96	291		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24218762_c1_18	1780	7002	137	414	64	0.015

Protein name

Locus Name

Acc#

ribosomal protein L5

gp:U17009

U17009

Description

Phytophthora infestans mitochondrion, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3163438_c2_19	1781	7003	406	1221	148	1.4e-07

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4806337_c3_21	1782	7004	93	282		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6445306_f2_8	1783	7005	212	639	186	1.7e-14

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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13065655_f3_2	1784	7006	67	201		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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1050026_f2_4	1785	7007	129	390	69	0.044
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Protein name

Locus Name

Acc#

transcription regulator, PbsX family

pir:H75270

H75270

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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14652161_f3_17	1786	7008	77	234	191	2.6e-14
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Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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16832885_f2_11	1787	7009	115	348	428	3.9e-40
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Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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22860128_f3_16	1788	7010	83	252	64	0.031
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Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24615625_c3_24	1789	7011	725	2178	2793	9.5e-291
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
alpha-glucosidase	gp:BTU66897				U66897	
<u>Description</u>	Bacteroides thetaiotaomicron neopullulanase (susA) and alpha-glucosidase (susB) genes, complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34382842_f1_3	1790	7012	113	342	170	5.1e-12
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
hypothetical protein				pir:JQ1020	JQ1020	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10644652_c3_306.....	1791	7013	628	1887	1058	6.8e-107
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:YFBS_ECOLI					
<u>Description</u>						
HYPOTHETICAL 65.9 KD PROTEIN IN LRHA-ACKA INTERGENIC REGION						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1070311_c3_324.....	1792	7014	355	1068		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10727040_c1_204	1793	7015	345	1038		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10968955_f3_167.....	1794	7016	237	714	546	1.2e-52

Protein name

Locus Name

Acc#

sp:PDXH_SYNY3

P74211

Description

PYRIDOXAMINE 5'-PHOSPHATE OXIDASE, (PNP/PMP OXIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11190877_c3_317.....	1795	7017	406	1221		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1214075_c2_259.....	1796	7018	215	648	364	2.4e-33

Protein name

Locus Name

Acc#

O-acetyl transferase

gp:SAU77308

U77308

Description

Staphylococcus aureus O-acetyl transferase (cap5H) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12985802_f2_99	1797	7019	245	738	84	0.0053

Protein name

Locus Name

Acc#

gp:D84670

D84670

Description

Pyrococcus furiosus gene for DNA polymerase II subunit 1, DNAPolymerase II subunit 2, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13851552_f3_168	1798	7020	363	1092		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13937556_c3_325.....	1799	7021	182	549		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14463512_f1_57.....	1800	7022	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14570327_f3_149	1801	7023	157	474	263	1.2e-22
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
orfX	gp:AB014440				AB014440	
<u>Description</u>	Staphylococcus aureus genes for orf1, orfX, orf2, orf3, partial andcomplete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16112682_f3_192	1802	7024	961	2886		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16223432_c2_284.....	1803	7025	198	597	187	1.3e-14
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
RNA polymerase ECF-type sigma factor homolog ylaC	pir:A69872				A69872	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1957187_c3_315.....	1804	7026	195	588		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19726375_c1_207	1805	7027	161	486	233	1.8e-19
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
unknown			gp:AF048749			AF048749
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20505007_c3_305	1806	7028	60	183		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2187550_f3_143.....	1807	7029	112	339		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22469452_c3_298.....	1808	7030	172	519	149	1.4e-10
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
unknown			gp:AF048749			AF048749
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23625302_c1_213	1809	7031	434	1305	1720	4.8e-177
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative UDP-galactose-6 dehydrogenase	gp:AF048749				AF048749	
<u>Description</u>	Bacteroides fragilis capsular polysaccharide biosynthesis operon,complete sequence.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23631637_f3_163	1810	7032	342	1029	902	2.3e-90
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
D-2-hydroxy-acid dehydrogenase,	pir:S76782				S76782	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23944510_f1_48.....	1811	7033	104	315		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24022212_c1_236.....	1812	7034	330	993	588	4.3e-57
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
conserved hypothetical protein			pir:A72335		A72335	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415952_c1_231	1813	7035	220	663	712	3.1e-70

Protein name

Locus Name

Acc#

ykvJ protein

pir:A69868

A69868

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24416062_c2_258	1814	7036	386	1161	117	0.00067

Protein name

Locus Name

Acc#

MURF1

gp:AF079967

AF079967

Description

Phytomonas serpens 12S large subunit ribosomal RNA and 9S small subunit ribosomal RNA, partial sequence; NADH dehydrogenase subunit 8 (ND8) cryptogene, NADH dehydrogenase subunit 9 (ND9) cryptogene, NADH dehydrogenase subunit 7 (ND7) cryptogene, ATPase subunit 6 (A6) cryptogene, G3 cryptogene, complete sequence; and MURF1 (MURF1) and MURF1 (MURF1) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24640887_c3_301	1815	7037	351	1056	615	5.9e-60

Protein name

Locus Name

Acc#

N-acetylneuraminic acid condensing enzyme

gp:LPN7311

AJ007311

Description

Legionella pneumophila serogroup 1 lipopolysaccharide biosynthesis gene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24641925_c1_214	1816	7038	388	1167	128	3.3e-05

Protein name

Locus Name

Acc#

probable lipopolysaccharide
N-acetylglucosaminyltransferase, rfbU

pir:F64500

F64500

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24642125_c3_304	1817	7039	442	1329		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24642813_c1_217.....	1818	7040	200	603	189	8.2e-15
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Protein name

Locus Name

Acc#

thiol:disulfide interchange protein

pir:F75549

F75549

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24647126_f1_19.....	1819	7041	431	1296	78	0.045
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Protein name

Locus Name

Acc#

sp:RS10_METTH

O27133

Description

30S RIBOSOMAL PROTEIN S10P

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24648510_c1_211.....	1820	7042	343	1032	424	1.0e-39
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Protein name

Locus Name

Acc#

unknown

gp:AF144879

AF144879

Description

Leptospira interrogans rfb locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24806575_c3_300	1821	7043	281	846	159	2.6e-09

Protein name

Locus Name

Acc#

galactosyl transferase

gp:AF030373

AF030373

Description

Streptococcus pneumoniae strain SP-264 alpha, 1-6-glucosidase(dexB) gene, complete cds; capsular polysaccharide biosynthetic locus, complete sequence; and oligopeptide binding protein (aliA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25431551_c1_212	1822	7044	238	717	289	2.1e-25

Protein name

Locus Name

Acc#

acetyltransferase, vatB

pir:T10903

T10903

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25815961_c2_248.....	1823	7045	647	1944		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25900252_c2_282.....	1824	7046	152	459	591	2.1e-57

Protein name

Locus Name

Acc#

conserved hypothetical protein ykvM

pir:D69868

D69868

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26847025_f2_134	1825	7047	167	504	843	4.1e-84

Protein name

Locus Name

Acc#

sp:FLP_YEAST

P03870

Description

RECOMBINASE FLP PROTEIN (PROTEIN ABLE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26847025_f3_195	1826	7048	167	504	843	4.1e-84

Protein name

Locus Name

Acc#

sp:FLP_YEAST

P03870

Description

RECOMBINASE FLP PROTEIN (PROTEIN ABLE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29484452_c1_216	1827	7049	433	1302	933	1.2e-93

Protein name

Locus Name

Acc#

Cps7G

gp:AF164515

AF164515

Description

Streptococcus suis putative glycosyltransferase Cps7E (cps7E) gene, partial cds; putative glycosyltransferase Cps7F (cps7F) and Cps7G (cps7G) genes, complete cds; and putative glycosyltransferase Cps7H (cps7H) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29506500_c2_257	1828	7050	481	1446	275	2.0e-21

Protein name

Locus Name

Acc#

Cps2J

gp:AF026471

AF026471

Description

Streptococcus pneumoniae DexB (dexB) gene, partial cds; putative transposase gene, complete cds; type 2 capsular polysaccharide biosynthesis operon, complete sequence; and AliA (aliA) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30509375_c1_198	1829	7051	246	741	117	0.00037

Protein name

Locus Name

Acc#

STARP antigen

gp:AF209925

AF209925

Description

Plasmodium falciparum STARP antigen (STARP) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31287_c2_255	1830	7052	236	711	347	1.5e-31

Protein name

Locus Name

Acc#

CMP-N-acetylneuraminic acid synthetase

gp:LPN7311

AJ007311

Description

Legionella pneumophila serogroup 1 lipopolysaccharide biosynthesis gene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31593_c2_243.....	1831	7053	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34019812_c2_283.....	1832	7054	272	819		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34180437_c2_280	1833	7055	172	519	209	6.3e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative ECF sigma factor RpoE1	gp:AF049107	AF049107

Description

Myxococcus xanthus response regulator FrzZ (frzZ) gene, partialcds; alanine dehydrogenase (aldA), putative ECF sigma factor RpoE1(rpoE1), and response regulator homolog (frzS) genes, complete cds;and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34562591_c3_296	1834	7056	352	1059		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34572201_c1_235.....	1835	7057	283	852		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35166265_c2_254.....	1836	7058	214	645	291	1.3e-25

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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putative acetyl transferase	gp:LPN7311	AJ007311
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Description

Legionella pneumophila serogroup 1 lipopolysaccharide biosynthesisgene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36135887_c1_219	1837	7059	68	207	73	0.016
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
water-stress inducible protein				gp:AF010584		AF010584
<u>Description</u>						
Oryza sativa water-stress inducible protein (WSI) mRNA, completecds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
39067_c2_256	1838	7060	443	1332	81	0.023
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:RK23_EUGGR				P19167	
<u>Description</u>						
CHLOROPLAST 50S RIBOSOMAL PROTEIN L23						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
391003_f2_101.....	1839	7061	311	936	129	5.6e-06
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
ubiquinone/menaquinone biosynthesis methyltransferase-related protein				pir:F72262	F72262	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3912637_f1_28.....	1840	7062	244	735	428	3.9e-40
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein sl11773			pir:S77110		S77110	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
392802_c2_261	1841	7063	198	597	541	4.1e-52

Protein name

Locus Name

Acc#

ORF8S

gp:AB028134

AB028134

Description

Shigella sonnei O-antigen gene cluster for ORF6S, ORF7S, ORF8S, ORF9S, ORF10S, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3957767_f2_69	1842	7064	372	1119	1076	8.4e-109

Protein name

Locus Name

Acc#

alanine dehydrogenase

gp:AF070716

AF070716

Description

Vibrio proteolyticus alanine dehydrogenase (ald) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4071052_c2_242	1843	7065	250	753	312	7.6e-28

Protein name

Locus Name

Acc#

Tou1

gp:AF058689

AF058689

Description

Neisseria meningitidis strain Z2491, genomic sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4117802_c1_225	1844	7066	608	1827	181	3.6e-09

Protein name

Locus Name

Acc#

hypothetical protein

pir:S75991

S75991

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4407580_c1_215	1845	7067	261	786	761	2.0e-75
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative glycosyl transferase			gp:AF048749		AF048749	
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4457808_c2_287	1846	7068	490	1470	189	3.8e-12
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein			pir:B72224		B72224	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4789052_c3_321.....	1847	7069	282	849	609	2.6e-59
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
quinolinate phosphoribosyl transferase			pir:B70375		B70375	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4975937_c2_281.....	1848	7070	230	693	266	5.7e-23
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein			pir:A72334		A72334	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
585312_f1_34	1849	7071	132	399	154	4.2e-11

Protein name

Locus Name

Acc#

sp:LGUL_NEIME

033393

Description

(S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
598150_f2_113	1850	7072	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
625933_c1_196.....	1851	7073	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6679812_c2_273.....	1852	7074	147	444		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7293_c3_288	1853	7075	85	258	263	1.2e-22

Protein name

Locus Name

Acc#

sp:REP1_YEAST

P03871

Description

TRANS-ACTING FACTOR B (REP1) (PROTEIN BAKER)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
907575_c1_208	1854	7076	412	1239	319	1.8e-30

Protein name

Locus Name

Acc#

putative epimerase/dehydratase WbiI

gp:AF064070

AF064070

Description

Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphateacyltransferase (plsC), putative diadenosine tetraphosphatase (apaH), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphateN-acetylglucosaminyltransferase, and putative

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
977202_c1_226	1855	7077	501	1506		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9859712_c3_299	1856	7078	406	1221	544	1.0e-56

Protein name

Locus Name

Acc#

aminotransferase homolog

gp:AF001497

AF001497

Description

Campylobacter jejuni polysaccharide biosynthesis protein homolog gene, partial cds, galactosyl transferase homolog, UDP-galactosephosphate transferase homolog, acetyl transferase homolog and aminotransferase homolog genes, complete cds, and polysaccharide biosynthesis enzyme homolog gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14722075_f1_6	1857	7079	77	234	137	2.7e-09
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ribosomal protein L30			pir:B72248		B72248	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14868817_f1_12	1858	7080	113	342		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
157552_c1_36	1859	7081	616	1851	266	3.1e-22
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:MUTS_AQUPY		P70755	
<u>Description</u>						

DNA MISMATCH REPAIR PROTEIN MUTS

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16595463_f1_4	1860	7082	193	582	458	2.6e-43
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ribosomal protein L6			pir:E72248		E72248	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16836062_f1_11	1861	7083	203	612	504	3.4e-48

Protein name

Locus Name

Acc#

sp:RS4_BACST

P81288

Description

30S RIBOSOMAL PROTEIN S4

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22540937_f3_29	1862	7084	162	489	318	1.8e-28

Protein name

Locus Name

Acc#

sp:RL17_PSEAE

O52761

Description

50S RIBOSOMAL PROTEIN L17

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23475302_f3_28	1863	7085	335	1008	634	5.8e-62

Protein name

Locus Name

Acc#

sp:RPOA_BACHD

O50634

Description

ALPHA CHAIN) (RNA POLYMERASE ALPHA SUBUNIT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
235677_f1_3	1864	7086	149	450	373	2.6e-34

Protein name

Locus Name

Acc#

gp:AB017508

AB017508

Description

Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23712803_f1_1	1865	7087	186	561	524	2.6e-50
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:RL5_BACSU				P12877	
<u>Description</u>						
50S RIBOSOMAL PROTEIN L5 (BL6)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24353377_f1_2	1866	7088	100	303	274	8.1e-24
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
ribosomal protein S14	pir:R3EC14					
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24353385_f1_10.....	1867	7089	73	222	287	3.4e-25
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
initiation factor IF1	gp:AF115283				AF115283	
<u>Description</u>						
Leptospira interrogans S10-spc-alpha locus, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25437550_f1_7.....	1868	7090	158	477	354	2.7e-32
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
ribosomal protein L15	pir:A72248				A72248	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3019182_f3_30	1869	7091	148	447		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3939377_f1_5	1870	7092	118	357	332	5.8e-30
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:RL18_BACSU		
<u>Description</u>						

50S RIBOSOMAL PROTEIN L18

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4040885_f3_26	1871	7093	127	384	413	1.5e-38
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
ribosomal protein S13				gp:AF115283		AF115283
<u>Description</u>						

Leptospira interrogans S10-spc-alpha locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4334377_f3_25	1872	7094	176	531	443	1.0e-41
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				gp:AB017508		AB017508
<u>Description</u>						

Bacillus halodurans C-125 genomic DNA, 32 kb fragment, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5117303_f1_9	1873	7095	267	804	673	4.2e-66

Protein name

Locus Name

Acc#

gp:AB017508

AB017508

Description

Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
578213_f3_31	1874	7096	215	648		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5897177_f2_20.....	1875	7097	134	405	392	2.5e-36

Protein name

Locus Name

Acc#

sp:RS11_STRCO

P72403

Description

30S RIBOSOMAL PROTEIN S11

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9969412_f2_18.....	1876	7098	452	1359	913	1.6e-91

Protein name

Locus Name

Acc#

preprotein translocase SecY

gp:AF115283

AF115283

Description

Leptospira interrogans S10-spc-alpha locus, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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10742027_c1_170	1877	7099	61	186		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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12533408_c1_171	1878	7100	177	534		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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13941932_f1_14	1879	7101	759	2280	1022	4.4e-103
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Protein name

Locus Name

Acc#

immunoreactive 89kD antigen PG87

gp:AF175722

AF175722

Description

Porphyromonas gingivalis strain W50 immunoreactive 89kD antigen PG87 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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14105438_f2_49	1880	7102	802	2409	991	8.5e-100
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Protein name

Locus Name

Acc#

hypothetical protein Rv0584

pir:G70934

G70934

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1453553_c2_174	1881	7103	1220	3663	1910	4.3e-222
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
beta-galactosidase			gp:AF055482		AF055482	
<u>Description</u>						
Thermotoga neapolitana galactose utilization operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22445937_f1_28	1882	7104	378	1137	146	4.2e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:A75327		A75327	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24301306_c2_179.....	1883	7105	64	195		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24414007_f1_22.....	1884	7106	234	705		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24415930_f2_56	1885	7107	736	2211	430	6.3e-38
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24422510_c3_237.....	1886	7108	347	1044	305	5.5e-27
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein RP407			pir:F71698		F71698	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24490937_f3_113.....	1887	7109	135	408		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24820301_c2_202.....	1888	7110	126	378	121	1.3e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YHI4_RHOCA		P30791	
<u>Description</u>						
HYPOTHETICAL PROTEIN IN HIMA 3'REGION (FRAGMENT)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24823562_c3_230	1889	7111	66	201		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2616636_f1_23	1890	7112	183	552	222	2.6e-18
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
conserved hypothetical protein ylbH				pir:E69874		E69874
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26351577_c2_177	1891	7113	389	1170	422	3.5e-38
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
sensory transduction histidine kinase slr2098:protein slr2098:protein slr2098				pir:S75130		S75130
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
272078_f3_112	1892	7114	375	1128	449	2.3e-42
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
3-dehydroquinate synthase PAB0298				pir:C75161		C75161
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29332532_c2_196	1893	7115	294	885	156	5.2e-09

Protein name

Locus Name

Acc#

pobR regulator

gp:PSEY18527

Y18527

Description

Pseudomonas sp. pobA, pobR, pcaQ, pcaH and pcaG genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29412805_f1_12	1894	7116	199	600	204	2.1e-16

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31328126_c1_149	1895	7117	478	1437	144	4.2e-12

Protein name

Locus Name

Acc#

hypothetical protein MJ1519

pir:F64489

F64489

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31408525_f3_121	1896	7118	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33366385_f1_15	1897	7119	766	2301	2410	3.6e-250
Protein name			Locus Name		Acc#	
immunoreactive 89kD antigen PG87			gp:AF175722		AF175722	
Description						
Porphyromonas gingivalis strain W50 immunoreactive 89kD antigenPG87 gene, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34179592_f2_74	1898	7120	430	1293	526	1.9e-61
Protein name			Locus Name		Acc#	
3-phosphoshikimate 1-carboxyvinyltransferase, :5-enolpyruvylshikimate-3-phosphate synthase			pir:JN0758			
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34251302_f3_83	1899	7121	876	2631	1368	3.2e-193
Protein name			Locus Name		Acc#	
alanyl-tRNA synthetase			gp:AF027500		AF027500	
Description						
Aquifex pyrophilus alanyl-tRNA synthetase (alaS) gene, completecds; and ATP-dependent Clp protease regulatory subunit (clpA) gene,partial cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4039063_c2_183	1900	7122	146	441		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4113941_c3_208	1901	7123	656	1971	379	3.2e-32
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
lacto-N-biosidase precursor			gp:SSU40488		U40488	
<u>Description</u>						
Streptomyces sp. lacto-N-biosidase precursor gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4173192_f2_57	1902	7124	196	591		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4692208_c2_173.....	1903	7125	499	1500	264	2.6e-49
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
alpha-1,3/4-fucosidase precursor			gp:SSU39394		U39394	
<u>Description</u>						
Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, completecds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4964055_f2_48.....	1904	7126	402	1209	598	3.8e-58
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative membrane transport protein.			gp:SCC75A		AL133220	
<u>Description</u>						
Streptomyces coelicolor cosmid C75A.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5162628_F2_60	1905	7127	281	846		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5319637_F2_58	1906	7128	385	1158		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
546925_C2_176	1907	7129	303	912	156	3.3e-11
Protein name			Locus Name		Acc#	
PobR			gp:RLU40388		U40388	
Description						

Rhizobium leguminosarum positive regulator of pobA (pobR) gene, complete cds, and 4-hydroxybenzoate hydroxylase (pobA) gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
625032_C2_184	1908	7130	989	2970	166	1.7e-15
Protein name			Locus Name		Acc#	
unknown			gp:AF007381		AF007381	
Description						

Flavobacterium johnsoniae gliding motility protein (gldA) gene, complete cds; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6306441_f1_17	1909	7131	422	1269	178	5.0e-10

Protein name: receptor antigen (RagA) Locus Name: gp:PGI130872 Acc#: AJ130872

Description: Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
634758_c1_140	1910	7132	79	240		

Protein name: Locus Name: Acc#:

Description: NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6761652_c2_185.....	1911	7133	503	1512	915	9.6e-92

Protein name: Locus Name: sp:YWNE_BACSU Acc#: P71040

Description: HYPOTHETICAL 55.8 KD PROTEIN IN SP011Q-MTA INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
796950_f2_50.....	1912	7134	342	1029	165	1.0e-09

Protein name: transmembrane sensor Locus Name: gp:AF051691 Acc#: AF051691

Description: Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor (fiuI), transmembrane sensor (fiuR), and hydroxamate-type ferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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1055303_f3_59	1913	7135	76	231		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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10797128_f3_58	1914	7136	384	1155	406	8.3e-38
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Protein name

Locus Name

Acc#

DNA processing chain A

pir:C72399

C72399

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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1293_f2_43	1915	7137	310	933	133	3.2e-06
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Protein name

Locus Name

Acc#

sp:EXSA_PSEAE

P26993

Description

EXOENZYME S SYNTHESIS REGULATORY PROTEIN EXSA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13157626_f1_17	1916	7138	85	258		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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134717_f1_12	1917	7139	322	969	107	0.0016
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Protein name

Locus Name

Acc#

hypothetical protein RP870

pir:F71649

F71649

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13678887_f3_67	1918	7140	72	219		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20734627_f2_40.....	1919	7141	341	1026		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22068817_c2_132.....	1920	7142	165	498	162	6.0e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

RNA polymerase sigma-E factor

pir:H75550

H75550

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22072175_f3_62.....	1921	7143	833	2502	192	5.0e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

tonB-linked receptor Tlr

gp:AF155223

AF155223

Description

Porphyromonas gingivalis tonB-linked receptor Tlr (tlr) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22460876_f2_42	1922	7144	342	1029	111	0.0052
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
71			gp:AF030027		AF030027	
<u>Description</u>						
Equine herpesvirus 4 strain NS80567, complete genome.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23634713_f1_22	1923	7145	377	1134	135	3.5e-11
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:PSEOPRC		D28119	
<u>Description</u>						
Pseudomonas aeruginosa oprC gene for outer membrane protein C, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23875636_c1_92	1924	7146	96	291	78	0.039
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YB05_YEAST		P33313	
<u>Description</u>						
HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24220312_f1_14	1925	7147	142	429	149	1.4e-10
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YE94_AQUAE		067466	
<u>Description</u>						
HYPOTHETICAL 15.3 KD PROTEIN AQ_1494						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24335967_c2_103	1926	7148	255	768	744	1.3e-73
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
putative reductase iron-sulfur protein			gp:SCM10			AL133469
<u>Description</u>						
Streptomyces coelicolor cosmid M10.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24486507_f3_69	1927	7149	211	636	187	3.1e-14
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:Y374_METJA			Q57819
<u>Description</u>						
HYPOTHETICAL PROTEIN MJ0374						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25397550_f2_31	1928	7150	342	1029	197	8.2e-19
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
probable UDP-glucose 4-epimerase			pir:A71183			A71183
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26345025_c1_95	1929	7151	164	495	160	9.7e-12
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
nimD protein			pir:I40187			
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31445427_c1_85	1930	7152	330	993	576	8.1e-56

Protein name

Locus Name

Acc#

sp:YACF_BACSU

P37567

Description

HYPOTHETICAL 37.1 KD PROTEIN IN FOLK-LYSS INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33397252_c3_140	1931	7153	652	1959	2133	8.2e-221

Protein name

Locus Name

Acc#

putative reductase flavoprotein subunit

gp:SCM10

AL133469

Description

Streptomyces coelicolor cosmid M10.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33728400_c3_138.....	1932	7154	292	879	138	7.2e-07

Protein name

Locus Name

Acc#

sp:EXSA_PSEAE

P26993

Description

EXOENZYME S SYNTHESIS REGULATORY PROTEIN EXSA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34197186_f2_30.....	1933	7155	300	903	494	3.9e-47

Protein name

Locus Name

Acc#

cation efflux system homolog ydIM

pir:C69781

C69781

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34379406_c1_78	1934	7156	74	225	74	0.013

Protein name

Locus Name

Acc#

citrate synthase

gp:BBU28076

U28076

Description

Bartonella bacilliformis citrate synthase (glTA) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36361057_f3_50	1935	7157	317	954	980	1.2e-98

Protein name

Locus Name

Acc#

O-acetylserine(thiol)-lyase-A related protein

gp:AF174138

AF174138

Description

Methanosarcina barkeri O-acetylserine(thiol)-lyase-A related protein (cysK) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4025375_f3_57	1936	7158	425	1278	1537	1.2e-157

Protein name

Locus Name

Acc#

collagenase

gp:AB006973

AB006973

Description

Porphyromonas gingivalis DNA for collagenase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4117202_f2_41	1937	7159	321	966	81	0.043

Protein name

Locus Name

Acc#

sp:RL12_HALVO

P41197

Description

50S RIBOSOMAL PROTEIN L12 ('A' TYPE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4789162_c1_91	1938	7160	718	2157	1190	7.0e-121
Protein name			Locus Name			Acc#
conserved hypothetical protein yvaJ			pir:G70027			G70027
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5095937_f1_21	1939	7161	409	1230		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5994790_f3_49	1940	7162	286	861	281	3.2e-24
Protein name			Locus Name			Acc#
probable lipase			pir:C75472			C75472
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6053885_c2_101	1941	7163	64	195		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6444187_c1_94	1942	7164	206	621		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
781703_f2_36	1943	7165	239	720	96	0.0070
Protein name			Locus Name		Acc#	
hypothetical protein			gp:PA0243397		AJ243397	
Description						
Pseudomonas aureofaciens partial bolA gene and ORF1 DNA.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
867012_c2_102	1944	7166	234	705	199	7.2e-16
Protein name			Locus Name		Acc#	
putative cytochrome B subunit			gp:SCM10		AL133469	
Description						
Streptomyces coelicolor cosmid M10.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2141962_c3_52	1945	7167	132	399	179	9.5e-14
Protein name			Locus Name		Acc#	
MecI protein			gp:SSK3MECA2		Y13095	
Description						
S.sciuri mecA2 gene, strain K3 (MM2).						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23634637_f1_14	1946	7168	291	876	113	0.0010
Protein name			Locus Name		Acc#	
immunoglobulin-Fc-binding protein			gp:SPFCRA2		X73159	
Description						
S.pyogenes fcrA2 gene for Ig-Fc-binding protein.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648410_c2_41	1947	7169	1097	3294	289	4.2e-37

Protein name Locus Name Acc#
hypothetical protein c0624 pir:S73091 S73091

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25822143_c3_53	1948	7170	731	2196	114	0.0037

Protein name Locus Name Acc#
sp:BLAR_STAAU P18357

Description

REGULATORY PROTEIN BLAR1

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35159632_F3_27	1949	7171	76	231	54	0.022

Protein name Locus Name Acc#
extracellular protein Exp4 precursor gp:LLU95836 U95836

Description

Lactococcus lactis extracellular protein Exp4 precursor, gene,partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4178387_c1_38	1950	7172	317	954	750	2.9e-74

Protein name Locus Name Acc#
sp:MDH_CHLAU P80040

Description

MALATE DEHYDROGENASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4725192_f3_26	1951	7173	676	2031	159	2.7e-13
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein F14F9.5			pir:T33774		T33774	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24337765_c3_16	1952	7174	762	2286	673	6.1e-69
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2477187_c3_15	1953	7175	60	183		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35235700_f2_6	1954	7176	62	189		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5991061_c1_11	1955	7177	227	684	859	8.3e-86

Protein name

Locus Name

Acc#

Phosphoenolpyruvate carboxykinase

gp:AB016600

AB016600

Description

Selenomonas ruminantium gene for Phosphoenolpyruvate carboxykinase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10009393_c1_53	1956	7178	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13103563_f3_37	1957	7179	375	1128	248	5.3e-21

Protein name

Locus Name

Acc#

probable histidinol phosphatase

pir:F75515

F75515

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14587752_f3_39	1958	7180	165	498	345	2.4e-31

Protein name

Locus Name

Acc#

sp:RISB_BACAM

Q44681

Description

(LUMAZINE SYNTHASE) (RIBOFLAVIN SYNTHASE BETA CHAIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
17092_c1_50	1959	7181	395	1188	474	5.2e-45

Protein name

Locus Name

Acc#

gp:AB013492

AB013492

Description

Bacillus halodurans C-125 genomic DNA, 9A/3S' fragment, cloneALBAC001.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1954562_f1_5	1960	7182	366	1101	1505	2.9e-154

Protein name

Locus Name

Acc#

sp:G3P_BACFR

Q59199

Description

(FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23958.125_c2_76.....	1961	7183	517	1554	1411	2.6e-144

Protein name

Locus Name

Acc#

sp:GUAA_ECOLI

P04079

Description

AMIDOTRANSFERASE) (GMP SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24017187_f2_25.....	1962	7184	236	711	109	0.00037

Protein name

Locus Name

Acc#

sp:YA57_ACTAC

O52728

Description

HYPOTHETICAL PROTEIN 1057

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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240762_c1_46	1963	7185	62	189		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24229038_f2_19	1964	7186	716	2151	1255	9.0e-128
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Protein name

Locus Name

Acc#

sp:OPDA_ECOLI

P27298

Description

OLIGOPEPTIDASE A,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24431425_f3_36	1965	7187	82	249	78	0.0054
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Protein name

Locus Name

Acc#

gp:MGU34967

U34967

Description

Mycoplasma genitalium repetitive sequence element mgp-r4.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24508512_c3_83	1966	7188	102	309	100	2.2e-05
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Protein name

Locus Name

Acc#

hypothetical protein

pir:D72328

D72328

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24645176_f3_41	1967	7189	427	1284	743	1.6e-73

Protein name

Locus Name

Acc#

probable oxidoreductase

gp:SCF11

AL132662

Description

Streptomyces coelicolor cosmid F11.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24648437_f2_20	1968	7190	171	516		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26595836_f1_6	1969	7191	147	444	292	1.0e-25

Protein name

Locus Name

Acc#

dCMP deaminase homolog

pir:C69470

C69470

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3009632_f2_16	1970	7192	675	2028		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34175162_f1_7	1971	7193	184	555	331	7.4e-30

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_1731

pir:C70449

C70449

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34407937_f3_35	1972	7194	494	1485	538	8.6e-52
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
carboxyl-terminal proteinase			pir:F70369		F70369	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36328387_c2_58	1973	7195	609	1830		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36370312_c2_75	1974	7196	148	447	405	1.1e-37
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:MSCL_ECOLI		P23867	
<u>Description</u>						
LARGE-CONDUCTANCE MECHANOSENSITIVE CHANNEL						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6538962_c1_49	1975	7197	138	417		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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782642_c2_77	1976	7198	66	201		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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16659411_f2_19	1977	7199	83	252	183	1.9e-13
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Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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2741687_c1_28	1978	7200	696	2091	281	1.4e-23
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Protein name

Locus Name

Acc#

conserved hypothetical protein MTH83

pir:F69210

F69210

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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3942136_c3_38	1979	7201	649	1950	1708	8.9e-176
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Protein name

Locus Name

Acc#

threonyl-tRNA synthetase

pir:B75317

B75317

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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47111562_f2_18	1980	7202	421	1266		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
7032800_c1_30	1981	7203	116	348	262	1.5e-22

Protein name

Locus Name

Acc#

sp:IF3_HAEIN

P43814

Description

TRANSLATION INITIATION FACTOR IF-3

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10741260_c2_21	1982	7204	74	225	110	1.9e-06

Protein name

Locus Name

Acc#

sp:RL29_BACST

P04457

Description

50S RIBOSOMAL PROTEIN L29

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1204063_c3_23	1983	7205	146	441	461	1.2e-43

Protein name

Locus Name

Acc#

sp:RL16_SYNY3

P73313

Description

50S RIBOSOMAL PROTEIN L16

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24399202_c1_16	1984	7206	244	735	639	1.7e-62

Protein name

Locus Name

Acc#

gp:AB017508

AB017508

Description

Bacillus halodurans C-125 genomic DNA, 32 kb fragment, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26600312_c1_14	1985	7207	210	633	486	2.8e-46

Protein name

Locus Name

Acc#

sp:RL4_BACST

P28601

Description

50S RIBOSOMAL PROTEIN L4

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31525257_c3_22	1986	7208	90	273	326	2.5e-29

Protein name

Locus Name

Acc#

ribosomal protein S19

pir:H72249

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4688811_c1_15	1987	7209	279	840	853	3.6e-85

Protein name

Locus Name

Acc#

gp:AB017508

AB017508

Description

Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4978427_c2_19	1988	7210	97	294	173	4.1e-13

Protein name

Locus Name

Acc#

sp:RL23_SYNY3

P73318

Description

50S RIBOSOMAL PROTEIN L23

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5976007_f3_12	1989	7211	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
659702_c1_18	1990	7212	89	270	278	3.1e-24

Protein name

Locus Name

Acc#

ribosomal protein S17

pir:C72249

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6829637_c2_20	1991	7213	143	432	231	2.9e-19

Protein name

Locus Name

Acc#

sp:RL22_ECOLI

P02423

Description

50S RIBOSOMAL PROTEIN L22

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11924131_f1_14	1992	7214	245	735		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12284405_f1_1	1993	7215	400	1203	279	7.7e-23

Protein name

Locus Name

Acc#

sp:RFBX_SALTY

P26400

Description

PUTATIVE O-ANTIGEN TRANSPORTER

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1251537_c2_67	1994	7216	61	186	81	0.014

Protein name

Locus Name

Acc#

gp:CEY39C12A

AL132859

Description

Caenorhabditis elegans cosmid Y39C12A, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1366500_f1_3	1995	7217	383	1152	158	9.7e-09

Protein name

Locus Name

Acc#

hypothetical protein 17.9

pir:S22619

S22619

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13710902_f3_32	1996	7218	407	1224	142	1.1e-06

Protein name

Locus Name

Acc#

putative membrane protein

gp:SPN131984

AJ131984

Description

Streptococcus pneumoniae cap37 locus.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14882818_c2_76	1997	7219	93	282	165	2.9e-12

Protein name

Locus Name

Acc#

sp:DBH_BACST

Description

DNA-BINDING PROTEIN II (HB) (HU)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15822135_f3_31	1998	7220	309	930	241	2.5e-20

Protein name

Locus Name

Acc#

sp:Y868_HAEIN

Description

PUTATIVE GLYCOSYL TRANSFERASE H10868,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
161592_f3_30	1999	7221	321	966	194	3.1e-13

Protein name

Locus Name

Acc#

WbCD

gp:YEU46859

Description

Yersinia enterocolitica lipopolysaccharide O-side chain biosynthesis genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19697126_f3_37	2000	7222	316	951	1366	1.6e-139

Protein name

Locus Name

Acc#

putative UDP-GlcNAc:undecaprenylphosphate

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1989077_f3_36	2001	7223	320	963	809	2.4e-147

Protein name

Locus Name

Acc#

UDP-glucose-4-epimerase/dTDP-glucose-4,6

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20350437_f2_15	2002	7224	253	762	362	3.8e-33

Protein name

Locus Name

Acc#

unknown

gp:AF078135

AF078135

Description

Leptospira borgpetersenii lipopolysaccharide o-antigen biosynthetic locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21879191_f3_40	2003	7225	239	720	129	2.6e-06

Protein name

Locus Name

Acc#

lipopeptide antibiotic iturin A biosynthesis
protein:protein slr0495:protein slr0495

pir:S74408

S74408

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22304007_f2_29	2004	7226	404	1215		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23945251_f1_11	2005	7227	453	1362	542	3.2e-52

Protein name Locus Name Acc#
hemolysin-related protein pir:F72326 F72326

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24410751_c2_85	2006	7228	64	195		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24426550_f1_8	2007	7229	370	1113	594	1.0e-57

Protein name Locus Name Acc#

A/G-specific adenine glycosylase homolog yfhQ pir:A69802 A69802

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24813137_f1_10	2008	7230	156	471	331	7.4e-30

Protein name Locus Name Acc#

single stranded DNA-binding protein gp:SHU64098 U64098

Description

Shewanella hanedai single stranded DNA-binding protein (ssb) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2537767_c2_88	2009	7231	105	315	76	0.0077

Protein name

Locus Name

Acc#

host shut off virion protein

gp:CHDNACSO

X89471

Description

Canine herpesvirus DNA for capsid and host shut off virion proteingenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26303426_c3_102	2010	7232	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26376260_f2_26.....	2011	7233	781	2346		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32637_f3_35.....	2012	7234	262	789	249	3.6e-21

Protein name

Locus Name

Acc#

rhamnosyl transferase

gp:AF097519

AF097519

Description

Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (rmlB), glucose-1-phosphate thymidyl transferase (rmlA), dTDP-4-keto-L-rhamnose reductase (rmlD), dTDP-4-keto-6-deoxy-D-glucose 3,5-epimerase (rmlC), and rhamnosyltransferase (wbbL) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34101512_c2_68	2013	7235	110	333	172	5.2e-13

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:G75347

G75347

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4023377_f1_2	2014	7236	318	957	79	0.023

Protein name

Locus Name

Acc#

ribosomal protein S10

gp:U17009

U17009

Description

Phytophthora infestans mitochondrion, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4719137_c1_65	2015	7237	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4728313_f2_16	2016	7238	254	765	348	1.2e-31

Protein name

Locus Name

Acc#

putative glycosyl transferase

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4875677_f1_9	2017	7239	526	1581	297	1.2e-45

Protein name

Locus Name

Acc#

sp:STS_HUMAN

P08842

Description

SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5273377_f3_33	2018	7240	299	900		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5287507_f1_13	2019	7241	291	876		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
582628_c3_92	2020	7242	123	372	118	2.8e-07

Protein name

Locus Name

Acc#

Yjdi-like protein

gp:LLLNISZ

Y13384

Description

Lactococcus lactis nisZ gene and 3 ORF's.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6015692_f3_45	2021	7243	68	207	86	0.0011

Protein name

Locus Name

Acc#

cryptogene protein G4

pir:S51910

S51910

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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7240938_c1_63	2022	7244	527	1584	631	5.5e-76
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Protein name

Locus Name

Acc#

sp:CAFA_HAEIN

P45175

Description

CYTOPLASMIC AXIAL FILAMENT PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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9954652_f3_34	2023	7245	207	624	424	1.0e-39
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Protein name

Locus Name

Acc#

sp:WBBJ_ECOLI

Description

(EC 2.3.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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10558252_f2_8	2024	7246	335	1008	88	0.0017
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Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12351376_f2_7	2025	7247	529	1590	1357	1.4e-138

Protein name

Locus Name

Acc#

unknown

gp:AF125164

AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16102032_f2_6	2026	7248	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25962692_c3_33.....	2027	7249	104	315		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
311770636_f2_4.....	2028	7250	305	918	95	0.013

Protein name

Locus Name

Acc#

gp:AB021078

AB021078

Description

plasmid ColIb-P9 DNA, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7089527_f3_11	2029	7251	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
196952_f3_10	2030	7252	509	1530		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
203177_f1_3	2031	7253	362	1089		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23633438_c3_38	2032	7254	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23635900_f2_6	2033	7255	344	1035		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24649063_f1_2	2034	7256	345	1038		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35632826_f2_7	2035	7257	227	684		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
45317951_f2_5	2036	7258	646	1941	233	4.5e-18

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
7275081_f1_1	2037	7259	246	741	157	4.8e-16

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10552188_c3_304	2038	7260	170	513	158	5.9e-14
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
glucosamine--fructose-6-phosphate aminotransferase PAB2201			pir:F75212		F75212	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10735812_f1_17	2039	7261	112	339	154	4.4e-10
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:ASNB_ECOLI		P22106	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10744013_c1_192	2040	7262	189	570	114	3.0e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein Rv1624c			pir:F70558		F70558	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10991288_f1_36	2041	7263	220	663	291	1.3e-25
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:TRPF_THEMA		Q56320	
<u>Description</u>						

N- (5'-PHOSPHORIBOSYL) ANTHRANILATE ISOMERASE, (PRAI)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11879400_c2_208	2042	7264	774	2325	243	6.9e-17

Protein name

Locus Name

Acc#

sp:CIRA_ECOLI

P17315

Description

COLICIN I RECEPTOR PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12125931_f3_144	2043	7265	214	645	220	4.3e-18

Protein name

Locus Name

Acc#

2,3,4,5-tetrahydropyridine-2-carboxylate
N-succinyltransferase-related protein

pir:H72245

H72245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12213186_f3_148	2044	7266	210	633	336	2.2e-30

Protein name

Locus Name

Acc#

flavodoxin

pir:H71850

H71850

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1228787_f3_136	2045	7267	486	1461	718	7.2e-71

Protein name

Locus Name

Acc#

anthranilate synthase, component I

pir:D72414

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12988762_f3_145	2046	7268	69	210	82	0.026

Protein name

Locus Name

Acc#

sp:NU5M_PETMA

Q35543

Description

NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14336463_c2_209	2047	7269	340	1023	332	6.1e-45

Protein name

Locus Name

Acc#

hypothetical protein

pir:D72115

D72115

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14354642_f1_8	2048	7270	449	1350		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14632808_f3_142	2049	7271	813	2442		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14726593_f1_24	2050	7272	101	306	163	2.7e-11

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76639

S76639

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15656537_c3_309	2051	7273	446	1341	133	1.3e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein aq_1059			pir:C70391		C70391	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c3_293.....	2052	7274	431	1296	1723	2.3e-177
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:JQ1020		JQ1020	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
182832_c1_203.....	2053	7275	384	1155	1034	2.4e-104
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
carbamoyl phosphate synthetase III			gp:FR24G11		Z93780	
<u>Description</u>						
Fugu rubripes genes encoding carbamoyl phosphate synthetase III, myosin light chain, MAP2.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19578255_f2_87.....	2054	7276	231	696	460	1.6e-43
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:TRPG_THEMEA		Q08654	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1964390_f2_83	2055	7277	97	294	83	0.035

Protein name

Locus Name

Acc#

hypothetical protein HeLE

pir:T08605

T08605

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19955328_f3_123.....	2056	7278	498	1497		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2111262_f1_37.....	2057	7279	362	1089	736	8.9e-73

Protein name

Locus Name

Acc#

sp:ASG1_ECOLI

P18840

Description

(L-ASNASE I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2131327_f1_40.....	2058	7280	386	1161	198	3.4e-32

Protein name

Locus Name

Acc#

Cps9F

gp:AF155805

AF155805

Description

Streptococcus suis strain 5218 Cps9D (cps9D) gene, partial cds; Cps9E (cps9E), Cps9F (cps9F), and Cps9G (cps9G) genes, complete cds; and Cps9H (cps9H) gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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22033141_c1_162	2059	7281	140	423		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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22270175_f1_21	2060	7282	300	903	186	1.8e-11
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Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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22304531_f1_31	2061	7283	401	1206	1218	7.5e-124
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Protein name

Locus Name

Acc#

sp:TRPB_THEMEA

P50909

Description

TRYPTOPHAN SYNTHASE BETA CHAIN,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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22460027_f3_151	2062	7284	90	273		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c1_190	2063	7285	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23600812_c1_169	2064	7286	104	315		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23650256_c3_289.....	2065	7287	382	1149	971	1.1e-97

Protein name

Locus Name

Acc#

sp:YQHD_ECOLI

Q46856

Description

HYPOTHETICAL OXIDOREDUCTASE IN METC-SUFI INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23851532_c1_204.....	2066	7288	1084	3255	3165	0.0

Protein name

Locus Name

Acc#

sp:PYRI_DICDI

P20054

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24022162_f3_147	2067	7289	395	1188	1161	8.2e-118
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:PU91_YEAST				P54113	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24026537_f1_23	2068	7290	313	942	962	1.0e-96
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
aspartate aminotransferase related protein	pir:E69168				E69168	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24081580_f3_121	2069	7291	505	1518	1698	1.0e-174
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	gp:AB025342				AB025342	
<u>Description</u>						
Moritella marina genes, complete cds, similar to eicosapentaenoic acid synthesis gene cluster.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24267843_f2_81	2070	7292	284	855	244	1.2e-20
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
exopolyphosphatase	pir:E70376				E70376	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24317552_f3_143	2071	7293	331	996		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24429187_f3_152.....	2072	7294	165	498	324	4.1e-29
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Protein name

Locus Name

Acc#

sp:THIO_BORBU

051088

Description

THIOREDOXIN (TRX)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24486082_f1_35.....	2073	7295	281	846	436	5.5e-41
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Protein name

Locus Name

Acc#

sp:TRPC_PSEPU

P20578

Description

INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE, (IGPS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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245927_c1_173.....	2074	7296	238	717		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24641962_f3_140	2075	7297	265	798	407	6.5e-38

Protein name

Locus Name

Acc#

sp:TRPA_METVO

P14637

Description

TRYPTOPHAN SYNTHASE ALPHA CHAIN,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24645650_c2_265	2076	7298	388	1167		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26820202_f3_131.....	2077	7299	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2744752_f2_71.....	2078	7300	269	810	148	8.9e-09

Protein name

Locus Name

Acc#

probable glycerophosphoryl diester
phosphodiesterase

pir:G75506

G75506

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2914202_c3_305	2079	7301	627	1884	151	1.2e-23

Protein name

Locus Name

Acc#

sp:PUR1_HAEIN

P43854

Description

PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPATASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2926562_f2_99	2080	7302	352	1059	221	5.2e-18

Protein name

Locus Name

Acc#

subunit of the terminal oxidase with unknown

gp:AADOXP24H

Y08730

Description

A.ambivalens doxA gene locus with doxD and doxA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2947687_c2_263	2081	7303	119	360	152	6.9e-11

Protein name

Locus Name

Acc#

probable thioredoxin

pir:T08271

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31672007_f3_130	2082	7304	692	2079	1338	1.4e-136

Protein name

Locus Name

Acc#

polyphosphate kinase

gp:AF083928

AF083928

Description

Vibrio cholerae polyphosphate kinase (ppk) and exopolyphosphatase (ppx) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31750887_c3_285	2083	7305	75	228	101	1.7e-05

Protein name Locus Name Acc#
hypothetical protein APE2554 pir:C72489 C72489

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32440650_c2_243.....	2084	7306	547	1644	79	0.0024

Protein name Locus Name Acc#
gp:CELB0454 AF025452

Description

Caenorhabditis elegans cosmid B0454.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32458331_f3_137.....	2085	7307	342	1029	541	4.1e-52

Protein name Locus Name Acc#
sp:TRPD_METUA Q57686

Description

ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33398412_c2_266.....	2086	7308	151	453	109	4.1e-05

Protein name Locus Name Acc#
immunoreactive 36 kDa antigen PG14 gp:AF145798 AF145798

Description

Porphyromonas gingivalis strain W50 immunoreactive 36 kDa antigenPG14 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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3376327_f3_106	2087	7309	64	195		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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34017302_f3_126	2088	7310	303	912	550	4.6e-53
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Protein name

Locus Name

Acc#

sp:DAPF_SYNY3

P74667

Description

DIAMINOPIMELATE EPIMERASE, (DAP EPIMERASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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34235700_f3_129	2089	7311	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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35345063_f3_161	2090	7312	66	201		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35392907_f2_75	2091	7313	92	279	258	7.2e-22
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
aspartate aminotransferase related protein			pir:E69168			E69168
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36136262_c2_216	2092	7314	210	633	136	5.5e-12
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
probable response regulator			pir:T34675			T34675
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4082762_c1_165	2093	7315	378	1137	474	5.2e-45
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:MAUG_PARDE			Q51658
<u>Description</u>						
METHYLAMINE UTILIZATION PROTEIN MAUG PRECURSOR						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4379433_f1_39	2094	7316	143	432	203	5.7e-15
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
bZIP histidine kinase			gp:PPUY18245			Y18245
<u>Description</u>						
Pseudomonas putida todX, todF, todC1, todC2, todB, todA, todD, todE, todG, todI, todH, todS, todT genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6057812_f1_43	2095	7317	134	405		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
806512_f1_5	2096	7318	321	966	194	1.2e-13

Protein name

Locus Name

Acc#

PobR protein

gp:PPU251792

AJ251792

Description

Pseudomonas putida pobR gene for PobR protein and pobA gene forPobA protein.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11816716_c3_86	2097	7319	78	237	119	2.8e-07

Protein name

Locus Name

Acc#

gp:D90701

Description

Escherichia coli genomic DNA. (13.6 - 14.0 min).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16051540_c1_63	2098	7320	122	369		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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20203951_c1_55	2099	7321	90	273		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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20895303_f1_11	2100	7322	1045	3138		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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22687817_c3_100	2101	7323	126	381		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24335781_f2_25	2102	7324	140	423	77	0.0064
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:NOLP_RHILP	P23717
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Description

NODULATION PROTEIN NOLP

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24727127_c3_102	2103	7325	155	468	243	2.1e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative oxygen-independent coproporphyrinogen	gp:AF157642	AF157642

Description

Desulfitobacterium dehalogenans putative oxygen-independent coproporphyrinogen III oxidase (hemN) gene, partial cds; Hrd22-1(hrd22-1) gene, complete cds; and two-component sensor histidine kinase homolog (hkhB) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25494062_c3_99	2104	7326	84	255		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26594127_f3_40.....	2105	7327	536	1611	2764	1.1e-287

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
mobilization protein C	gp:AF118243	AF118243

Description

Bacteroides fragilis mobilization protein C (mobC) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26602175_c1_62.....	2106	7328	229	690	171	6.7e-13

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
RNA polymerase sigma factor SigZ-like protein	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33708427_c1_43	2107	7329	157	474		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34412578_f1_1	2108	7330	102	309		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36367837_c1_44	2109	7331	423	1272	531	4.0e-55
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

sp:YBDN_ECOLI P77216

Description

HYPOTHETICAL 47.8 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4032950_f1_3	2110	7332	296	891		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4103377_f2_28	2111	7333	118	357		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4180181_c2_68.....	2112	7334	126	381	265	7.3e-23
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Protein name

Locus Name

Acc#

unknown

gp:AF118244

AF118244

Description

Bacteroides fragilis unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4406908_c1_46.....	2113	7335	69	210	199	7.2e-16
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Protein name

Locus Name

Acc#

sp:YBDM_ECOLI

P77174

Description

HYPOTHETICAL 23.9 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4486052_f1_2.....	2114	7336	69	210		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6287687_f1_10	2115	7337	439	1320	130	3.1e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
M protein			gp:SSGEMM		X60098	
<u>Description</u>						
Streptococcus sp. (group G) emm gene for M protein.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6522533_c2_81	2116	7338	213	642	120	4.3e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable transposase for IS1558			pir:F70678		F70678	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9897137_c3_103	2117	7339	102	309	83	0.0087
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
coproporphyrinogen III oxidase			gp:BSHRCA		Y09446	
<u>Description</u>						
B.stearothermophilus hemN gene (partial) and hrcA gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14463305_c3_24	2118	7340	520	1563	1215	1.6e-123
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
50 kD antigen PG1			gp:AF144076		AF144076	
<u>Description</u>						
Porphyromonas gingivalis strain W50 50 kD antigen PG1 gene,complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16603425_c1_18	2119	7341	361	1083	558	1.7e-68
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
NqrB					gp:AF165980	AF165980
<u>Description</u>						
Vibrio harveyi Na+-translocating NADH-quinone oxidoreductase complex operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19775252_f2_8	2120	7342	432	1299		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30728302_c3_23.....	2121	7343	355	1068	707	1.1e-69
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					sp:BLMH_RAT	P70645
<u>Description</u>						
BLEOMYCIN HYDROLASE, (BLM HYDROLASE) (BMH)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13845052_c3_49.....	2122	7344	812	2439	649	3.1e-82
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein	pir:JC6027				JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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1953386_f3_23	2123	7345	148	447		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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19553528_c1_32	2124	7346	101	306	99	2.8e-05
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Protein name

Locus Name

Acc#

sp:Y660_HAEIN

P44031

Description

HYPOTHETICAL PROTEIN HI0660

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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21988900_f2_17	2125	7347	316	951		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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23492761_f1_6	2126	7348	89	270		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23610933_c1_26	2127	7349	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23643903_f1_3	2128	7350	121	366		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24494056_f1_7	2129	7351	498	1494	481	1.1e-44
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Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24892087_c1_36	2130	7352	332	996	178	2.9e-10
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Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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29691536_f2_13	2131	7353	89	270		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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31414132_c2_41	2132	7354	68	207		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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7245312_c3_47	2133	7355	101	306	101	1.7e-05
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Protein name

Locus Name

Acc#

putative transcriptional regulator

gp:YPPCP1

AL109969

Description

Yersinia pestis plasmid pPCP1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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1360802_f3_34	2134	7356	373	1122		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13884652_f3_32	2135	7357	125	378	259	2.2e-21

Protein name

Locus Name

Acc#

sp:TRA2_BACFR

Q45119

Description

TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS21-LIKE

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14556510_f3_30	2136	7358	209	630	396	9.6e-37

Protein name

Locus Name

Acc#

YadS

gp:AF198617

AF198617

Description

Aeromonas caviae polar flagella locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
195337_f3_33	2137	7359	103	312		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20815912_c2_56	2138	7360	446	1341	494	3.9e-47

Protein name

Locus Name

Acc#

lipopolysaccharide biosynthesis protein bplD
homolog

pir:G64487

G64487

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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25422952_f1_12	2139	7361	165	498		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26174037_f1_9	2140	7362	88	267		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26581625_f3_35	2141	7363	320	963		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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30523513_c1_47	2142	7364	731	2193	122	0.00035
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Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4006551_f1_10	2143	7365	110	333		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4087502_c1_45	2144	7366	179	540		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4100342_f1_8	2145	7367	65	198		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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7034587_f2_22	2146	7368	104	315	81	0.0058
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Protein name

Locus Name

Acc#

sp:ZN90_HUMAN

Q03938

Description

ZINC FINGER PROTEIN 90 (ZINC FINGER PROTEIN HTF9) (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16525383_c2_37	2147	7369	119	360		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32665833_c1_32	2148	7370	577	1731	150	3.4e-07

Protein name

Locus Name

Acc#

immunoreactive 53 kD antigen PG123

gp:AF144641

AF144641

Description

Porphyromonas gingivalis strain W50 immunoreactive 53 kD antigenPG123 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36226558_c1_31	2149	7371	118	357		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36363967_c2_34	2150	7372	109	330		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36525317_c1_28	2151	7373	95	288		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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36679717_c2_33	2152	7374	61	186		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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5332628_c3_42	2153	7375	73	222		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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6459782_c2_35	2154	7376	138	417		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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23992175_c3_29	2155	7377	432	1296		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24006387_f1_4	2156	7378	763	2292	613	6.0e-59
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Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24511625_f1_5	2157	7379	70	213	52	0.042

Protein name Locus Name Acc#
heat shock transcription factor HSF21 pir:S59537

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24666656_f2_6	2158	7380	397	1194	229	1.5e-16

Protein name Locus Name Acc#
dipeptidase homolog gp:AF060858 AF060858

Description

Salmonella dublin regulatory protein CopR (copR), histidine kinase(copS), SPI-4 pathogenicity island containing dipeptidase homolog(pipD), SopB (sopB), PipC (pipC), PipB (pipB), and PipA (pipA)genes, complete cds; and tRNA-Ser gene, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33412762_f1_2	2159	7381	586	1761	1163	5.0e-118

Protein name Locus Name Acc#
sp:YHXB_BACSU P18159

Description

PROBABLE PHOSPHOMANNOMUTASE, (PMM)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34119717_f3_12	2160	7382	64	195		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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3912688_c2_26	2161	7383	81	246		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4344035_f3_13	2162	7384	314	945	135	2.4e-06
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Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor (fiuI), transmembrane sensor (fiuR), and hydroxamate-type ferrisiderophore receptor (fiuA) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4735655_f2_9	2163	7385	195	588	199	7.2e-16
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Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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3001688_f3_13	2164	7386	629	1890	1567	7.8e-161
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Protein name

Locus Name

Acc#

sp:PARE_BORBU

Q59189

Description

TOPOISOMERASE IV SUBUNIT B,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33361630_f2_9	2165	7387	160	483	305	4.2e-27

Protein name

Locus Name

Acc#

probable KDO transferase

pir:T35652

T35652

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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33707761_g3_32	2166	7388	146	441	131	1.2e-08
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Protein name

Locus Name

Acc#

hypothetical protein PH0474

pir:E71159

E71159

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4038927_f1_1	2167	7389	381	1146	331	7.4e-30
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Protein name

Locus Name

Acc#

hypothetical protein b2981

pir:C65084

C65084

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4195250_f3_11	2168	7390	323	972	627	3.2e-61
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Protein name

Locus Name

Acc#

conserved hypothetical protein aq_066

pir:E70306

E70306

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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5126407_f2_10	2169	7391	306	921	409	4.0e-38
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Protein name

Locus Name

Acc#

carboxy-terminal processing proteinase
ctpA, :tail-specific endopeptidase Prc

pir:B69610

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14664017_c3_5	2170	7392	209	627	376	1.9e-33

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24257800_f2_2	2171	7393	398	1197	343	4.0e-31

Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12687687_f3_16	2172	7394	156	471	147	2.5e-10

Protein name

Locus Name

Acc#

sp:CUTF_ECOLI

P40710

Description

COPPER HOMEOSTASIS PROTEIN CUTF PRECURSOR (LIPOPROTEIN NLPE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14067057_f1_8	2173	7395	738	2217	863	3.1e-86

Protein name

Locus Name

Acc#

Na⁺/H⁺-exchanging protein slr1595:Na⁺/H⁺ antiporter:Na⁺/H⁺ antiporter

pir:S74951

S74951

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14354762_f3_15	2174	7396	117	354	90	0.0020

Protein name

Locus Name

Acc#

gp:CEY111B2C

AL132906

Description

Caenorhabditis elegans cosmid Y111B2C, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f2_14	2175	7397	182	546	702	3.6e-69

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f3_25.....	2176	7398	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24412566_f2_13.....	2177	7399	358	1077	153	1.1e-07

Protein name

Locus Name

Acc#

KIAA0850 protein

gp:AB020657

AB020657

Description

Homo sapiens mRNA for KIAA0850 protein, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34181531_c1_33	2178	7400	402	1209	86	0.0058

Protein name

Locus Name

Acc#

sp:Y414_HAEIN

Description

HYPOTHETICAL PROTEIN HI0414

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5172277_c2_40	2179	7401	466	1401		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16270793_c2_53	2180	7402	87	264		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2007255_c3_60	2181	7403	419	1260	759	3.3e-75

Protein name

Locus Name

Acc#

hypothetical protein

pir:G72244

G72244

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22150262_c2_47	2182	7404	211	636	570	3.5e-55

Protein name

Locus Name

Acc#

sp:Y168_HAEIN

Description

HYPOTHETICAL PROTEIN HI0168/169

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24744125_c1_44	2183	7405	164	495	276	5.0e-24

Protein name

Locus Name

Acc#

macrophage infectivity potentiator

gp:LSU92222

U92222

Description

Legionella spiritensis macrophage infectivity potentiator (mip) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24804642_c1_41	2184	7406	429	1290	1031	4.9e-104

Protein name

Locus Name

Acc#

Na+-translocating NADH-ubiquinone oxidoreductase, beta chain

pir:D64052

D64052

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26214062_c1_46	2185	7407	152	456	155	1.5e-10

Protein name

Locus Name

Acc#

sp:T2H2_HAEPA

P36433

Description

(R.HPA11)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26456280_c1_42	2186	7408	471	1416	452	1.5e-51

Protein name

Locus Name

Acc#

sp:DEAD_BACSU

P42305

Description

PROBABLE ATP-DEPENDENT RNA HELICASE DEAD

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30105385_c3_61	2187	7409	183	552	221	3.3e-18

Protein name

Locus Name

Acc#

sp:AB014075

AB014075

Description

Clostridium histolyticum genes for hypoxanthine-guaninephosphoribosyl-transferase (HGPRTase), GTPase and 12 ORFs, complete and partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34174063_c3_55	2188	7410	214	645	626	4.1e-61

Protein name

Locus Name

Acc#

sp:NQRE_HAEIN

P71342

Description

(NA-NQR COMPLEX SUBUNIT 5)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35806324_c1_40	2189	7411	84	255	102	4.8e-05

Protein name

Locus Name

Acc#

Na+-translocating NADH-ubiquinone oxidoreductase, gamma chain

pir:S65528

S65528

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4142191_c1_43	2190	7412	365	1098	839	1.1e-83

Protein name

Locus Name

Acc#

sp:SERC_BACSU

Description

PROTEIN 234) (VEG234)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
916577_c3_59	2191	7413	327	984	1049	6.1e-106

Protein name

Locus Name

Acc#

D-3-phosphoglycerate dehydrogenase

gp:AF079881

AF079881

Description

Entodinium caudatum D-3-phosphoglycerate dehydrogenase mRNA,partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
984752_c2_3	2192	7414	110	333	460	1.6e-43

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
116052_c2_50	2193	7415	86	261	96	5.9e-05

Protein name

Locus Name

Acc#

hypothetical protein MJ1608

pir:G64500

G64500

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12704377_f2_10	2194	7416	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f1_6	2195	7417	271	813	1021	5.6e-103

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19923150_c3_61	2196	7418	175	528		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20500430_f3_31	2197	7419	115	348	72	0.020

Protein name

Locus Name

Acc#

PRO1914

gp:AF118084

AF118084

Description

Homo sapiens PRO1914 mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f2_21	2198	7420	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24229677_c3_60	2199	7421	113	342		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25835942_c1_41	2200	7422	161	486		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34173157_c1_37	2201	7423	198	597	483	5.8e-46

Protein name

Locus Name

Acc#

conserved hypothetical protein CAB06296

pir:T17189

T17189

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34407161_c3_65	2202	7424	339	1020	652	7.1e-64
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
low specificity L-threonine aldolase			gp:AB001577		AB001577	
<u>Description</u>						
Pseudomonas sp. DNA for low specificity L-threonine aldolase, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35166557_f3_22	2203	7425	736	2211	120	0.0012
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein T13D8.29			pir:T02292		T02292	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4329831_c2_51	2204	7426	186	561	218	7.0e-18
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
AlgT			gp:AF190580		AF190580	
<u>Description</u>						
Pseudomonas syringae pv. syringae AlgT (algT) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5188937_f1_4	2205	7427	146	441		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
582552_f3_29	2206	7428	601	1806	1549	6.3e-159

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
pyruvate dehydrogenase	pir:T34668	T34668

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
595700_g2_46	2207	7429	89	270		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7167057_g2_45	2208	7430	90	273	100	0.00069

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

sp:YHV8_YEAST	P38853
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Description

HYPOTHETICAL 131.1 KD PROTEIN IN REC104-SOL3 INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11049030_g1_97	2209	7431	70	213	109	3.3e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

hypothetical protein APE0580	pir:D72643	D72643
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f3_63	2210	7432	431	1296	1723	2.3e-177

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

hypothetical protein	pir:JQ1020	JQ1020
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Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21519061_f2_39	2211	7433	262	789	175	3.8e-11

Protein name

Locus Name

Acc#

sp:Y612_METJA

Q58029

Description

HYPOTHETICAL PROTEIN MJ0612

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22689083_f1_16	2212	7434	396	1191	766	5.9e-76

Protein name

Locus Name

Acc#

aminotransferase (AspC family)

pir:B70325

B70325

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22860128_f1_14	2213	7435	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23626550_c2_121	2214	7436	306	921	391	3.2e-36

Protein name

Locus Name

Acc#

sp:NPL_ECOLI

P06995

Description

ACID ALDOLASE) (N-ACETYLNEURAMINATE PYRUVATE LYASE) (NALASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24229677_c3_127	2215	7437	165	498		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24329587_c1_104	2216	7438	1102	3309	421	9.0e-71

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24800675_f1_20	2217	7439	683	2052	738	6.2e-77

Protein name

Locus Name

Acc#

sp:PRIM_CLOAB

P33655

Description

DNA PRIMASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26287762_c3_133	2218	7440	534	1605	232	1.3e-38

Protein name

Locus Name

Acc#

sp:STS_RAT

P15589

Description

SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26595402_f2_38	2219	7441	355	1068	380	4.7e-35

Protein name

Locus Name

Acc#

phospho-2-dehydro-3-deoxyheptonate
aldolase/chorismate mutase

pir:A75449

A75449

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3.1.7.26635_f3_64.....	2220	7442	300	903	363	3.0e-33

Protein name

Locus Name

Acc#

sp:PHEA_ERWHE

Q02286

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35234800_c1_88.....	2221	7443	521	1566	254	1.3e-38

Protein name

Locus Name

Acc#

sp:STS_MOUSE

P50427

Description

SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3.9.108.75_f3_84.....	2222	7444	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3930163_c3_129	2223	7445	313	942	167	4.3e-10

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3937927_f3_83	2224	7446	99	300	106	1.3e-05

Protein name

Locus Name

Acc#

unknown

gp:SPU59236

U59236

Description

Synechococcus PCC7942 ribosomal protein S1 of 30S ribosome (rps1), ORF271, ORF231, ORF341, carboxyltransferase alpha subunit (accA), ORF245, ORF227, and GTP cyclohydrolase I (fole) genes, completecds, and ORF205 gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3985936_c3_128	2225	7447	195	588	163	4.7e-12

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4117167_c3_130	2226	7448	1128	3387	737	4.6e-71

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4875001_c2_126	2227	7449	493	1482	172	9.1e-14

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5941260_c2_106	2228	7450	199	600	557	8.3e-54

Protein name

Locus Name

Acc#

sp:GCH1_SYNY3

Q55759

Description

GTP CYCLOHYDROLASE I, (GTP-CH-I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
678385_c1_103	2229	7451	286	861	168	1.2e-11

Protein name

Locus Name

Acc#

sp:YCBG_BACSU

P42239

Description

(ORF6)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9953161_c1_87	2230	7452	542	1629	171	4.3e-13
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:U96771		U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11953382_f2_22	2231	7453	133	402	98	0.00012
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein F19H6.4			pir:T21123		T21123	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14507137_f1_12	2232	7454	201	606		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16116655_c2_76	2233	7455	183	552	323	5.2e-29
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:DYR_NEIGO		P04174	
<u>Description</u>						
DIHYDROFOLATE REDUCTASE,						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16832885_f1_18	2234	7456	405	1218	1614	8.2e-166
Protein name			Locus Name			Acc#
hypothetical protein			pir:JQ1020			JQ1020
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16882762_c1_55	2235	7457	291	876	112	0.0015
Protein name			Locus Name			Acc#
hypothetical protein			pir:T29116			T29116
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16884630_f1_1	2236	7458	88	267	123	5.6e-07
Protein name			Locus Name			Acc#
probable oxidoreductase			pir:F70970			F70970
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16886405_c3_107	2237	7459	132	399	120	2.6e-07
Protein name			Locus Name			Acc#
hypothetical protein PH1073			pir:F71101			F71101
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20901531_c3_99	2238	7460	271	816	1030	6.3e-104
Protein name			Locus Name			Acc#
thymidylate synthase			gp:NGU86637			U86637
Description						

Neisseria gonorrhoeae thymidylate synthase (thyA) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22165933_c1_51	2239	7461	190	573		
Protein name					Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22860128_f2_34	2240	7462	83	252	64	0.031
Protein name					Locus Name	Acc#

sp:SPRC_XENLA P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2370340_f3_37	2241	7463	526	1581	604	8.7e-59
Protein name					Locus Name	Acc#

probable oxidoreductase

pir:F70970 F70970

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24222175_f1_10	2242	7464	281	846	208	8.0e-17
Protein name					Locus Name	Acc#

sp:YA22_METTH 027101

Description

PUTATIVE BIOPOLYMER TRANSPORT PROTEIN EXBB HOMOLOG

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24509675_f3_44	2243	7465	155	468		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26382062_f1_6	2244	7466	239	720	139	2.2e-07
Protein name			Locus Name		Acc#	
siderophore-mediated iron transport protein			pir:F71829		F71829	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32244077_f3_38	2245	7467	290	873	377	9.9e-35
Protein name			Locus Name		Acc#	
UBE-1a			gp:AB030503		AB030503	
Description						

Mus musculus mRNA for UBE-1a, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3242201_f2_30	2246	7468	69	210		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34417255_f1_11	2247	7469	158	477	107	0.00056
Protein name			Locus Name		Acc#	
hypothetical protein PH1889			pir:D71202		D71202	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34504015_f1_8	2248	7470	244	735		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34573385_f3_43.....	2249	7471	347	1044	517	1.4e-49
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
bifunctional short chain isoprenyl diphosphate synthase (idsA) homolog				pir:F69535		F69535
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35756562_f3_36.....	2250	7472	457	1374	972	8.8e-98
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
citrate synthase				gp:AF088222		AF088222
<u>Description</u>						

Lactococcus lactis subsp. lactis citrate synthase, aconitate hydratase, and truncated isocitrate dehydrogenase genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36367125_f1_16.....	2251	7473	160	483	311	9.7e-28
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:ASNC_HAEIN		P44337
<u>Description</u>						

REGULATORY PROTEIN ASNC

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4428518_c1_67	2252	7474	317	954	428	3.9e-40
Protein name			Locus Name			Acc#
LytB protein			pir:G70449			G70449
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4881510_c3_109	2253	7475	278	837	464	6.0e-44
Protein name			Locus Name			Acc#
			sp:KCY_BACSU			P38493
Description						
(CMP KINASE)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5114062_c3_111	2254	7476	331	996	834	3.7e-83
Protein name			Locus Name			Acc#
			sp:K6P1_THETH			P21777
Description						
(PFK1)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5884637_f1_9	2255	7477	259	780	411	2.5e-38
Protein name			Locus Name			Acc#
			sp:YABD_BACSU			P37545
Description						
HYPOTHETICAL 29.2 KD PROTEIN IN METS-KSGA INTERGENIC REGION						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
829417_f1_13	2256	7478	61	186		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9894067_c2_78	2257	7479	213	642	130	4.5e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:T29116		T29116	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10555302_f3_105	2258	7480	350	1053	255	8.4e-22
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein AF2231			pir:G69528		G69528	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10757817_c1_149	2259	7481	152	459		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10805308_c2_174	2260	7482	62	189		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12147561_c1_120	2261	7483	705	2118	169	8.1e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 53 kD antigen PG123	gp:AF144641	AF144641

Description
 Porphyromonas gingivalis strain W50 immunoreactive 53 kD antigenPG123 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12697180_c3_207	2262	7484	378	1137		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16140752_f1_27	2263	7485	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16621087_f1_10	2264	7486	134	405		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1954412_f1_29	2265	7487	173	522	181	5.8e-14
Protein name			Locus Name			Acc#
RNA polymerase ECF-type sigma factor sigW			pir:H69706			H69706
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22145627_c2_180	2266	7488	565	1698	263	1.1e-19
Protein name			Locus Name			Acc#
hypothetical protein aq_1220			pir:C70405			C70405
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23486536_f2_65	2267	7489	85	258		
Protein name			Locus Name			Acc#
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23704675_f3_114	2268	7490	551	1656	2162	6.9e-224
Protein name			Locus Name			Acc#
chaperonin groEL			pir:S47530			S47530
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24347332_f1_8	2269	7491	338	1017	896	9.9e-90
Protein name			Locus Name			Acc#
cysteine synthase			gp:MLCB22			Z98741
Description						
Mycobacterium leprae cosmid B22.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24414553_c1_143	2270	7492	63	192		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24415892_c1_121	2271	7493	181	546		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2463451_f3_79	2272	7494	270	813		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24805302_f1_16	2273	7495	232	699	432	1.5e-40
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

hypothetical protein yugP

pir:F70011

F70011

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24806517_f2_49	2274	7496	684	2055	231	1.6e-26
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
dipeptidyl peptidase III			gp:D89340		D89340	
<u>Description</u>						
Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25429837_c2_154	2275	7497	294	885	1200	6.1e-122
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:JQ1020		JQ1020	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25585781_c3_234.....	2276	7498	225	678	167	5.5e-12
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:Y374_METJA		Q57819	
<u>Description</u>						
HYPOTHETICAL PROTEIN MJ0374						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25641942_c3_219.....	2277	7499	231	696		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25911662_f2_52	2278	7500	166	501	216	1.1e-17

Protein name

Locus Name

Acc#

sp:FUR_CAMJE

Description

FERRIC UPTAKE REGULATION PROTEIN (FERRIC UPTAKE REGULATOR)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25978462_c1_142	2279	7501	608	1827	1308	2.2e-133

Protein name

Locus Name

Acc#

sp:RECQ_HABIN

P71359

Description

ATP-DEPENDENT DNA HELICASE RECQ,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26598467_f3_106	2280	7502	194	585		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2923517_f1_17	2281	7503	395	1188		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29455156_c1_129	2282	7504	624	1875	434	2.1e-40
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
acylamino-acid-releasing enzyme, (acyl-peptide hydrolase) (aph) (acylaminoacyl-peptidase) PAB1300			pir:H75007		H75007	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29926562_c3_208	2283	7505	276	831		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31447702_c1_128.....	2284	7506	273	822	535	2.9e-51
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
immunoreactive 89kD antigen PG87			gp:AF175722		AF175722	
<u>Description</u>						

Porphyromonas gingivalis strain W50 immunoreactive 89kD antigenPG87 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3323437_f2_77.....	2285	7507	345	1038		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33238187_c2_159	2286	7508	389	1170		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33287775_c2_158	2287	7509	506	1521		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33402001_c2_160	2288	7510	375	1128		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35781576_f1_30	2289	7511	297	894	582	1.9e-56
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
conserved hypothetical protein					pir:D75557	D75557

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3906380_f2_54	2290	7512	69	210	70	0.033
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
hypothetical protein Y68A4B.3					pir:T27307	T27307

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4022312_f3_113	2291	7513	93	282	393	2.0e-36

Protein name

Locus Name

Acc#

sp:CH10_PORGI

P42376

Description

10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4695302_c2_175	2292	7514	422	1269		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4718760_f3_88.....	2293	7515	300	903	193	4.1e-13

Protein name

Locus Name

Acc#

conserved hypothetical protein MTH83

pir:F69210

F69210

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4798465_f1_26.....	2294	7516	386	1161	291	1.3e-25

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:C72340

C72340

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4883437_f1_15	2295	7517	426	1281	967	3.0e-97

Protein name

Locus Name

Acc#

sp:PURA_YEAST

P80210

Description

ADENYLOSUCCINATE SYNTHETASE, (IMP--ASPARTATE LIGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
526637_f3_96	2296	7518	457	1374	429	3.0e-40

Protein name

Locus Name

Acc#

probable glycosyl hydrolase

pir:T36467

T36467

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5351687_f2_67	2297	7519	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
643818_c3_233	2298	7520	504	1515	424	5.9e-42

Protein name

Locus Name

Acc#

sp:YC46_HAEIN

P44135

Description

HYPOTHETICAL PROTEIN HI1246

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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6462751_f2_50	2299	7521	221	666		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

7222125_c3_218	2300	7522	474	1425	545	1.6e-52
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Protein name

Locus Name

Acc#

putative secreted protein

gp:SCM11

AL133278

Description

Streptomyces coelicolor cosmid M11.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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822137_c2_195	2301	7523	713	2142	121	5.4e-10
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Protein name

Locus Name

Acc#

heme receptor

gp:VIBHUTA

L27149

Description

Vibrio cholerae heme receptor (huta) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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9797180_f1_18	2302	7524	471	1416	535	1.5e-65
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Protein name

Locus Name

Acc#

sp:SYH_HUMAN

P12081

Description

(HISRS)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

9883507_c3_238	2303	7525	359	1080		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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9953556_f3_91	2304	7526	158	477	135	3.2e-08
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Protein name

Locus Name

Acc#

response regulator

gp:SPAJ6396

AJ006396

Description

Streptococcus pneumoniae rr07 and hk07 genes; two component system07.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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11906705_c1_6	2305	7527	303	912	1115	6.2e-113
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Protein name

Locus Name

Acc#

beta-glucosidase

gp:AF006658

AF006658

Description

Bacteroides fragilis beta-glucosidase gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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19578130_f2_3	2306	7528	66	201		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1276700_F1_1	2307	7529	102	309		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
162937_F2_83	2308	7530	707	2124	1709	7.0e-176
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16500342_c3_176	2309	7531	1335	4008	280	1.4e-39
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hybrid histidine kinase			gp:AF029704		AF029704	
<u>Description</u>						

Dictyostelium discoideum hybrid histidine kinase (dhkD) mRNA, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19564077_c3_177	2310	7532	180	543	247	2.1e-20
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable chromate transport protein			pir:G71379		G71379	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20830137_c2_135	2311	7533	459	1380	267	7.9e-25

Protein name

Locus Name

Acc#

sucrose transporter 1

sp:AF191024

AF191024

Description

Asarina barclaiana sucrose transporter 1 (SUT1) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22534633_c3_175	2312	7534	1294	3885	1006	2.8e-207

Protein name

Locus Name

Acc#

sp:PUR4_DROME

P35421

Description

(ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22712880_c1_123	2313	7535	1021	3066	661	3.6e-62

Protein name

Locus Name

Acc#

cation efflux system (AcrB/AcrD/AcrF family)

pir:F70342

F70342

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24234676_c3_174	2314	7536	437	1314		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24486562_f2_36	2315	7537	165	498		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24509680_c3_165	2316	7538	354	1065	254	1.1e-21
Protein name			Locus Name		Acc#	
cation efflux system (czcB-like)			pir:C70415		C70415	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24644812_c3_164	2317	7539	773	2322	1663	5.2e-171
Protein name			Locus Name		Acc#	
			sp:YVDK_BACSU		006993	
Description						

HYPOTHETICAL 88.3 KD PROTEIN IN CLPP-CRH INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2928461_f1_27	2318	7540	97	294		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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29892568_f3_91	2319	7541	80	243		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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30116437_c3_163	2320	7542	341	1026	451	1.4e-42
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Protein name

Locus Name

Acc#

transcription regulator, LacI family

pir:F72282

F72282

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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3944562_f3_90	2321	7543	279	840	645	3.9e-63
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Protein name

Locus Name

Acc#

YngK

gp:AF184956

AF184956

Description

Bacillus subtilis mycosubtilin operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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422776_c3_181	2322	7544	937	2814	1529	4.7e-234
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Protein name

Locus Name

Acc#

excinuclease ABC chain A:uvrA protein

pir:H69157

H69157

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4583338_f3_84	2323	7545	256	771	293	7.9e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
H. influenzae predicted coding region HI1127	gp:U32792	

Description

Haemophilus influenzae Rd section 107 of 163 of the complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5109662_c1_128	2324	7546	184	555	254	1.1e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable chromate transport protein	pir:C70068	C70068

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5110712_c1_124	2325	7547	426	1281	182	5.2e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 52kD antigen PG41	gp:AF175716	AF175716

Description

Porphyromonas gingivalis strain W50 immunoreactive 52kD antigen PG41 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7032127_f2_70	2326	7548	89	270		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
838142_f1_4	2327	7549	254	765	374	2.1e-34
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
YngK			gp:AF184956		AF184956	
<u>Description</u>						
Bacillus subtilis mycosubtilin operon, complete sequence.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
17048331_c3_60	2328	7550	406	1221	367	1.2e-32
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:AMPN_STRLI		Q11010	
<u>Description</u>						
(ALANINE AMINOPEPTIDASE)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
246445.75_c1_50	2329	7551	522	1569	155	2.0e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:AAP1_YEAST		P37898	
<u>Description</u>						
ALANINE/ARGININE AMINOPEPTIDASE,						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
246490.17_c3_58	2330	7552	415	1248	651	2.1e-66
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein SC4H2.17 SC4H2.17			pir:T35116		T35116	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26365961_c1_47	2331	7553	470	1413	139	2.1e-07

Protein name

Locus Name

Acc#

receptor antigen B (RagB)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29350375_c3_59	2332	7554	468	1407	345	1.9e-30

Protein name

Locus Name

Acc#

hypothetical protein TP0851

pir:C71274

C71274

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31496067_c1_49	2333	7555	227	684		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33439010_c3_57	2334	7556	982	2949	448	4.6e-86

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4738761_c2_55	2335	7557	433	1299	1622	1.2e-166
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
fumarate hydratase, fumB, iron-dependent:fumarase B			pir:B44511			
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
48828124_c1_4	2336	7558	178	537	410	3.1e-38
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein F36H12.3			pir:T33457		T33457	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
48828124_c2_5.....	2337	7559	179	540	407	6.5e-38
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein F36H12.3			pir:T33457		T33457	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
48828124_c3_6	2338	7560	188	567	412	1.9e-38
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein F36H12.3			pir:T33457		T33457	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4485917_c2_3	2339	7561	104	312		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10742905_f2_80	2340	7562	97	294	105	4.2e-05

Protein name conserved hypothetical protein Locus Name pir:A72220 Acc# A72220

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11210313_c3_276.....	2341	7563	281	846	645	3.9e-63

Protein name CysQ protein Locus Name pir:A70330 Acc# A70330

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11796876_c3_240.....	2342	7564	159	480		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1296950_c2_225.....	2343	7565	522	1569	381	6.0e-67

Protein name Locus Name sp:Y640_SYNY3 Acc# P72958

Description

HYPOTHETICAL 66.7 KD PROTEIN SLL0640

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1348563_c1_151.....	2344	7566	166	501	715	1.5e-70

Protein name hypothetical protein Locus Name pir:JQ1020 Acc# JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13837817_f2_54	2345	7567	272	819	101	0.0055

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
otnG protein	pir:S70954	S70954

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13859376_f2_77	2346	7568	391	1176	687	1.4e-67

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
galactokinase	pir:C72283	C72283

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14648312_c1_199	2347	7569	376	1131	363	3.0e-33

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 42kD antigen PG33	gp:AF175715	AF175715

Description

Porphyromonas gingivalis strain W50 immunoreactive 42kD antigenPG33 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16801507_f1_32	2348	7570	280	843	226	9.9e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) homolog	pir:G69278	G69278

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16832885_f2_51	2349	7571	90	273	312	7.6e-28
Protein name			Locus Name		Acc#	
hypothetical protein			pir:JQ1020		JQ1020	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1.7187...c3_273	2350	7572	64	195		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
18.7502...c2_235	2351	7573	364	1095		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
18.7502...f1_10	2352	7574	522	1569		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20110930_f2_82	2353	7575	63	192		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22470301_f2_73	2354	7576	131	396	71	0.026

Protein name

Locus Name

Acc#

unknown protein

gp:BACATPA

Description

B.megaterium ATP synthase i,a,c,b,delta,alpha,gamma,beta andepsilon subunit genes, complete cds, and ORF.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22660002_f3_129	2355	7577	103	312		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f3_106.....	2356	7578	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23554687_f1_35.....	2357	7579	305	918		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23631562_f3_133	2358	7580	460	1383	330	9.4e-30

Protein name

Locus Name

Acc#

sp:GLUP_BRUAB

Q44623

Description

GLUCOSE/GALACTOSE TRANSPORTER

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23907956_f1_22	2359	7581	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24069755_c2_222	2360	7582	279	840	503	4.4e-48

Protein name

Locus Name

Acc#

hypothetical protein sir1117

pir:S74480

S74480

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24237507_f1_28	2361	7583	396	1191	747	6.1e-74

Protein name

Locus Name

Acc#

sp:GALM_ACICA

P05149

Description

ALDOSE 1-EPIMERASE PRECURSOR, (MUTAROTASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24242327_f3_143	2362	7584	173	522	140	1.3e-09

Protein name

Locus Name

Acc#

sp:RFAY_XANCP

P46358

Description

PROBABLE RNA POLYMERASE SIGMA FACTOR RFAY

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24253316_c3_239	2363	7585	209	630		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24260885_c1_153	2364	7586	480	1443	213	1.4e-16

Protein name

Locus Name

Acc#

vitellogenin

sp:CHKVITB

K02113

Description

Gallus gallus vitellogenin gene coding for phosvitin, exons 23 and 24.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24298137_f2_65	2365	7587	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24353377_f2_81	2366	7588	76	231	170	8.5e-13

Protein name

Locus Name

Acc#

hypothetical protein TM1758

pir:G72214

G72214

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24406536_f2_79	2367	7589	149	450	367	1.1e-33

Protein name

Locus Name

Acc#

sugar-phosphate isomerase

pir:H72296

H72296

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415877_c3_272	2368	7590	166	501	99	0.0018

Protein name

Locus Name

Acc#

sp:Y896_HAEIN

Description

HYPOTHETICAL PROTEIN HI0896

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415888_c1_154	2369	7591	528	1587	69	0.0075

Protein name

Locus Name

Acc#

outer membrane protein

gp:HEAOMPP1B

Description

Haemophilus influenzae outer membrane protein (OMPP1) gene, complete CDS.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24645262_f3_109	2370	7592	375	1128	377	9.9e-35
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
immunoreactive 42kD antigen PG33	gp:AF175715				AF175715	
<u>Description</u>	Porphyromonas gingivalis strain W50 immunoreactive 42kD antigenPG33 gene, complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648563_c3_271	2371	7593	258	777	575	1.0e-55
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
PksB	gp:AF019986				AF019986	
<u>Description</u>	Dictyostelium discoideum PksB (pksB) mRNA, complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24692212_c1_187	2372	7594	293	882	940	2.2e-94
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
sulfate adenylyltransferase, small chain:ATP-sulfurylase:sulfurylase	pir:D65056					
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24890887_f2_89.....	2373	7595	75	228		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25600262_c3_278	2374	7596	79	240	174	6.6e-13

Protein name

Locus Name

Acc#

ATP sulfurylase small subunit

gp:AF035608

AF035608

Description

Pseudomonas aeruginosa ATP sulfurylase small subunit (cysD) and ATPsulfurylase GTP-binding subunit/APS kinase (cysN) genes, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25792127_f3_124	2375	7597	84	255		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26289761_c3_279	2376	7598	491	1476	1334	3.8e-136

Protein name

Locus Name

Acc#

ATP sulfurylase GTP-binding subunit/APS kinase

gp:AF035608

AF035608

Description

Pseudomonas aeruginosa ATP sulfurylase small subunit (cysD) and ATPsulfurylase GTP-binding subunit/APS kinase (cysN) genes, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26359760_c1_152	2377	7599	82	249	61	0.048

Protein name

Locus Name

Acc#

sp:COX3_PYLLI

Q37600

Description

CYTOCHROME C OXIDASE POLYPEPTIDE III,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29298205_c2_237	2378	7600	145	438	202	3.5e-16

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76868

S76868

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29722915_f3_107	2379	7601	356	1071	1412	2.1e-144

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31878250_f3_147	2380	7602	185	558	396	9.6e-37

Protein name

Locus Name

Acc#

conserved hypothetical protein ykna

pir:F69857

F69857

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32304817_f2_90	2381	7603	216	651		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32422553_f1_31	2382	7604	659	1980	96	0.044

Protein name

Locus Name

Acc#

sp:YC8B_METJA

P81319

Description

HYPOTHETICAL PROTEIN MJ1282.2

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33476517_f1_30	2383	7605	369	1110	994	4.1e-100
Protein name			Locus Name		Acc#	
hypothetical protein TM1759			pir:H72214		H72214	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34191425_f2_50.....	2384	7606	332	999		
Protein name			Locus Name		Acc#	
Description			NO-HIT			

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34242212_f3_145.....	2385	7607	153	462	92	0.039
Protein name			Locus Name		Acc#	
PfEMP1 fragment PFB1045w			pir:F71600		F71600	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34407937_f3_142.....	2386	7608	330	993	260	2.5e-22
Protein name			Locus Name		Acc#	
			sp:YISS_BACSU			
Description						
HYPOTHETICAL 37.5 KD PROTEIN IN DEGA-NPRB INTERGENIC REGION						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34609450_c3_242	2387	7609	376	1131	117	0.0016
Protein name			Locus Name		Acc#	
complement C7			gp:AF162274		AF162274	
Description						
Sus scrofa complement C7 mRNA, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36226562_c1_190	2388	7610	325	978		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36604663_f1_27.....	2389	7611	411	1236	992	6.7e-100
Protein name			Locus Name		Acc#	
			sp:RHLE_ECOLI		P25888	
Description						
PUTATIVE ATP-DEPENDENT RNA HELICASE RHLE						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3917130_c3_268.....	2390	7612	332	999	488	1.7e-46
Protein name			Locus Name		Acc#	
mannose-6-phosphate isomerase homolog yjdB			pir:H69848		H69848	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3939003_f2_84	2391	7613	185	558	294	1.4e-25
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
2-oxoacid--ferredoxin oxidoreductase, beta chain:2-oxoisovalerate oxidoreductase alpha chain (misidentification)	pir:B69194				B69194	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
40888_c1_200	2392	7614	185	558	301	1.1e-26
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:DEF_THEMA				P96113	
<u>Description</u>						

DEFORMYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4115930_f3_134	2393	7615	312	939	1046	1.3e-105
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative transketolase				gp:BOU15179		U15179
<u>Description</u>						

Bacteroides ovatus arabinosidase (asdII) gene, complete cds and putative transketolase, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4145331_f1_29	2394	7616	376	1131	645	3.9e-63
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:TKT_BACSU				P45694	
<u>Description</u>						

TRANSKETOLASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4485917_f2_56	2395	7617	135	408	98	0.00035

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
XylS/AraC family transcriptional regulatory	gp:AF039207	AF039207

Description

Listeria monocytogenes putative transcriptional attenuator leaderpeptide (attM), LapA (lapA), XylS/AraC family transcriptional regulatory protein homolog (lapB), and NADH-dependent dehydrogenase homolog (lapC) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4719011_c3_277	2396	7618	205	618	476	3.2e-45

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:NODQ_AZOBR	P28604

Description

SULFURYLASE) (NODULATION PROTEIN Q)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4722176_f3_121	2397	7619	898	2697	367	4.0e-85

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:BGAL_THEET	P77989

Description

BETA-GALACTOSIDASE, (LACTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4867167_c1_198	2398	7620	418	1257		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5259437_c3_287	2399	7621	253	762	106	0.00070

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
otnG protein	pir:S70954	S70954

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5273312_f3_128	2400	7622	73	222	81	0.0035

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
gas vesicle protein GvpP	gp:AF053765	AF053765

Description

Bacillus megaterium AraC (araC) gene, partial cds; gas vesicle proteins GvpU (gvpU), GvpT (gvpT), GvpJ (gvpJ), GvpK (gvpK), GvpS (gvpS), GvpL (gvpL), GvpG (gvpG), GvpF (gvpF), GvpN (gvpN), GvpR (gvpR), GvpB (gvpB), GvpQ (gvpQ), GvpP (gvpP), and GvpA (gvpA) genes, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5284453_c2_202	2401	7623	138	417	114	1.2e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein (eggshell protein gene region)	pir:D44805	D44805

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6143800_c1_189	2402	7624	390	1173	393	2.0e-36

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YU43_MYCTU	Q50695

Description

HYPOTHETICAL 46.1 KD PROTEIN CY339.43

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6381932_f2_53	2403	7625	269	810		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6647927_f1_36	2404	7626	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6851562_f2_83	2405	7627	257	774	633	7.3e-62

Protein name

Locus Name

Acc#

2-oxoacid--ferredoxin oxidoreductase, beta
chain:2-oxoisovalerate oxidoreductase alpha
chain (misidentification)

pir:B69194

B69194

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
687_c2_234	2406	7628	410	1233	389	5.3e-36

Protein name

Locus Name

Acc#

integrase

gp:BFU75371

U75371

Description

Bacteroides fragilis transposon Tn4555 TnpA (tnpA), integrase(int), TnpC (tnpC), excisionase (xis), mobilization protein (mobA), and beta-lactamase (cfxA) genes, complete cds; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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9782302_f1_43	2407	7629	83	252		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

10369011_f3_154	2408	7630	283	852		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

1057958_f2_73	2409	7631	188	567	212	3.0e-17
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Protein name

Locus Name

Acc#

sensory transduction system regulatory
protein slr1982:protein slr1982:protein
slr1982

pir:S75663

S75663

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

1176517_f1_52	2410	7632	66	201		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12343962_f2_59	2411	7633	742	2229	156	1.1e-06

Protein name

Locus Name

Acc#

hypothetical protein

pir:C72351

C72351

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13787952_f1_53	2412	7634	312	939		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13861037_f1_46	2413	7635	156	471		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13865891_c2_277	2414	7636	428	1287	712	3.1e-70

Protein name

Locus Name

Acc#

sp:BIOF_BACSH

P22806

Description

LIGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13882887_f1_44	2415	7637	146	441	155	3.3e-11

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF158372

AF158372

Description

Flavobacterium johnsoniae hypothetical protein gene, partial cds;GldB (gldB), GldC (gldC), and hypothetical protein genes, completecds; and hypothetical protein gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14459637_f1_49	2416	7638	605	1818	207	4.3e-14

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF158372

AF158372

Description

Flavobacterium johnsoniae hypothetical protein gene, partial cds;GldB (gldB), GldC (gldC), and hypothetical protein genes, completecds; and hypothetical protein gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14492062_f3_147	2417	7639	143	432		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14564003_f2_71	2418	7640	290	873	140	4.2e-07

Protein name

Locus Name

Acc#

MigA

gp:PAU70729

U70729

Description

Pseudomonas aeruginosa MigA (migA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14631406_f1_14	2419	7641	322	969	257	2.6e-25
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
glycosyltransferase			gp:AF146532		AF146532	
<u>Description</u>						
Klebsiella pneumoniae waa gene cluster.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14642175_f1_38	2420	7642	1035	3108	96	4.2e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
DNA helicase homolog			pir:G69494		G69494	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14646926_f3_144.....	2421	7643	141	426	175	2.5e-13
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			gp:AF158372		AF158372	
<u>Description</u>						
Flavobacterium johnsoniae hypothetical protein gene, partial cds;GldB (gldB), GldC (gldC), and hypothetical protein genes, completecds; and hypothetical protein gene, partial cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14651638_f2_68.....	2422	7644	120	363		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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1550_f2_88	2423	7645	259	780		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

15761062...c2...283.....	2424	7646	72	219	209	1.2e-16
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Protein name

Locus Name

Acc#

integrase

gp:D50438

D50438

Description

Serratia marcescens DNA for integrase,
metallo-beta-lactamase, aminoglycoside acetyltransferase, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

16100927...c1...194.....	2425	7647	280	843	109	0.00011
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Protein name

Locus Name

Acc#

sp:YBEU_ECOLI

P77427

Description

HYPOTHETICAL 27.0 KD PROTEIN IN LEUS-GLTL INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

16603377...f1...51.....	2426	7648	326	981		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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194765_c3_348	2427	7649	135	408		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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19695302_f2_58	2428	7650	293	882		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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20026537_c1_190	2429	7651	330	993	297	3.0e-26
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Protein name

Locus Name

Acc#

sp:Y4QK_RHISN

P55632

Description

PUTATIVE INTEGRASE/RECOMBINASE Y4QK

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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20705385_c2_281	2430	7652	227	684	110	0.00019
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Protein name

Locus Name

Acc#

LanK

gp:AF080235

AF080235

Description

Streptomyces cyanogenus landomycin biosynthetic gene cluster, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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20912537_f3_151	2431	7653	235	708		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

20953211_f3_124	2432	7654	251	756	136	9.7e-07
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Protein name

Locus Name

Acc#

hypothetical protein

pir:F75494

F75494

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

212762_f1_43	2433	7655	828	2487	827	4.1e-145
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Protein name

Locus Name

Acc#

ClpB

gp:AB012390

AB012390

Description

Thermus thermophilus genes for DnaK, GrpE, DnaJ, DnaA, ClpB, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

21507765_c3_369	2434	7656	76	231		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23547157_c2_286	2435	7657	162	489		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23632793_c1_189.....	2436	7658	87	264	72	0.048
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Protein name

Locus Name

Acc#

ubiquinone biosynthesis protein coq7 (coq7)
RP190

pir:A71730

A71730

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24063450_f3_101.....	2437	7659	419	1260	115	0.0028
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Protein name

Locus Name

Acc#

outer membrane protein

pir:C70412

C70412

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24065927_f2_90.....	2438	7660	293	882		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24257700_c3_353	2439	7661	584	1755	1657	2.3e-170

Protein name

Locus Name

Acc#

sp:YJJK_ECOLI

P37797

Description

ABC TRANSPORTER ATP-BINDING PROTEIN YJJK

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24258437_f3_103	2440	7662	306	921	271	5.1e-32

Protein name

Locus Name

Acc#

rhamnosyl transferase related protein PAB0795

pir:F75099

F75099

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24398442_f1_45	2441	7663	152	459	94	0.00014

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF158372

AF158372

Description

Flavobacterium johnsoniae hypothetical protein gene, partial cds;GldB (gldB), GldC (gldC), and hypothetical protein genes, completecds; and hypothetical protein gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24407563_f3_155	2442	7664	389	1170		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640881_f1_24	2443	7665	408	1227	210	1.2e-14
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hyaluronan synthase related PAB1314			pir:G75005		G75005	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640952_c1_193.....	2444	7666	152	459		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24843877_f3_148.....	2445	7667	150	453	77	0.024
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:AB030825		AB030825	
<u>Description</u>						
Pseudomonas aeruginosa genomic DNA, partial sequence, strain:PA01.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25584626_c1_191.....	2446	7668	132	399		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25906913_f3_104	2447	7669	437	1314	184	3.3e-11

Protein name

Locus Name

Acc#

gp:PWQRRMP

L39794

Description

Plasmid pWQ799 RNAI and RNAI genes, complete sequence; RNAI modulator protein (Rom), mobilization proteins (mbeC, mbeA, mbeB, and mbeD), N-acetylmannosamine transferase (wbbE), wbbF, and UDP-N-acetylglucosamine 2-epimerase (wecB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2929813_c2_306	2448	7670	93	282	66	0.035

Protein name

Locus Name

Acc#

plasma membrane protein

pir:T03680

T03680

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29479667_f1_34	2449	7671	100	303		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29820341_f3_102	2450	7672	467	1404	116	0.0010

Protein name

Locus Name

Acc#

sp:RFC_SALMU

Q00474

Description

O-ANTIGEN POLYMERASE

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

32225307_c3_350	2451	7673	149	450		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

32698450_f3_153	2452	7674	269	810	197	1.2e-15
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Protein name

Locus Name

Acc#

outer membrane protein mom72,
72K:hypothetical protein sll1667:hypothetical
protein sll1667

pir:S74665

S74665

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

33400252_c2_290	2453	7675	632	1899	82	0.028
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Protein name

Locus Name

Acc#

MHC class II protein

gp:AF030872

AF030872

Description

Poeciliopsis occidentalis occidentalis MHC class II protein gene, partial
exon II, and partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

34022837_f1_42	2454	7676	464	1395		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34164777_f1_25	2455	7677	801	2406	390	2.4e-36
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
sensory transduction histidine kinase slr2104:protein slr2104:protein slr2104			pir:S75136		S75136	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34179562_f1_41	2456	7678	154	465		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34569676_c3_354	2457	7679	934	2805	178	1.5e-10
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35156933_c1_192	2458	7680	84	255		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35188568_f1_13	2459	7681	72	219		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35351502_f1_54	2460	7682	495	1488		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
39660_f3_152	2461	7683	262	789	292	1.0e-25
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

outer membrane protein mom72, 72K:hypothetical protein sll1667:hypothetical protein sll1667	pir:S74665	S74665
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3984442_f2_84	2462	7684	60	183		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4100635_f1_50	2463	7685	771	2316		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4109715_f1_56	2464	7686	321	966		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4110211_f1_21	2465	7687	307	924		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4119010_c2_285	2466	7688	158	477	97	0.0046
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
ABC transporter protein				gp:CJAJ0856		AJ000856
<u>Description</u>						

Campylobacter jejuni kpsM, kpsT genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4566502_f1_33	2467	7689	106	321		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4798388_f3_141	2468	7690	64	195	114	7.3e-07
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein MTH1606	pir:E69081	E69081
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4884686_c2_284	2469	7691	287	864		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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5339133_c3_367	2470	7692	65	198		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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6338916_f3_157	2471	7693	112	336		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
644125_c2_309	2472	7694	104	315	87	0.00083

Protein name

Locus Name

Acc#

sp:INVA_BARBA

P35640

Description

INVASION PROTEIN A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6814062_f2_70	2473	7695	1248	3747	423	2.7e-38

Protein name

Locus Name

Acc#

biosynthesis of teichuronic acid tuaB

pir:D69727

D69727

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6851660_f2_96	2474	7696	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6923378_f3_150	2475	7697	488	1467		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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85901_c3_366	2476	7698	119	360		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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915912_f3_143	2477	7699	130	393	194	2.4e-15
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Protein name

Locus Name

Acc#

hypothetical protein

gp:AF158372

AF158372

Description

Flavobacterium johnsoniae hypothetical protein gene, partial cds;GldB (gldB), GldC (gldC), and hypothetical protein genes, completedcds; and hypothetical protein gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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975262_f3_149	2478	7700	611	1836		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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979137_f1_26	2479	7701	183	552		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9959463_f3_146	2480	7702	331	996	150	9.7e-07
Protein name			Locus Name		Acc#	
serine/threonine-specific protein kinase, PFB0150c			pir:H71621		H71621	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2350306_f3_12	2481	7703	100	303	105	6.6e-06
Protein name			Locus Name		Acc#	
hypothetical protein PH0217			pir:G71244		G71244	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24335131_f2_8	2482	7704	63	192	106	5.1e-06
Protein name			Locus Name		Acc#	
hypothetical protein PH0219			pir:A71245		A71245	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3.1539640_c1_14	2483	7705	62	189		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11756280_f2_12	2484	7706	667	2004	1546	1.3e-158

Protein name

Locus Name

Acc#

gp:CEY51H4A

AL132952

Description

Caenorhabditis elegans cosmid Y51H4A, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1198528_c1_58	2485	7707	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1203442_f2_15	2486	7708	211	636	364	2.4e-33

Protein name

Locus Name

Acc#

sp:SCE4_METEX

Q49135

Description

PUTATIVE SERINE CYCLE ENZYME (ORF4)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12673767_f1_3	2487	7709	327	984	510	7.9e-49

Protein name

Locus Name

Acc#

histidine ammonia-lyase

pir:F75610

F75610

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12947255_f1_1	2488	7710	309	930	855	2.2e-85

Protein name Locus Name Acc#
 hypothetical protein TM0843 pir:D72326 D72326

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21680317_f3_40.....	2489	7711	102	309	73	0.016

Protein name Locus Name Acc#
 hypothetical protein aq_862 pir:F70374 F70374

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21932163_f3_45.....	2490	7712	75	228		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2350306_c2_69.....	2491	7713	100	303	111	1.5e-06

Protein name Locus Name Acc#
 hypothetical protein PH0217 pir:G71244 G71244

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24431500_f3_42.....	2492	7714	310	933		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24804561_f1_5	2493	7715	220	663	122	4.7e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable transcription regulator	pir:T29062	T29062

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25813300_f3_39.....	2494	7716	1021	3066	1244	1.3e-126

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
acriflavine resistance protein (acrB)	gp:AE001125	

Description

Borrelia burgdorferi (section 11 of 70) of the complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26204716_f2_18.....	2495	7717	64	195		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33398568_c3_101.....	2496	7718	75	228	61	0.044

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
MADS box-like protein	gp:AB003323	AB003323

Description

Oryza sativa mRNA for MADS box-like protein, complete cds, clone:E20969.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34409692_f1_2	2497	7719	419	1260	847	1.5e-84

Protein name

Locus Name

Acc#

sp:HUTI_BACSU

P42084

Description

HYDROLASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34651386_f2_24	2498	7720	489	1470		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3916638_f3_30	2499	7721	213	642		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4103137_f1_6	2500	7722	309	930	200	6.7e-18

Protein name

Locus Name

Acc#

hypothetical protein sll0141

pir:S76434

S76434

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4141887_f3_38	2501	7723	453	1362	840	8.5e-84

Protein name

Locus Name

Acc#

immunoreactive 52kD antigen PG41

gp:AF175716

AF175716

Description

Porphyromonas gingivalis strain W50 immunoreactive 52kD antigenPG41 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4422500_f3_37	2502	7724	159	480	308	1.4e-26

Protein name

Locus Name

Acc#

sp:HUTH_HUMAN

P42357

Description

HISTIDINE AMMONIA-LYASE, (HISTIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5331665_f1_9	2503	7725	525	1578	745	1.1e-77

Protein name

Locus Name

Acc#

AlgI

gp:AF027499

AF027499

Description

Azotobacter vinelandii mannuronan C-5-epimerase (algG) gene,partial cds; and AlgX, alginate lyase (algL), AlgI, and AlgV genes,complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7057792_f2_19	2504	7726	63	192	88	0.0036

Protein name

Locus Name

Acc#

gp:D85752

D85752

Description

Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE,bacF, bacG, bacH and bacI genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14664052_c1_25	2505	7727	197	594	217	8.9e-18

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23495336_c1_24	2506	7728	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24035707_c1_27.....	2507	7729	811	2436	515	5.2e-46

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29296910_c1_26.....	2508	7730	346	1041	113	0.00087

Protein name

Locus Name

Acc#

sp:FECR_ECOLI

P23485

Description

FECR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35328313_c2_31	2509	7731	381	1146	328	2.6e-28

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3906250_f2_14	2510	7732	167	504		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3947287_c3_38	2511	7733	95	285		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10250001_c2_207	2512	7734	109	330		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10735692_f1_26	2513	7735	431	1296	967	3.0e-97

Protein name

Locus Name

Acc#

sp:PUR2_HAEIN

P43845

Description

RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10937551_c2_210	2514	7736	246	741	94	0.036

Protein name

Locus Name

Acc#

DNA alkylation repair enzyme

gp:BAJ10128

AJ010128

Description

Bacillus cereus bc297a, alkD genes and partial glyS gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11203138_c2_205	2515	7737	65	198	60	0.048

Protein name

Locus Name

Acc#

alpha 1,2 fucosyltransferase

gp:AF042743

AF042743

Description

Rattus norvegicus alpha 1,2 fucosyltransferase mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1194632_c3_244	2516	7738	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12350205_f3_94	2517	7739	614	1845	1095	8.1e-111

Protein name

Locus Name

Acc#

sp:UVRC_BACSU

P14951

Description

EXCINUCLEASE ABC SUBUNIT C

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12542657_f3_111	2518	7740	288	867	533	2.9e-51

Protein name

Locus Name

Acc#

ABC-type transport protein slr2044:protein
slr2044:protein slr2044

pir:S75197

S75197

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12973466_c1_168.....	2519	7741	530	1593	175	1.0e-16

Protein name

Locus Name

Acc#

Cps2J

gp:AF026471

AF026471

Description

Streptococcus pneumoniae DexB (dexB) gene, partial cds; putativetransposase gene, complete cds; type 2 capsular polysaccharidebiosynthesis operon, complete sequence; and AliA (aliA) gene,partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16047502_f1_4.....	2520	7742	451	1356	434	9.0e-41

Protein name

Locus Name

Acc#

spore maturation protein B:hypothetical
protein sll1677:hypothetical protein sll1677

pir:S74647

S74647

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16228385_f3_108	2521	7743	159	480	163	4.7e-12

Protein name

Locus Name

Acc#

alkaline phosphatase homolog ykoX

pir:B69861

B69861

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16508444_c1_123	2522	7744	408	1227		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20734688_c1_146	2523	7745	253	762	231	2.9e-19

Protein name

Locus Name

Acc#

sp:YEHT_ECOLI

Description

HYPOTHETICAL 27.9 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20798338_f1_27	2524	7746	245	738	86	0.0026

Protein name

Locus Name

Acc#

orf98

sp:AF160864

AF160864

Description

Tetrahymena pyriformis mitochondrial DNA, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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20882827_f1_34	2525	7747	1119	3360		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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21907892_f2_67	2526	7748	305	918	175	2.2e-26
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Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:C75368

C75368

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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21991656_f1_28	2527	7749	323	972	498	1.5e-47
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Protein name

Locus Name

Acc#

adhesion protein

pir:C69180

C69180

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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23477186_f1_14	2528	7750	243	732		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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23595331_c3_251	2529	7751	293	879	343	1.7e-30
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Protein name

Locus Name

Acc#

hypothetical protein sll1151

pir:S74882

S74882

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23631937_f3_88	2530	7752	143	432	177	1.5e-13

Protein name

Locus Name

Acc#

conserved hypothetical protein TP0650

pir:A71300

A71300

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24259677_f3_101	2531	7753	120	363		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24651660_c3_243	2532	7754	409	1230		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2516025_c1_126	2533	7755	405	1218		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26359436_f1_17	2534	7756	140	423	91	0.015

Protein name

Locus Name

Acc#

gp:PFMAL3P8

Description

Plasmodium falciparum MAL3P8, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26598453_f3_96	2535	7757	302	909	544	2.0e-52

Protein name

Locus Name

Acc#

sp:DEOC_CAEEL

Q19264

Description

(PHOSPHODEOXYRIBOALDOLASE) (DEOXYRIBOALDOLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29558432_f1_25	2536	7758	627	1884	818	1.8e-81

Protein name

Locus Name

Acc#

X-Pro dipeptidyl-peptidase,

pir:JC5142

JC5142

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30276587_c1_157	2537	7759	132	399		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30479750_f2_56	2538	7760	151	456	191	5.1e-15

Protein name

Locus Name

Acc#

sp:YPJD_BACSU

P42979

Description

HYPOTHETICAL 13.0 KD PROTEIN IN QCRC-DAPB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30664678_c2_173	2539	7761	377	1134	131	1.8e-05

Protein name

Locus Name

Acc#

glucose-binding protein

gp:PPU74323

U74323

Description

Pseudomonas putida glucose-binding protein (glbB) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31444012_c1_161	2540	7762	304	915	91	0.017

Protein name

Locus Name

Acc#

Gly1ORF1

gp:AF003941

AF003941

Description

Neisseria gonorrhoeae Gly1ORF1 and Gly1ORF2 genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33400260_f1_6	2541	7763	544	1635	123	0.00055

Protein name

Locus Name

Acc#

hypothetical protein F56H9.1

pir:T22808

T22808

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

33678186_c2_202	2542	7764	154	465		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

33992811_f3_95	2543	7765	158	477	379	6.1e-35
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Protein name

Locus Name

Acc#

hypothetical protein

pir:S39974

S39974

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

34183407_f2_72	2544	7766	191	576		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

4314637_f1_22	2545	7767	303	912	698	9.5e-69
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Protein name

Locus Name

Acc#

sp:SRPH_SYNP7

Q59967

Description

SERINE ACETYLTRANSFERASE, PLASMID, (SAT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4490938_f3_93	2546	7768	631	1896	1457	3.5e-149

Protein name

Locus Name

Acc#

sp:GIDA_PSEPU

P25756

Description

GLUCOSE INHIBITED DIVISION PROTEIN A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4579011_f3_100	2547	7769	454	1365	667	1.8e-65

Protein name

Locus Name

Acc#

sp:Y064_SYNY3

Q55156

Description

HYPOTHETICAL 43.0 KD PROTEIN SLR0064

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4687757_c3_242	2548	7770	566	1701		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4719528_f1_36	2549	7771	312	939	541	4.1e-52

Protein name

Locus Name

Acc#

sp:YJES_ECOLI

P39288

Description

HYPOTHETICAL 43.1 KD PROTEIN IN PSD-AMIB INTERGENIC REGION (F379)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4766461_f2_52	2550	7772	240	723	396	9.6e-37

Protein name

Locus Name

Acc#

sp:APT1_WHEAT

Q43199

Description

ADENINE PHOSPHORIBOSYLTRANSFERASE 1, (APRT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4804652_c1_145	2551	7773	679	2040	225	3.6e-15

Protein name

Locus Name

Acc#

gp:D90868

Description

E.coli genomic DNA, Kohara clone #414(53.8-54.2 min.).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5292206_f2_75	2552	7774	207	624	222	2.6e-18

Protein name

Locus Name

Acc#

sp:YFU2_BACST

Q04729

Description

(ORF2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6254457_c3_248	2553	7775	371	1116	989	1.4e-99

Protein name

Locus Name

Acc#

sp:RUVB_PSEAE

Q51426

Description

HOLLIDAY JUNCTION DNA HELICASE RUVB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6525_c1_151	2554	7776	354	1065	478	2.0e-45

Protein name

Locus Name

Acc#

octylprenyl diphosphate synthase-like protein

gp:AF153713

AF153713

Description

Pseudomonas sp. BG33R strain BG33R octylprenyl diphosphatesynthase-like protein gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7078137_c2_200	2555	7777	136	411		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
894058_f2_60.....	2556	7778	1001	3006	2069	5.0e-214

Protein name

Locus Name

Acc#

DNA polymerase I

gp:AF121780

AF121780

Description

Rhodothermus obamensis DNA polymerase I (polA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10187642_f1_26.....	2557	7779	256	771	112	6.3e-05

Protein name

Locus Name

Acc#

immunity region protein in prophage homolog ydcM

pir:B69774

B69774

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1035311_f2_115	2558	7780	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10354011_c2_312.....	2559	7781	266	801		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10550306_c3_436.....	2560	7782	352	1059		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11989088_c2_364.....	2561	7783	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1220317_f2_113	2562	7784	309	930	264	9.3e-23

Protein name

Locus Name

Acc#

sp:DDH_CORGL

P04964

Description

MESO-DIAMINOPIMELATE D-DEHYDROGENASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12306502_f1_44	2563	7785	205	618	353	3.4e-32

Protein name

Locus Name

Acc#

sp:KGUA_YEAST

P15454

Description

GUANYLATE KINASE, (GMP KINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12391401_f1_34	2564	7786	152	459	385	1.4e-35

Protein name

Locus Name

Acc#

probable permease b1828

pir:D64944

D64944

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12774028_f3_202	2565	7787	819	2460	355	3.5e-71

Protein name

Locus Name

Acc#

sp:NRDD_HAEIN

P43752

Description

ANAEROBIC RIBONUCLEOSIDE-TRIPHOSPHATE REDUCTASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1281260_c2_372	2566	7788	481	1446	454	6.8e-43

Protein name

Locus Name

Acc#

O-unit flippase-like protein

gp:YPE251713

AJ251713

Description

Yersinia pestis strain EV76 hemH gene (partial) and O-antigen genecluster for ddhD gene, ddhA gene, ddhB pseudogene, ddhC gene, prt gene, wbyH gene, wzx gene, wbyI pseudogene, wbyJ gene, wzypseudogene, wbyK gene, gmd pseudogene, fcl pseudogene, manC gene, wbyL gene, manB gene, wzz gene and gsk gene (partial).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14496090_c2_321	2567	7789	94	285		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15812885_c3_448	2568	7790	334	1005	358	1.0e-32

Protein name

Locus Name

Acc#

galactosyl transferase

gp:AF030373

AF030373

Description

Streptococcus pneumoniae strain SP-264 alpha, 1-6-glucosidase(dexB) gene, complete cds; capsular polysaccharide biosynthetic locus, complete sequence; and oligopeptide binding protein (aliA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16056682_c1_245	2569	7791	96	291	74	0.013

Protein name

Locus Name

Acc#

hypothetical protein

gp:SSU18930

Y18930

Description

Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19551535_f3_192	2570	7792	118	357	113	9.3e-07

Protein name

Locus Name

Acc#

unknown

gp:LLU35629

U35629

Description

Lactococcus lactis plasmid pSRQ802 abortive infection protein K(abiK) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1994055_c3_451	2571	7793	239	720	104	0.0028

Protein name

Locus Name

Acc#

capsular polysaccharide biosynthesis homolog
ywqE

pir:H70066

H70066

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20492137_f3_188.....	2572	7794	167	504		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22292513_f2_109.....	2573	7795	185	558	179	9.5e-14

Protein name

Locus Name

Acc#

Phosphinothricin acetyltransferase (EC

gp:D90784

Description

E.coli genomic DNA, Kohara clone #273(32.5-32.8 min.).

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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23486536_c2_340	2574	7796	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

23554651_c2_349	2575	7797	370	1113	1086	7.3e-110
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Protein name

Locus Name

Acc#

PhnW

gp:STU69493

U69493

Description

Salmonella typhimurium ThiJ and Orf1 genes, partial cds, and PhnX, PhnW, PhnR, PhnS, PhnT, PhnU and PhnV genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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23565628_f3_241	2576	7798	69	210		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

23625311_c3_415	2577	7799	388	1167	745	5.0e-96
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Protein name

Locus Name

Acc#

dTDPglucose
4,6-dehydratase, :dTDP-D-glucose-4,6-dehydratas
e:dTDP-glucose dehydratase

pir:T00102

T00102

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23631627_c2_346	2578	7800	456	1371	340	8.2e-31

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_1964

pir:D70468

D70468

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23632211_i3_239	2579	7801	221	666		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23632880_c2_341	2580	7802	245	738	199	7.2e-16

Protein name

Locus Name

Acc#

hypothetical protein

gp:EFY17797

Y17797

Description

Enterococcus faecalis gph, ydjH, ydjG, ydjI, pbp4 and ydiC, ORF2and ORF3 genes, partial.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23697051_c2_357	2581	7803	305	918	305	4.2e-27

Protein name

Locus Name

Acc#

sp:RUVA_PSEAE

Q51425

Description

HOLLIDAY JUNCTION DNA HELICASE RUVA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24066055_f3_173	2582	7804	310	933	107	0.022

Protein name

Locus Name

Acc#

gp:SCYDL057W

Description

S.cerevisiae chromosome IV reading frame ORF YDL057w.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24353386_f1_45	2583	7805	202	609	301	1.1e-26

Protein name

Locus Name

Acc#

sp:YQEU_BACSU

P54455

Description

HYPOTHETICAL 22.2 KD PROTEIN IN AROD-COMER INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24412952_c3_452.....	2584	7806	146	441	128	2.4e-08

Protein name

Locus Name

Acc#

cold shock protein homolog cspC

pir:S43618

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24469555_c1_275.....	2585	7807	438	1317	988	1.8e-99

Protein name

Locus Name

Acc#

UDP-N-acetylglucosamine
1-carboxyvinyltransferase (murA) homolog

pir:G70158

G70158

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24644068_f3_203	2586	7808	154	465	322	6.6e-29

Protein name

Locus Name

Acc#

sp:NRDG_HAEIN

P45080

Description

(EC 1.97.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24645138_c3_444	2587	7809	210	633	110	3.5e-06

Protein name

Locus Name

Acc#

unknown

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648443_c3_394.....	2588	7810	474	1425	451	1.4e-42

Protein name

Locus Name

Acc#

sp:YEBU_ECOLI

Description

HYPOTHETICAL 53.2 KD PROTEIN IN PRC-PRPA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24804691_f2_152.....	2589	7811	1032	3099	1980	1.3e-204

Protein name

Locus Name

Acc#

cation efflux system protein czcA-1:protein
slr0794:protein slr0794

pir:S77008

S77008

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2538562_c3_406	2590	7812	139	420	191	5.1e-15

Protein name

Locus Name

Acc#

response regulator homolog

pir:A69531

A69531

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2540885_f1_5	2591	7813	483	1452	119	0.00070

Protein name

Locus Name

Acc#

receptor antigen B (RagB)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25510927_f3_242	2592	7814	429	1290	677	1.6e-66

Protein name

Locus Name

Acc#

sp:YWNE_BACSU

P71040

Description

HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25594152_c1_269	2593	7815	448	1347	262	4.2e-22

Protein name

Locus Name

Acc#

probable phosphoesterase, ykuE

pir:B69865

B69865

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26212837_c3_465	2594	7816	482	1449	1671	7.4e-172

Protein name

Locus Name

Acc#

polyA polymerase

gp:AB022867

AB022867

Description

Prevotella ruminicola genes for polyA polymerase, D-alanineglycinepermease and cellulase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26305136_c3_418	2595	7817	205	618	130	1.5e-08

Protein name

Locus Name

Acc#

sp:RIMM_HAEIN

P44568

Description

16S RRNA PROCESSING PROTEIN RIMM

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26360762_c2_352.....	2596	7818	98	297		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26367332_f3_232.....	2597	7819	404	1215	135	4.7e-06

Protein name

Locus Name

Acc#

cation efflux system membrane protein czCC

pir:C33830

C33830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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26600682_f2_110	2598	7820	176	531		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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2775312_f2_96.....	2599	7821	300	903	153	9.6e-09
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Protein name

Locus Name

Acc#

hypothetical protein aq_1477

pir:D70428

D70428

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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29347260_c3_438.....	2600	7822	105	318		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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29412901_c2_334.....	2601	7823	295	888	1030	6.3e-104
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Protein name

Locus Name

Acc#

glucose-1-phosphate thymidyltransferase,

pir:C69106

C69106

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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29475312_c1_276.....	2602	7824	395	1188	866	1.5e-86
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Protein name

Locus Name

Acc#

sp:DXR_SYNY3

Q55663

Description

REDUCTOISOMERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30164137_c3_422	2603	7825	292	879	460	1.6e-43
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
2-phosphonoacetaldehyde hydrolase	gp:PAU45309				U45309	
<u>Description</u>	Pseudomonas aeruginosa 2-phosphonoacetaldehyde hydrolase gene, complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31307880_f2_133	2604	7826	108	327		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31836562_f1_56.....	2605	7827	95	288	115	1.6e-06
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
sperm-specific protein component	gp:DMU90537				U90537	
<u>Description</u>						
Drosophila melanogaster sperm-specific protein component (dj) mRNA, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32614052_f3_204.....	2606	7828	562	1689	921	2.2e-92
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
probable permease b1828	pir:D64944				D64944	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33252182_c3_437	2607	7829	237	714	392	2.5e-36

Protein name

Locus Name

Acc#

ribose 5-phosphate isomerase (rpi) homolog

pir:G69367

G69367

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33400268_c3_467	2608	7830	701	2106	170	1.1e-09

Protein name

Locus Name

Acc#

sp:YE09_SYNY3

P73594

Description

HYPOTHETICAL WD-REPEAT PROTEIN SLR1409

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33992130_f1_57	2609	7831	138	417		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34022765_f3_184	2610	7832	99	300		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34172765_c3_449	2611	7833	373	1122	122	0.00018

Protein name

Locus Name

Acc#

hypothetical protein 4

pir:E22845

E22845

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34181500_f1_6	2612	7834	955	2868	651	1.1e-61

Protein name

Locus Name

Acc#

immunoreactive 106 kDa antigen PG115

gp:AF153767

AF153767

Description

Porphyromonas gingivalis strain W50 immunoreactive 106 kDa antigenPG115 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34181587_f2_103	2613	7835	720	2163	202	4.6e-15

Protein name

Locus Name

Acc#

gp:U93688

U93688

Description

Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34572182_c3_468.....	2614	7836	921	2766	127	0.00026

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_854

pir:B70374

B70374

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36329426_f1_54.....	2615	7837	700	2103	1174	3.4e-119

Protein name

Locus Name

Acc#

sp:PPK_ECOLI

P28688

Description

POLYPHOSPHATE KINASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
39242137_c2_306	2616	7838	120	363	464	6.0e-44

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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3960126_c1_249.....	2617	7839	377	1134	108	0.0045
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Protein name

Locus Name

Acc#

gp:UMCRG1

X92509

Description

U.maydis crg1 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4023452_f3_175.....	2618	7840	400	1203		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4062817_f1_58.....	2619	7841	417	1254	233	1.0e-17
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Protein name

Locus Name

Acc#

cation efflux system (czcB-like)

pir:E70342

E70342

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4094787_f3_174	2620	7842	1019	3060	745	1.9e-73

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4100377_c2_370	2621	7843	166	501	201	4.4e-16

Protein name

Locus Name

Acc#

unknown

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4104687_f1_20	2622	7844	105	318	116	4.5e-07

Protein name

Locus Name

Acc#

sp:Y4DJ_RHISN

P55409

Description

HYPOTHETICAL TRANSCRIPTIONAL REGULATOR Y4DJ

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4110262_c3_446	2623	7845	179	540	312	7.6e-28

Protein name

Locus Name

Acc#

sp:CAPG_STAAU

P39856

Description

CAPG PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4114692_f3_229	2624	7846	547	1644	1069	4.6e-108

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ABC-type transport protein slr0864:protein slr0864:protein slr0864	pir:S74849	S74849

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4141886_f3_187.....	2625	7847	473	1422	107	0.029

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
middle molecular weight neurofilament protein	gp:XLU85969	U85969

Description

Xenopus laevis middle molecular weight neurofilament proteinNF-M(1) mRNA,
complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4187767_f3_414.....	2626	7848	189	570	120	1.2e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YH74_METTH	O27802

Description

HYPOTHETICAL PROTEIN MJ1774

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4412550_f2_104.....	2627	7849	165	498	105	6.6e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:IHFA_HAEIN	P43723

Description

INTEGRATION HOST FACTOR ALPHA-SUBUNIT (IHFA-ALPHA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4457750_c2_342	2628	7850	208	627		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4719385_c2_344.....	2629	7851	290	873	235	1.1e-19

Protein name

Locus Name

Acc#

lipoprotein

gp:AF000945

AF000945

Description

Vibrio cholerae lipoprotein (nlpD) gene, partial cds, sigma S(rpoS) gene, complete cds, and methyl-directed mismatch repairprotein (mutS) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4726557_f2_160.....	2630	7852	185	558	246	7.5e-21

Protein name

Locus Name

Acc#

AlgT

gp:AF190580

AF190580

Description

Pseudomonas syringae pv. syringae AlgT (algT) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4876252_c3_447.....	2631	7853	341	1026	108	0.0038

Protein name

Locus Name

Acc#

galactosyl transferase

gp:SPN239004

AJ239004

Description

Streptococcus pneumoniae type 8 capsular gene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4885937_f1_49	2632	7854	301	906	446	4.8e-42

Protein name

Locus Name

Acc#

putative 1,4-dihydroxy-2-naphthoate

gp:AF101047

Description

Haemophilus ducreyi putative
1,4-dihydroxy-2-naphthoate octaprenyltransferase, YadR (yadR), cytidine
5'monophosphate N-acetylneuraminic acid synthetase (neuA),
lipooligosaccharide sialyltransferase (lst), and putative
dTDP-D-glucose 4,6-dehydratase (rmlB) genes, complete cds; and

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5178800_f2_114	2633	7855	240	723	325	3.2e-29

Protein name

Locus Name

Acc#

sp:HLY3_BACCE

P54176

Description

HEMOLYSIN III (HLY-III)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5863277_c2_371	2634	7856	368	1107	406	8.3e-38

Protein name

Locus Name

Acc#

flm protein

pir:A55856

A55856

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5892183_f3_198	2635	7857	143	432	121	1.3e-07

Protein name

Locus Name

Acc#

conserved hypothetical protein MTH700

pir:E69193

E69193

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5937787_f3_227	2636	7858	775	2328	152	2.0e-10

Protein name

Locus Name

Acc#

sp:YG04_HAEIN

P45268

Description

PUTATIVE PHOSPHATE PERMEASE HI1604

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6066040_f3_208	2637	7859	297	894		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6345012_f1_43	2638	7860	304	915	360	6.2e-33

Protein name

Locus Name

Acc#

conserved hypothetical protein yloC

pir:A69878

A69878

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6428430_c3_450	2639	7861	376	1131	746	7.8e-74

Protein name

Locus Name

Acc#

cpsF protein, 40,6K

pir:S70157

S70157

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6835285_c3_393	2640	7862	125	378		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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7148412_f3_240	2641	7863	113	342		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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14178177_c3_105.....	2642	7864	64	195		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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19744643_c2_85.....	2643	7865	151	456		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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23468752_c2_84.....	2644	7866	206	621	97	0.010
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Protein name

Locus Name

Acc#

sp:VGP8_EBV

P03224

Description

PROBABLE MEMBRANE ANTIGEN GP85

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24337765_f1_23	2645	7867	267	804	365	3.0e-32

Protein name Locus Name Acc#

115K outer membrane protein precursor:SusC protein pir:JC6027 JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24390925_f2_41	2646	7868	540	1623	2188	1.2e-226

Protein name Locus Name Acc#

sp:PPCK_ANASU 009460

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24432692_g2_78	2647	7869	538	1617	92	0.031

Protein name Locus Name Acc#

MerC protein gp:EAMMRTRAN Y08992

Description

E.agglomerans pKLH272 incomplete unit of mosaic mercury resistancetransposon.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2477187_f1_22	2648	7870	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24803760_f2_36	2649	7871	637	1914	1489	1.4e-152

Protein name

Locus Name

Acc#

putative oxidoreductase alpha-subunit

gp:SCAH10

AL132824

Description

Streptomyces coelicolor cosmid AH10.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25444787_c3_98	2650	7872	222	669	784	7.3e-78

Protein name

Locus Name

Acc#

Uracil phosphoribosyltransferase

gp:AB016085

AB016085

Description

Porphyromonas gingivalis Port, upp, and prtQ genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26056588_f2_37	2651	7873	337	1014	819	1.4e-81

Protein name

Locus Name

Acc#

probable oxidoreductase

pir:E70864

E70864

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26364836_c1_70	2652	7874	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26562750_c1_69	2653	7875	415	1248	196	9.6e-13

Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26854808_f1_2	2654	7876	117	354		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29290000_f1_11	2655	7877	300	903	148	4.2e-08

Protein name

Locus Name

Acc#

sp:MSMR_STRMU

Q00753

Description

MSM OPERON REGULATORY PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32455077_c1_73	2656	7878	261	786		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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32602012_f2_43	2657	7879	81	246		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

33647142_c2_76	2658	7880	277	834	280	1.9e-24
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Protein name

Locus Name

Acc#

glycerophosphodiester phosphodiesterase
homolog yhdW

pir:E69827

E69827

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

35235700_c1_60	2659	7881	62	189		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

36520931_f2_42	2660	7882	798	2397	376	5.7e-31
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Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC
protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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392005_c1_72	2661	7883	579	1740		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3959677_c1_71	2662	7884	189	570		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4876450_c2_88	2663	7885	392	1179	88	0.00068
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Protein name

Locus Name

Acc#

gp:D42067

D42067

Description

Porphyromonas gingivalis DNA for Fimbriilin, ORF1-4, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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822135_c3_106	2664	7886	90	273		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

9933530_c2_77	2665	7887	66	201		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

23487680_f2_13	2666	7888	443	1332	110	3.1e-10
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Protein name

Locus Name

Acc#

conserved hypothetical protein yknZ

pir:E69858

E69858

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

24641677_f2_14	2667	7889	425	1278	128	1.4e-05
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Protein name

Locus Name

Acc#

conserved hypothetical protein yvrM

pir:G70047

G70047

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

24664700_f3_22	2668	7890	113	342		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

30347807_c3_46	2669	7891	304	915	132	3.4e-08
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Protein name

Locus Name

Acc#

gp:AP000342

AP000342

Description

Plasmid R100 genomic DNA.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32072162_f2_12	2670	7892	429	1290	123	0.00013

Protein name

Locus Name

Acc#

sp:Y797_METJA

Q58207

Description

HYPOTHETICAL PROTEIN MJ0797

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3932937_f2_17	2671	7893	427	1284	219	7.5e-15

Protein name

Locus Name

Acc#

sp:YBJZ_ECOLI

P75831

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3960882_f3_23	2672	7894	224	675	602	1.4e-58

Protein name

Locus Name

Acc#

sp:YF08_METJA

Q58903

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ1508

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4898552_f1_10	2673	7895	401	1206	120	0.00028

Protein name

Locus Name

Acc#

gp:D85752

D85752

Description

Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE, bacF, bacG, bacH and bacI genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7220142_f2_11	2674	7896	215	648	127	3.1e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein yvrM	pir:G70047	G70047

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10289015_f1_15.....	2675	7897	81	246		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10328155_c1_403.....	2676	7898	133	402	88	0.035

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

hypothetical protein sli0241	pir:S75099	S75099
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1054188_c1_358.....	2677	7899	127	384		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10970392_f1_119.....	2678	7900	107	324		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11109662_f1_92	2679	7901	203	612	515	2.3e-49
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
immunoreactive 21 kD antigen PG10			gp:AF144077		AF144077	
<u>Description</u>						
Porphyromonas gingivalis strain W50 immunoreactive 21 kD antigenPG10 gene, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11132800_f1_31	2680	7902	499	1500	1616	5.0e-166
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:SAHH_MESCR		P93253	
<u>Description</u>						
HYDROLASE) (ADOHCYASE)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11725312_f3_261	2681	7903	120	363	240	3.2e-20
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:RS15_BORBU		051744	
<u>Description</u>						
30S RIBOSOMAL PROTEIN S15						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1219437_c1_425	2682	7904	532	1599	255	1.1e-34
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:STS_HUMAN		P08842	
<u>Description</u>						
SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13757180_f2_220	2683	7905	60	183	70	0.033

Protein name	Locus Name	Acc#
hypothetical protein APE1598	pir:A72539	A72539

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14063750_f1_124	2684	7906	452	1359	114	2.6e-05

Protein name	Locus Name	Acc#
hypothetical protein PH0212	pir:B71244	B71244

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14173331_c2_516	2685	7907	113	342	103	1.1e-05

Protein name	Locus Name	Acc#
hypothetical protein APE0625	pir:C72649	C72649

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14536453_c1_372	2686	7908	78	237		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14720052_f3_345	2687	7909	329	990	553	2.2e-53

Protein name	Locus Name	Acc#
clindamycin resistance transfer factor btgB	pir:B41656	B41656

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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14885826_f3_296	2688	7910	64	195		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

15039137_c2_505	2689	7911	682	2049		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

167802_f3_342	2690	7912	323	972	151	5.7e-15
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Protein name

Locus Name

Acc#

hypothetical protein SCJ12.27c

pir:T37044

T37044

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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16986252_c2_479	2691	7913	261	786	595	7.8e-58
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Protein name

Locus Name

Acc#

hypothetical protein jhp1180

pir:A71838

A71838

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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19551337_c2_474	2692	7914	262	789	225	1.3e-18
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Protein name

Locus Name

Acc#

hypothetical protein b2381

pir:B65012

B65012

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19625177_f2_232	2693	7915	353	1062	423	1.3e-39

Protein name

Locus Name

Acc#

thiamin monphosphate kinase

pir:G69052

G69052

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19719812_f3_346.....	2694	7916	440	1323	432	1.5e-40

Protein name

Locus Name

Acc#

NcoI DNA modification methyltransferase

gp:AF068761

AF068761

Description

Nocardia corallina NcoI DNA modification methyltransferase (ncoIM) and NcoI restriction endonuclease (ncoIR) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1992707_c1_402.....	2695	7917	167	504		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20742167_f3_344.....	2696	7918	112	339		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
210937_c2_462	2697	7919	232	699		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21520936_f3_348.....	2698	7920	180	543		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21600627_f2_230.....	2699	7921	613	1842	888	7.0e-89

Protein name

Locus Name

Acc#

sp:SPPA_SYNY3

P73689

Description

PROTEASE IV HOMOLOG, (ENDOPEPTIDASE IV)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21673205_c1_423.....	2700	7922	1178	3537	633	2.2e-62

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21673332_c1_424	2701	7923	656	1971		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21757701_f1_93	2702	7924	95	288		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22064087_c2_458	2703	7925	66	201	51	0.016

Protein name

Locus Name

Acc#

cytochrome oxidase subunit II

gp:TIMY18821

Y18821

Description

Timarcha metallica mitochondrial tRNA-Leu and partial COII genes, isolate Forest d'Anlier.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22078391_f3_333	2704	7926	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22462842_c1_397	2705	7927	375	1128		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22687827_c3_551	2706	7928	443	1332	136	9.8e-05

Protein name

Locus Name

Acc#

hypothetical protein

pir:H75507

H75507

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22838405_c3_598	2707	7929	1251	3756	333	5.6e-47

Protein name

Locus Name

Acc#

hybrid histidine kinase

gp:AF029704

AF029704

Description

Dictyostelium discoideum hybrid histidine kinase (dhkD) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23492786_c1_395	2708	7930	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2350306_f1_106	2709	7931	100	303	105	6.6e-06

Protein name

Locus Name

Acc#

hypothetical protein PH0217

pir:G71244

G71244

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23537750_f2_168	2710	7932	567	1704	269	3.5e-21

Protein name

Locus Name

Acc#

Immunoreactive 53 kD antigen PG123

gp:AF144641

AF144641

Description

Porphyromonas gingivalis strain W50 immunoreactive 53 kD antigenPG123 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23625061_f2_247	2711	7933	246	741		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23629407_f2_244.....	2712	7934	410	1233	184	1.3e-13

Protein name

Locus Name

Acc#

hypothetical protein (avrc 3' region)

pir:C43649

C43649

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23633430_c3_552.....	2713	7935	435	1308		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23875636_f2_151	2714	7936	87	264		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23876527_c1_356.....	2715	7937	61	186	53	0.016

Protein name

Locus Name

Acc#

TrkA

gp:BSU62055

U62055

Description

Bacillus subtilis Czcd (czcd) gene, partial cds, TrkA (trkA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23939825_f3_341.....	2716	7938	633	1902	224	4.5e-30

Protein name

Locus Name

Acc#

sp:YF65_METJA

Q58960

Description

HYPOTHETICAL PROTEIN MJ1565

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23985687_f2_231.....	2717	7939	285	858	736	8.9e-73

Protein name

Locus Name

Acc#

purine nucleoside phosphorylase

pir:H72217

H72217

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24250953_f3_254	2718	7940	640	1923	941	1.9e-98

Protein name Locus Name Acc#
hypothetical protein F10M10.30 pir:T04772 T04772

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24257177_f3_297	2719	7941	688	2067	1426	4.9e-173

Protein name Locus Name Acc#
methionyl-tRNA synthetase (mets) PAB2364 pir:B75074 B75074

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2428417_c3_594	2720	7942	67	204		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24335131_f2_222	2721	7943	64	195	106	5.1e-06

Protein name Locus Name Acc#
hypothetical protein PH0219 pir:A71245 A71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24343756_f3_255	2722	7944	62	189		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24401002_c2_500	2723	7945	114	345		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24412626_f2_140.....	2724	7946	682	2049		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
244636_c3_591.....	2725	7947	321	966		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24487752_f2_249.....	2726	7948	349	1050	109	0.012

Protein name

Locus Name

Acc#

DNA-directed RNA polymerase, beta'-2
chain:RNA polymerase rpoC2

pir:S72284

S72284

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24494067_f2_169	2727	7949	357	1074	138	1.1e-08

Protein name	Locus Name	Acc#
thiol:disulfide interchange protein homolog yneN	pir:E69891	E69891

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24503502_f2_143.....	2728	7950	98	297	124	7.3e-08

Protein name	Locus Name	Acc#
hypothetical protein	gp:SSU18930	Y18930

Description

Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24642312_c2_464.....	2729	7951	105	318		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24646916_f1_52.....	2730	7952	185	558	203	2.7e-16

Protein name	Locus Name	Acc#
RNA polymerase sigma factor SigZ-like protein	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24647188_c2_502	2731	7953	209	630	77	0.019

Protein name

Locus Name

Acc#

gp:HIVY16028

Y16028

Description

HIV-1 vif, vpr, tat, vpu genes, strain 95CAMP448.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648417_f3_309	2732	7954	291	876	375	1.4e-41

Protein name

Locus Name

Acc#

macrophage infectivity potentiator

gp:LAU91606

U91606

Description

Legionella adelaidensis macrophage infectivity potentiator (mip) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648442_c3_553.....	2733	7955	504	1515	131	0.00012

Protein name

Locus Name

Acc#

gp:SCYDL057W

Description

S.cerevisiae chromosome IV reading frame ORF YDL057w.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24650150_c1_396.....	2734	7956	466	1401		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24798157_c2_460	2735	7957	119	360		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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2531537_f2_197	2736	7958	370	1113		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

25547302_c1_379	2737	7959	355	1068	205	3.1e-14
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Protein name

Locus Name

Acc#

AlgZ

gp:PAU52431

U52431

Description

Pseudomonas aeruginosa AlgR-cognate sensor AlgZ (algZ) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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25578342_f1_120	2738	7960	380	1143		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25632882_f1_108	2739	7961	384	1155	321	8.5e-29

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_1656

pir:C70443

C70443

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26290890_f3_256.....	2740	7962	1087	3264	422	1.1e-73

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26364458_c1_433.....	2741	7963	638	1917	1704	2.4e-175

Protein name

Locus Name

Acc#

GTP-binding elongation factor family protein TypA/BipA

pir:E75426

E75426

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26445263_c1_378.....	2742	7964	435	1308	252	5.8e-19

Protein name

Locus Name

Acc#

immunoreactive 52kD antigen PG41

gp:AF175716

AF175716

Description

Porphyromonas gingivalis strain W50 immunoreactive 52kD antigenPG41 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26595663_c3_550	2743	7965	358	1077		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26619587_c2_504.....	2744	7966	392	1179	271	3.6e-27

Protein name

Locus Name

Acc#

coenzyme PQQ synthesis protein (pqqE) homolog

pir:F69551

F69551

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26640807_f3_252.....	2745	7967	496	1491		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
282708_f3_320.....	2746	7968	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29479502_f2_246.....	2747	7969	243	732	126	2.3e-06

Protein name

Locus Name

Acc#

probable transcription regulator

pir:T34578

T34578

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29479676_c2_461	2748	7970	106	321	202	3.5e-16

Protein name

Locus Name

Acc#

sp:DBH_BACST

Description

DNA-BINDING PROTEIN II (HB) (HU)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29775466_c1_427	2749	7971	126	381	103	1.1e-05

Protein name

Locus Name

Acc#

hypothetical protein APE0626

pir:D72649

D72649

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30345437_c1_420.....	2750	7972	419	1260	589	3.4e-57

Protein name

Locus Name

Acc#

hypothetical protein

gp:PGI237898

AJ237898

Description

Porphyromonas gingivalis olpA and rbfA genes and ORF3 (partial), strain ATCC33277.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30563152_c3_574.....	2751	7973	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30681581_f3_311	2752	7974	104	315		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3134627_c1_419	2753	7975	486	1461	1062	2.5e-107

Protein name

Locus Name

Acc#

sp:KPYK_BORBU

O51323

Description

PYRUVATE KINASE, (PK)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3156300_f2_172	2754	7976	403	1212	100	0.016

Protein name

Locus Name

Acc#

hypothetical protein DKFZp566D1824.1

pir:T14767

T14767

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31676317_f1_122	2755	7977	194	585		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31750058_f2_128	2756	7978	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3176437_f2_170	2757	7979	514	1545	1367	1.2e-139

Protein name

Locus Name

Acc#

hypothetical protein slr0904

pir:S75721

S75721

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32064193_c1_387	2758	7980	404	1215	1403	1.9e-143

Protein name

Locus Name

Acc#

UDP-ManNAc dehydrogenase

gp:AF125164

AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3234530_f2_127	2759	7981	379	1140	150	1.1e-07

Protein name

Locus Name

Acc#

hypothetical protein

pir:G75375

G75375

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33390680_f1_84	2760	7982	222	669	101	0.047

Protein name

Locus Name

Acc#

otoferlin

gp:AF107403

AF107403

Description

Homo sapiens otoferlin (OTOF) mRNA, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33792160_f2_138	2761	7983	87	264	82	0.020

Protein name

Locus Name

Acc#

gp:PFMAL3P7

Description

Plasmodium falciparum MAL3P7, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34081405_c1_376.....	2762	7984	88	267	110	1.9e-06

Protein name

Locus Name

Acc#

hypothetical protein PHS004

pir:F71245

F71245

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34094141_f2_248.....	2763	7985	229	690	156	2.6e-11

Protein name

Locus Name

Acc#

clindamycin resistance transfer factor btgA

pir:A41656

A41656

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34172157_c3_543	2764	7986	110	333	80	0.022

Protein name

Locus Name

Acc#

transposase

gp:EFENT1JO

Y16413

Description

Enterococcus faecium entI and entJ genes and two open readingframes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34176550_c3_549	2765	7987	346	1041	201	1.7e-13

Protein name

Locus Name

Acc#

integrase IntN1

gp:BUU51917

U51917

Description

Bacteroides uniformis insertion element NBUI fragment, integraseIntN1 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34198800_f1_107.....	2766	7988	60	183	58	0.024

Protein name

Locus Name

Acc#

immunoglobulin heavy chain variable region

gp:BTU49783

U49783

Description

Bos taurus immunoglobulin rearranged heavy chain variable regionmRNA, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34259628_c1_398.....	2767	7989	104	315		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35172150_f2_152	2768	7990	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35839375_c1_351	2769	7991	370	1113	1470	1.5e-150

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36072640_c3_588	2770	7992	111	336	99	2.8e-05

Protein name

Locus Name

Acc#

hypothetical protein PH0994

pir:E71091

E71091

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3912762_f2_245	2771	7993	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3914093_f2_228	2772	7994	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4032890_c1_429	2773	7995	537	1614	441	3.2e-40
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Protein name	Locus Name	Acc#
sensory transduction histidine kinase slr2098:protein slr2098:protein slr2098	pir:S75130	S75130

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4067837_f1_123	2774	7996	146	441		
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Protein name	Locus Name	Acc#
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4095080_c1_401	2775	7997	692	2079	620	5.1e-92
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Protein name	Locus Name	Acc#
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sp:Y590_METJA	Q58010
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Description

HYPOTHETICAL PROTEIN MJ0590

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4117188_c2_463	2776	7998	282	849	455	3.3e-58
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Protein name	Locus Name	Acc#
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helicase	gp:RNDNAB	Y13813
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Description

Rhodothermus marinus dnaB gene.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4117336_f1_90	2777	7999	260	783	368	8.9e-34

Protein name

Locus Name

Acc#

hypothetical protein jhp0094

pir:E71975

E71975

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4157880_c1_388	2778	8000	380	1143	1207	1.1e-122

Protein name

Locus Name

Acc#

putative UDP-N-acetylglucosamine 2-epimerase

gp:ALW243431

AJ243431

Description

Acinetobacter lwoffii wzc, wzb, wza, weeA, weeB, weeC, wzx, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeJ, weeK, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4320288_c2_473	2779	8001	1014	3045	712	3.0e-68

Protein name

Locus Name

Acc#

sp:Y895_HAEIN

Description

HYPOTHETICAL PROTEIN HI0895

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4411636_c1_361	2780	8002	122	369		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4491411_f2_133	2781	8003	213	642	121	5.4e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative large secreted protein			gp:SCF12		AL117669	
<u>Description</u>						
Streptomyces coelicolor cosmid F12.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4494028_f3_299	2782	8004	396	1191	222	1.1e-16
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
capsular polysaccharide biosynthesis protein			pir:F70441		F70441	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4562683_f1_76	2783	8005	165	498		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4580050_c1_399	2784	8006	401	1206		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4694410_f3_343	2785	8007	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4801588_f3_300	2786	8008	339	1020	96	0.0092

Protein name

Locus Name

Acc#

hypothetical protein F13H8.1

pir:T16066

T16066

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4860650_f1_14	2787	8009	95	288	75	0.0099

Protein name

Locus Name

Acc#

ct602 hypothetical protein

pir:F72036

F72036

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4881301_c1_363	2788	8010	306	921		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4884681_c1_365	2789	8011	99	300	113	9.3e-07

Protein name

Locus Name

Acc#

protein gp57

pir:T13144

T13144

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4886652_f3_280	2790	8012	574	1725	84	0.045

Protein name

Locus Name

Acc#

hypothetical protein PFB0765w

pir:E71606

E71606

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4898437_f2_167	2791	8013	320	963	580	3.0e-56

Protein name

Locus Name

Acc#

tyrosine recombinase XerD

gp:AF093548

AF093548

Description

Staphylococcus aureus tyrosine recombinase XerD (xerD) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4945451_f2_205	2792	8014	417	1254	214	7.8e-15

Protein name

Locus Name

Acc#

probable mannosyltransferase

pir:C75423

C75423

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4960907_f2_229	2793	8015	174	525	206	1.3e-16

Protein name

Locus Name

Acc#

hypothetical protein APE1457

pir:A72625

A72625

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
506502_f2_145	2794	8016	203	612	522	4.3e-50

Protein name

Locus Name

Acc#

epoxidase

pir:F69187

F69187

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5093790_c3_571	2795	8017	89	270		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5110212_c1_364	2796	8018	338	1017		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5116680_f2_146	2797	8019	560	1683	1827	2.2e-188

Protein name

Locus Name

Acc#

probable acid--CoA ligase, MTH657

pir:D69187

D69187

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5273337_f1_24	2798	8020	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5275263_c3_567	2799	8021	348	1047	226	5.0e-17

Protein name

Locus Name

Acc#

cation efflux system (czcB-like)

pir:C70415

C70415

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5332506_f2_221	2800	8022	95	288	73	0.034

Protein name

Locus Name

Acc#

hypothetical protein PH0220

pir:B71245

B71245

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
589038_f3_325.....	2801	8023	96	291		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6095461_c1_418.....	2802	8024	143	432	379	6.1e-35

Protein name

Locus Name

Acc#

3-dehydroquinate dehydratase, :carbonic
3-dehydroquinase:protein sll1112:carbonic
3-dehydroquinase:protein sll1112

pir:S77551

S77551

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6407762_c2_510.....	2803	8025	117	354	358	1.0e-32

Protein name

Locus Name

Acc#

RBFA, putative

gp:PGI237898

AJ237898

Description

Porphyromonas gingivalis olpA and rbfA genes and ORF3 (partial), strain ATCC33277.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6586_f2_129	2804	8026	587	1764		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6829052_f3_298.....	2805	8027	458	1377	542	3.2e-52

Protein name

Locus Name

Acc#

O-antigen repeat unit transporter Wzx

gp:AF172324

AF172324

Description

Escherichia coli GalF (galF) gene, partial cds; O-antigen repeatunit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy(wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE),UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenaseGnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF)genes, complete cds; and chain length determinant

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7142501_f3_304.....	2806	8028	439	1320	344	3.1e-31

Protein name

Locus Name

Acc#

hypothetical protein RP336

pir:B71690

B71690

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
791436_c3_612.....	2807	8029	220	663	363	3.0e-33

Protein name

Locus Name

Acc#

O-methyltransferase

pir:B70431

B70431

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
797311_f2_234	2808	8030	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
838915_f2_188.....	2809	8031	101	306	112	1.2e-06

Protein name

Locus Name

Acc#

hypothetical protein PH1791

pir:G71189

G71189

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
8501_c1_422.....	2810	8032	329	990		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9765652_f3_330.....	2811	8033	90	273	77	0.014

Protein name

Locus Name

Acc#

yhcV homolog 2:inosine-monophosphate
dehydrogenase (guaB-2) homolog (misnomer)

pir:F69514

F69514

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
976577_f2_150	2812	8034	832	2499	104	6.1e-05
Protein name			Locus Name			Acc#
hypothetical protein			gp:SSU18930			Y18930
Description						
Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
993811_f3_310	2813	8035	162	489	282	1.2e-24
Protein name			Locus Name			Acc#
			sp:ASNC_ECOLI			P03809
Description						
REGULATORY PROTEIN ASNC						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9959637_c3_595.....	2814	8036	417	1254	101	0.0013
Protein name			Locus Name			Acc#
thiol:disulfide interchange protein			pir:C70314			C70314
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10191317_f1_20.....	2815	8037	128	387	93	2.1e-06
Protein name			Locus Name			Acc#
hypothetical protein Jv0534			gp:AF121009			AF121009
Description						
Mycobacterium tuberculosis H37Rv hypothetical protein Jv0534(Jv0534) mRNA, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14566582_c1_74	2816	8038	635	1908	473	1.2e-43

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sensory transduction histidine kinase slr2098:protein slr2098:protein slr2098	pir:S75130	S75130

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14574068_c1_99.....	2817	8039	78	234		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14629712_f2_34.....	2818	8040	1066	3201	469	7.1e-80

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14944534_c3_164.....	2819	8041	68	207		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16132962_c3_126	2820	8042	206	621	239	2.4e-19
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein RP329			pir:C71689			C71689
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1953877_f1_26	2821	8043	66	201		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19578827_f2_33	2822	8044	282	849		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20437662_f3_54	2823	8045	309	930	151	2.2e-08
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
regulatory protein hpaA			pir:A55349			
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22348262_c2_124	2824	8046	754	2265	510	4.6e-46
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
cation efflux (AcrB/AcrD/AcrF family)			pir:F70368			F70368
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22365790_f1_8	2825	8047	76	231	83	0.012

Protein name: unknown

Locus Name: gp:AF007157

Acc#: AF007157

Description: Homo sapiens clone 23856 unknown mRNA, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23546890_c2_120	2826	8048	253	762	275	6.3e-24

Protein name:

Locus Name: sp:YEHT_ECOLI

Acc#:

Description: HYPOTHETICAL 27.9 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23572188_f2_39.....	2827	8049	568	1707	392	4.1e-50

Protein name:

Locus Name: sp:ACDB_BACSU

Acc#: P45857

Description: ACYL-COA DEHYDROGENASE,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24250285_c3_151.....	2828	8050	81	246		

Protein name:

Locus Name:

Acc#:

Description: NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24407552_c2_102	2829	8051	317	954	357	1.2e-55

Protein name

Locus Name

Acc#

sp:DNAJ_THETH

Description

DNAJ PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24495463_f2_38	2830	8052	344	1035	710	5.1e-70

Protein name

Locus Name

Acc#

sp:FIXB_CLOAB

P53578

Description

FIXB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24644011_f2_36	2831	8053	628	1887	441	1.6e-41

Protein name

Locus Name

Acc#

gp:ATAC005851

AC005851

Description

Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2845068_f3_56	2832	8054	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29476553_f1_6	2833	8055	62	189		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29851437_f2_29	2834	8056	435	1308	101	1.1e-07
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

cysteine proteinase CP1

pir:S67481

S67481

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3324133_c1_92	2835	8057	62	189		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33619587_c1_96	2836	8058	250	753	132	1.6e-09
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

conserved hypothetical protein

pir:B75483

B75483

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3395627_f2_37	2837	8059	323	972	446	3.9e-47
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

sp:ETFB_CLOAB

P52040

Description

TRANSFER FLAVOPROTEIN SMALL SUBUNIT) (ETFSS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34172130_f3_65	2838	8060	1348	4047	1255	1.3e-170

Protein name

Locus Name

Acc#

sp:BGAL_BACME

052847

Description

BETA-GALACTOSIDASE, (LACTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35556713_c2_100	2839	8061	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36226538_c3_155.....	2840	8062	406	1221	247	2.8e-18

Protein name

Locus Name

Acc#

sp:YEHU_ECOLI

Description

HYPOTHETICAL 62.1 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4020962_c2_103.....	2841	8063	106	321	90	0.00026

Protein name

Locus Name

Acc#

transcription regulator MerR family

pir:D70361

D70361

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4475281_f1_14	2842	8064	587	1764	187	3.4e-11
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:U96771		U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6694586_c3_139	2843	8065	62	189		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15633577_f2_1.....	2844	8066	66	201	103	0.00016
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
penicillin-binding protein 2			gp:AF147448		AF147448	
<u>Description</u>						
Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 2 (pbpA), rod-shape-determining protein (rodA), membrane-bound lytic transglycosylase (mltB), rare lipoprotein A (rlpA), penicillin-binding protein 5 (dacA), and lipote biosynthesis protein B (lipB) genes, complete cds; and unknown gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26595675_f3_5	2845	8067	437	1314	187	2.3e-26
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:RODA_HAEIN				P44468	
<u>Description</u>						
ROD SHAPE-DETERMINING PROTEIN RODA						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14865875_f3_5	2846	8068	346	1041	784	7.3e-78

Protein name

Locus Name

Acc#

sp:FE0B_METJA

Q57986

Description

FERROUS IRON TRANSPORT PROTEIN B HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36382950_f2_3	2847	8069	94	285		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10734635_f2_10.....	2848	8070	830	2493	135	1.0e-05

Protein name

Locus Name

Acc#

unknown

gp:AF124349

AF124349

Description

Zymomonas mobilis ZM4 fosmid clone 41A4, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10740952_f1_3.....	2849	8071	247	744	121	2.1e-05

Protein name

Locus Name

Acc#

sp:PAIB_RAT

O35264

Description

ACTIVATING FACTOR ACETYLHYDROLASE ALPHA 2 SUBUNIT) (PAF-AH ALPHA 2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24694837_f1_2	2850	8072	189	570		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34252176_c3_33.....	2851	8073	559	1680	567	9.4e-54
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
adenylate cyclase homolog			pir:T17197		T17197	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34406517_f3_16.....	2852	8074	1008	3027	822	6.9e-82
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)			gp:PGI130872		AJ130872	
<u>Description</u>						

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6257826_f3_12.....	2853	8075	311	936	113	0.012
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
cyclic beta 1-2 glucan synthetase			pir:T31419		T31419	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11925285_f2_7	2854	8076	90	273	187	1.3e-14
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:Y328_SYNY3		Q55535
<u>Description</u>						
(EC 3.1.3.48)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11930451_f1_2	2855	8077	112	339	118	2.8e-07
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:Y328_SYNY3		Q55535
<u>Description</u>						
(EC 3.1.3.48)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21875776_c1_27	2856	8078	67	204		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
237905_f2_10	2857	8079	63	192		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24629781_f1_1	2858	8080	494	1485		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25958125_f1_5	2859	8081	392	1179	643	4.2e-84

Protein name

Locus Name

Acc#

sp:SYE_BACST

P22249

Description

(GLURS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9765657_c2_36	2860	8082	704	2115	692	4.1e-68

Protein name

Locus Name

Acc#

sp:YQFF_BACSU

Description

HYPOTHETICAL 79.2 KD PROTEIN IN PHOH-DGKA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11756330_f1_2	2861	8083	107	324	142	7.9e-10

Protein name

Locus Name

Acc#

sp:YEAQ_ECOLI

P76246

Description

HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12189053_f2_10	2862	8084	183	552	418	4.5e-39

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
30S ribosomal protein S7	gp:AF087414	AF087414

Description

Haemophilus ducreyi OapA (oapA), OapB (oapB), RfaF (rfaF), 30S ribosomal protein S12, and 30S ribosomal protein S7 genes, complete cds; and elongation factor G gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
192812_c1_28	2863	8085	161	486		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2238400_c3_63.....	2864	8086	147	444	147	1.9e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein Jv0166c	gp:AF121004	AF121004

Description

Mycobacterium tuberculosis H37Rv hypothetical protein Jv0166c(Jv0166c) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22394692_c1_23.....	2865	8087	167	504	245	7.0e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YHA2_EIKCO	P35649

Description

HYPOTHETICAL 66.3 KD PROTEIN IN HAG2 5' REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22460877_f2_9	2866	8088	139	420	517	1.4e-49

Protein name

Locus Name

Acc#

sp:RS12_ANANI

P18662

Description

30S RIBOSOMAL PROTEIN S12

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24275036_c3_56	2867	8089	90	273		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24804717_f1_4	2868	8090	709	2130	2946	0.0

Protein name

Locus Name

Acc#

EF-G

gp:AB035469

AB035469

Description

Porphyromonas gingivalis gene for EF-G, complete cds, strain:SUNY1021.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2945300_f1_5	2869	8091	105	318	326	2.5e-29

Protein name

Locus Name

Acc#

ribosomal protein S10

gp:AF115283

AF115283

Description

Leptospira interrogans S10-spc-alpha locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34275250_f3_16	2870	8092	87	264	73	0.022

Protein name Locus Name Acc#
D-29 protein gp:GHLEA29 X13203

Description
Cotton set 5A Lea gene for seed protein D-29.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4064027_c1_29	2871	8093	382	1149	128	1.0e-10

Protein name Locus Name Acc#
hypothetical protein RP338 pir:D71690 D71690

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4562800_f2_7	2872	8094	1437	4314	4541	0.0

Protein name Locus Name Acc#
sp:RPOC_PORCN 033431

Description
BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT) (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4773262_f1_3	2873	8095	110	333		

Protein name Locus Name Acc#

Description
NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4881260_f1_6	2874	8096	125	378	293	7.9e-26

Protein name

Locus Name

Acc#

sp:RL3_THETH

P52860

Description

50S RIBOSOMAL PROTEIN L3

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
501401_c1_21	2875	8097	64	195	109	3.2e-05

Protein name

Locus Name

Acc#

sp:YHA2_EIKCO

P35649

Description

HYPOTHETICAL 66.3 KD PROTEIN IN HAG2 5'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
666025_f3_12	2876	8098	276	831	892	2.6e-89

Protein name

Locus Name

Acc#

DNA-dependent RNA polymerase subunit beta

gp:LMY16468

Y16468

Description

Listeria monocytogenes unidentified gene and partial rpoB gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
985967_c1_22	2877	8099	142	429	245	7.0e-20

Protein name

Locus Name

Acc#

sp:YHA2_EIKCO

P35649

Description

HYPOTHETICAL 66.3 KD PROTEIN IN HAG2 5'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11027152_c1_174	2878	8100	95	288	102	1.4e-05
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein PH0133			pir:C71234			C71234
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11803111_f2_79	2879	8101	132	399	95	7.5e-05
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:YGJM_ECOLI			P42594
<u>Description</u>						

HYPOTHETICAL 15.0 KD PROTEIN IN EBGX-UXAA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12376457_c3_246	2880	8102	495	1488	1521	5.8e-156
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:IMDH_AQUAE			067820
<u>Description</u>						

DEHYDROGENASE) (IMPDH) (IMPD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
136412_c3_263	2881	8103	788	2367		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13757180_f3_171	2882	8104	60	183	70	0.033
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein APE1598			pir:A72539		A72539	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13798132_f2_69	2883	8105	68	207		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14890637_c1_200	2884	8106	87	264		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14890637_c1_202	2885	8107	89	270		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15117081_c1_182	2886	8108	259	780		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16445385_c3_248	2887	8109	102	309		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16617812_c1_172.....	2888	8110	195	588	127	3.1e-08

Protein name

Locus Name

Acc#

hypothetical protein aq_1103

pir:A70395

A70395

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c1_194.....	2889	8111	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16835962_c2_206.....	2890	8112	63	192	162	6.0e-12

Protein name

Locus Name

Acc#

sp:RL32_BACST

P07840

Description

50S RIBOSOMAL PROTEIN L32 (RIBOSOMAL PROTEIN I) (BL37)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16839002_c1_181.....	2891	8113	728	2187	1183	3.8e-120

Protein name

Locus Name

Acc#

DNA helicase RecQ

pir:G75413

G75413

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19537662_c3_251	2892	8114	398	1197		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19725256_c1_192.....	2893	8115	424	1275		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20007287_c3_234.....	2894	8116	312	939	677	1.6e-66
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:ERA_BACSU		P42182
<u>Description</u>						

GTP-BINDING PROTEIN ERA HOMOLOG (BEX PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20527135_c1_199.....	2895	8117	423	1272	273	3.1e-22
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
probable lipopolysaccharide N-acetylglucosaminyltransferase, rfbU				pir:F64500		F64500
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20579552_c3_261	2896	8118	495	1488	172	2.1e-10

Protein name

Locus Name

Acc#

sp:Y907_METJA

Q58317

Description

HYPOTHETICAL PROTEIN MJ0907

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21490762_c1_191	2897	8119	413	1242		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22475317_f1_16.....	2898	8120	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22697055_c2_218.....	2899	8121	88	267		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22833311_c3_258	2900	8122	214	645		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c2_225.....	2901	8123	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23448251_f1_37.....	2902	8124	571	1716		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23626500_c2_211.....	2903	8125	75	228		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24252127_c3_255	2904	8126	458	1377		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24407802_c1_198.....	2905	8127	264	795		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24500762_c2_228.....	2906	8128	203	612		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24509632_c1_173.....	2907	8129	438	1317	978	2.0e-98
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Protein name

Locus Name

Acc#

sp:YPHC_BACSU

P50743

Description

REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24642262_c3_247	2908	8130	519	1560	133	8.0e-06

Protein name

Locus Name

Acc#

sp:PRSA_BACSU

P24327

Description

PROTEIN EXPORT PROTEIN PRSA PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24651442_c1_197	2909	8131	627	1884	121	0.00098

Protein name

Locus Name

Acc#

MAR binding filament-like protein 1:MFP1 protein

pir:T07111

T07111

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25391905_c1_184	2910	8132	571	1716		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25781265_c3_256	2911	8133	107	324		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25907687_f1_26	2912	8134	69	210		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26289002_c3_233.....	2913	8135	339	1020	698	9.5e-69

Protein name Locus Name Acc#

synthase III pir:F70394 F70394

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
265955_f1_52.....	2914	8136	130	393	221	3.3e-18

Protein name Locus Name Acc#

RNA-binding protein gp:SYORBPA L48548

Description

Synechococcus sp. PCC 7942 RNA-binding protein (rbpA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
27137_c2_226.....	2915	8137	62	189		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30120936_c3_240	2916	8138	257	774	933	1.2e-93

Protein name

Locus Name

Acc#

gp:PGPUT

X97228

Description

P.gingivalis gpdxJ, put, and yhbG-pg genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31447126_c1_203	2917	8139	224	675	290	1.9e-25

Protein name

Locus Name

Acc#

CMP-N-acetylneuraminic acid synthetase

gp:MMU6215

AJ006215

Description

Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33640927_c1_177	2918	8140	455	1368	205	1.8e-13

Protein name

Locus Name

Acc#

trigger factor

pir:C70416

C70416

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34081405_c3_231	2919	8141	88	267	110	1.9e-06

Protein name

Locus Name

Acc#

hypothetical protein PHS004

pir:F71245

F71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34165705_f2_114	2920	8142	80	243		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34406640_f3_134	2921	8143	96	291	127	3.1e-08

Protein name

Locus Name

Acc#

sp:YGJN_ECOLI

P42595

Description

HYPOTHETICAL 12.1 KD PROTEIN IN EBGC-UXAA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35343757_f2_104	2922	8144	260	783	453	8.7e-43

Protein name

Locus Name

Acc#

probable ribonucleotide transport ATP-binding protein mkl (mkl) RP097

pir:H71718

H71718

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35661528_f1_47	2923	8145	84	255	119	2.7e-07

Protein name

Locus Name

Acc#

hypothetical protein

gp:BSZ75208

Z75208

Description

B.subtilis genomic sequence 89009bp.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3929055_c3_260	2924	8146	410	1233		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4073567_c2_229.....	2925	8147	403	1212		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4100002_c1_201.....	2926	8148	83	252	72	0.020
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:MT13_MYTED		P80248
<u>Description</u>						

METALLOTHIONEIN 10-III (MT-10-III)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4178555_c1_193.....	2927	8149	167	504		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
42700_c1_195	2928	8150	268	807		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4490938_c2_215.....	2929	8151	418	1257	1153	5.8e-117

Protein name

Locus Name

Acc#

ClpX protein

gp:BSCLPXGEN

X95306

Description

B.subtilis clpX gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
48776_c3_242.....	2930	8152	246	741	585	9.0e-57

Protein name

Locus Name

Acc#

ATP-dependent protease proteolytic subunit
ClpP

gp:AF127082

AF127082

Description

Myxococcus xanthus ATP-dependent protease proteolytic subunit ClpP (clpP), ATP-dependent protease ATPase subunit ClpX (clpX), prolylendopeptidase precursor Pep (pep), ATP-dependent protease LonV (lonV), oligopeptide permease homolog OppA (oppA), oligopeptidepermease homolog OppB (oppB), and oligopeptide permease homolog OppC (oppC) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4882801_c2_227.....	2931	8153	139	420		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4957677_c1_183	2932	8154	459	1380	252	5.2e-19

Protein name

Locus Name

Acc#

sp:SURA_ECOLI

Description

SURA), (PPIASE) (ROTAMASE C)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6695412_f3_159	2933	8155	323	972	333	4.5e-30

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_355

pir:E70331

E70331

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6757757_c3_249	2934	8156	634	1905	838	1.4e-83

Protein name

Locus Name

Acc#

sp:MUTL_BACSU

P49850

Description

DNA MISMATCH REPAIR PROTEIN MUTL

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781290_c3_236	2935	8157	236	711	268	3.5e-23

Protein name

Locus Name

Acc#

vsrD protein

pir:I40540

I40540

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
818785_c3_262	2936	8158	410	1233		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
130278_c3_244	2937	8159	539	1620	1138	2.3e-115

Protein name Locus Name Acc#

phosphoribosylaminoimidazolecarboxamide
formyltransferase

pir:C70468 C70468

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13688436_c1_177	2938	8160	127	384	171	6.7e-13

Protein name Locus Name Acc#

YHCF

gp:AB024564 AB024564

Description

Bacillus halodurans gene for TNPA, ERMK, YCBJ, YHCG, YHCF and YHCE, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14570812_c1_175	2939	8161	220	663	94	0.0032

Protein name Locus Name Acc#

sp:EXB1_XANCP 034259

Description

BIOPOLYMER TRANSPORT EXBD1 PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15714000_f2_81	2940	8162	473	1422	895	1.3e-89

Protein name

Locus Name

Acc#

gp:BNRRTEAB

Description

Bacteroides thetaiotaomicron rteA and rtaB genes involved in production of plasmid-like forms, complete cds, and tetQ gene, 3'end.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f1_22	2941	8163	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
17079008_c1_179.....	2942	8164	288	867	162	3.5e-10

Protein name

Locus Name

Acc#

unknown

gp:AF062647

AF062647

Description

Butyrivibrio fibrisolvens butyrivibriocin OR79 (bvi79) gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19570256_c1_180.....	2943	8165	513	1542		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
195812_c1_178	2944	8166	269	810	75	0.048

Protein name

Locus Name

Acc#

gp:YSCMTRF21

Description

Yeast (S.uvarum) mitochondria RF2 gene, segment 1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f2_77	2945	8167	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2350306_f3_169.....	2946	8168	100	303	105	6.6e-06

Protein name

Locus Name

Acc#

hypothetical protein PH0217

pir:G71244

G71244

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23625127_c1_173.....	2947	8169	283	852	197	1.2e-15

Protein name

Locus Name

Acc#

TolQ protein

gp:PPPAL1

X74218

Description

Pseudomonas putida ruvB, tolQ, tolR, tolA, tolB and oprL genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23870287_f3_126	2948	8170	65	198		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23944506_f1_45	2949	8171	64	195	106	5.1e-06
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
hypothetical protein PH0219				pir:A71245		A71245
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24015950_c2_208	2950	8172	792	2379	107	0.00022
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
outer membrane protein Omp85				gp:AF021245		AF021245
<u>Description</u>						
Neisseria meningitidis outer membrane protein Omp85 (omp85) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24229677_c3_238	2951	8173	283	852	388	6.7e-36
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
NorM				gp:AB010463		AB010463
<u>Description</u>						
Vibrio parahaemolyticus gene for NorM, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24484666_c2_215	2952	8174	347	1044	761	2.0e-75
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
rod shape determining protein MreB			pir:B70373			B70373
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24487803_f2_93.....	2953	8175	70	213		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24641925_c3_243.....	2954	8176	798	2397	110	0.033
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
115K outer membrane protein precursor:SusC protein			pir:JC6027			JC6027
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24647752_c3_225.....	2955	8177	479	1440	178	1.2e-10
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
conserved hypothetical protein MTH83			pir:F69210			F69210
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25635393_c3_245.....	2956	8178	187	564		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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266067_f1_27	2957	8179	102	309		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26673162_f3_152	2958	8180	65	198		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26767842_c2_216	2959	8181	364	1092	442	1.8e-41
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Protein name

Locus Name

Acc#

penicillin-binding protein 2

gp:AF147448

AF147448

Description

Pseudomonas aeruginosa strain PA01 penicillin-binding protein 2 (pbpA), rod-shape-determining protein (rodA), membrane-bound lytic transglycosylase (mltB), rare lipoprotein A (rlpA), penicillin-binding protein 5 (dacA), and lipote biosynthesis protein B (lipB) genes, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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282708_f2_107	2960	8182	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29350402_c1_196	2961	8183	290	873	193	5.0e-14
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
rod shape-determining protein (mreC) homolog			pir:C70189		C70189	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30656500_c2_214.....	2962	8184	681	2046	1802	9.8e-186
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
PepO			gp:AB010440		AB010440	
<u>Description</u>						
Porphyromonas gingivalis gene for PepO, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3157802_c2_204.....	2963	8185	422	1269	514	3.0e-49
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:Y4WA_RHISN		P55679	
<u>Description</u>						
HYPOTHETICAL ZINC PROTEASE Y4WA,						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31813761_f1_37.....	2964	8186	85	258		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33210875_c1_182	2965	8187	252	759	647	2.4e-63

Protein name

Locus Name

Acc#

sp:FABG_BACSU

Description

ACYL CARRIER PROTEIN REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34081405_c3_220	2966	8188	88	267	110	1.9e-06

Protein name

Locus Name

Acc#

hypothetical protein PHS004

pir:F71245

F71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36151575_c3_228.....	2967	8189	462	1389	212	2.5e-14

Protein name

Locus Name

Acc#

erythromycin esterase homolog ybfO

pir:A69750

A69750

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3937535_c3_236.....	2968	8190	200	603	166	1.6e-11

Protein name

Locus Name

Acc#

NorM

gp:AB010463

AB010463

Description

Vibrio parahaemolyticus gene for NorM, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
394135_c3_231	2969	8191	243	732	276	5.0e-24

Protein name

Locus Name

Acc#

sp:YG29_SYNY3

P74346

Description

HYPOTHETICAL 36.0 KD PROTEIN SLR1629

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4040878_c3_239	2970	8192	767	2304	725	1.9e-75

Protein name

Locus Name

Acc#

tetracycline resistance element regulator
RteA

pir:A41860

A41860

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4741507_c2_198.....	2971	8193	319	960	154	4.6e-14

Protein name

Locus Name

Acc#

phosphate ABC transporter, periplasmic
phosphate-binding protein

pir:C72276

C72276

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4806377_c1_174.....	2972	8194	205	618	109	4.2e-06

Protein name

Locus Name

Acc#

ExbD2

gp:AF047974

AF047974

Description

Vibrio cholerae TolR (tolR), ExbB2 (exbB2), ExbD2 (exbD2), and TonB2 (tonB2) genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4877187_c3_224	2973	8195	274	825	153	8.2e-09

Protein name

Locus Name

Acc#

sp:TONB_HELPY

025899

Description

TONB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4880452_c2_200	2974	8196	300	903	512	4.9e-49

Protein name

Locus Name

Acc#

ABC transporter MutF

gp:AF082183

AF082183

Description

Streptococcus mutans ABC transporter MutF (mutF), membrane spanning protein MuteE (muteE), and membrane protein MutG (mutG) genes, complete cds; and fructose bi-phosphate aldolase (fba) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4954682_c1_176	2975	8197	275	828		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5120327_c2_199	2976	8198	286	861	457	3.3e-43

Protein name

Locus Name

Acc#

ABC transporter, ATP-binding protein homolog

pir:D70171

D70171

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5132937_c2_213	2977	8199	653	1962	1066	9.6e-108
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ABC-type transport protein slr0864:protein slr0864:protein slr0864			pir:S74849		S74849	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6369006_c1_181	2978	8200	199	600	143	6.2e-10
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YP23_STAAU		P23217	
<u>Description</u>						

HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN QACA 5' REGION (ORF 188)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6425_c3_222	2979	8201	165	498		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
663463_c2_207	2980	8202	1518	4557		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6966_f2_109	2981	8203	76	228	54	0.034
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
unknown			gp:MHU75508			U75508
<u>Description</u>						
Marinococcus halophilus plasmid pPL1, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7225883_c3_235	2982	8204	301	906	165	1.3e-22
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
CGI-124 protein			gp:AF151882			AF151882
<u>Description</u>						
Homo sapiens CGI-124 protein mRNA, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
865757_f2_103	2983	8205	128	387		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9845313_c2_209	2984	8206	333	1002		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24644061_c2_20	2985	8207	256	771		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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3.02.7206.7_f2_6.....	2986	8208	726	2181	567	4.7e-56
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Protein name

Locus Name

Acc#

hybrid histidine kinase homolog

gp:AF024619

AF024619

Description

Pseudomonas fluorescens hybrid histidine kinase homolog (styS) and response regulatory protein (styR) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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33400260_c1_15.....	2987	8209	536	1611	124	0.00030
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Protein name

Locus Name

Acc#

STARP antigen

gp:PFSTARP

Z26314

Description

P.falciparum gene for STARP antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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830003_f2_10.....	2988	8210	73	222		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9862501_f2_9	2989	8211	109	330		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10547781_f1_4	2990	8212	124	375	145	3.8e-10

Protein name

Locus Name

Acc#

hypothetical protein sll0939

pir:S74723

S74723

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c3_86	2991	8213	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22475387_c2_82	2992	8214	76	231	74	0.013

Protein name

Locus Name

Acc#

envelope glycoprotein

gp:AF113578

AF113578

Description

HIV-1 isolate 302_04 group O from Spain envelope glycoprotein (env) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22848261_f3_53	2993	8215	687	2064	110	1.0e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein MTH695			pir:F69192		F69192	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c1_54	2994	8216	83	252		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23453775_f1_11	2995	8217	837	2514	170	2.7e-09
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein			pir:G72385		G72385	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23525938_c3_103	2996	8218	85	258		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25816887_f2_17	2997	8219	148	447		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26598385_c3_96	2998	8220	456	1371	772	1.4e-76
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
transcription regulator NtrC family			pir:C70396		C70396	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30276562_f3_47.....	2999	8221	495	1488	148	4.2e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
immunoreactive 52kD antigen PG41			gp:AF175716		AF175716	
<u>Description</u>						

Porphyromonas gingivalis strain W50 immunoreactive 52kD antigenPG41 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31486011_c3_102.....	3000	8222	153	462		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31486011_f2_15.....	3001	8223	74	225		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33244627_f3_34	3002	8224	212	639	122	0.00016
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein H02F09.3			pir:T33369		T33369	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33382801_f3_39	3003	8225	81	246	65	0.0051
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YF03_MYCPN		P75445	
<u>Description</u>						
HYPOTHETICAL 85.3 KD PROTEIN F10_ORF750						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33407256_f2_26	3004	8226	434	1305	172	4.3e-10
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein aq_294			pir:H70326		H70326	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3407187_g2_81	3005	8227	429	1290	260	2.8e-20
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
sensor			gp:PSEFLESR		L41213	
<u>Description</u>						

Pseudomonas aeruginosa (strain PAK) putative fleR kinase (fleS) andtranscriptional activator (fleR) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3937553_c1_66	3006	8228	417	1254	115	2.5e-06

Protein name

Locus Name

Acc#

integrase

gp:BFU75371

U75371

Description

Bacteroides fragilis transposon Tn4555 TnpA (tnpA), integrase(int), TnpC (tnpC), excisionase (xis), mobilization protein (mobA), and beta-lactamase (cfxA) genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4179002_c1_67	3007	8229	210	633	106	0.014

Protein name

Locus Name

Acc#

high-molecular-weight surface-exposed protein
HMW1

pir:A43855

A43855

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6651552_f3_35	3008	8230	125	378		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10640787_f2_57	3009	8231	229	690	541	4.1e-52

Protein name

Locus Name

Acc#

yhgF protein

pir:B65136

B65136

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10664125_c2_136	3010	8232	982	2949	578	1.2e-93
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative secreted protein			gp:SCM11		AL133278	
<u>Description</u>						
Streptomyces coelicolor cosmid M11.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10822142_c2_148	3011	8233	60	183	94	0.00081
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
transposase			gp:AF038866		AF038866	
<u>Description</u>						
Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10945937_c3_159	3012	8234	104	315	137	2.6e-08
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YDEG_SCHPO		Q10449	
<u>Description</u>						
HYPOTHETICAL 57.2 KD PROTEIN C12B10.16C IN CHROMOSOME I						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
193757_c2_135	3013	8235	1054	3165	874	2.1e-87
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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19688750_f2_41	3014	8236	61	186		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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21484385_f3_81	3015	8237	78	237		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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23469015_c2_152	3016	8238	250	753		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24039688_c1_115	3017	8239	391	1176	457	6.4e-53
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Protein name

Locus Name

Acc#

alkaline phosphatase

pir:B72410

B72410

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24219562_c1_111	3018	8240	98	297	102	7.3e-05
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Protein name

Locus Name

Acc#

glucokinase

pir:F72246

F72246

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24226532_f3_92	3019	8241	407	1224	423	1.3e-39

Protein name

Locus Name

Acc#

sp:XYLR_HAEIN

P45043

Description

XYLOSE OPERON REGULATORY PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24308311_f2_49	3020	8242	135	408	141	2.0e-09

Protein name

Locus Name

Acc#

transposase slr0511:protein slr0511:protein
slr0511

pir:S76643

S76643

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24645312_f3_87.....	3021	8243	291	876	104	0.0026

Protein name

Locus Name

Acc#

homolog yvqC

pir:E70045

E70045

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25662812_f3_86.....	3022	8244	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25976567_f2_55	3023	8245	397	1194	113	0.0015

Protein name

Locus Name

Acc#

immunoreactive 42kD antigen PG33

gp:AF175715

AF175715

Description

Porphyromonas gingivalis strain W50 immunoreactive 42kD antigenPG33 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
262_c2_134	3024	8246	143	432		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26699155_c3_181.....	3025	8247	184	555		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2923212_c2_154.....	3026	8248	565	1698		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31929762_c2_138	3027	8249	391	1176	779	2.5e-77

Protein name

Locus Name

Acc#

sp:YDEG_SCHPO

Q10449

Description

HYPOTHETICAL 57.2 KD PROTEIN C12B10.16C IN CHROMOSOME I

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33709813_f3_84	3028	8250	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34429807_f2_52	3029	8251	207	624		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36230267_c3_180	3030	8252	376	1131	237	5.0e-24

Protein name

Locus Name

Acc#

immunoreactive 53 kD antigen PG123

gp:AF144641

AF144641

Description

Porphyromonas gingivalis strain W50 immunoreactive 53 kD antigenPG123 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3914587_c1_112	3031	8253	193	582	236	8.6e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:S76053	S76053

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4104637_c1_133	3032	8254	381	1146	115	0.00058

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
clostripain-related protein	pir:B72365	B72365

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4149180_c2_150	3033	8255	61	186	54	0.0081

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein T03F7.4	pir:T24404	T24404

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4192187_c1_129	3034	8256	481	1446	210	3.6e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transposase	gp:AF038866	AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4423386_c3_157	3035	8257	290	873	152	2.6e-08
Protein name			Locus Name			Acc#
Hyp1 protein			gp:HVHYPIPRO			Y09797
Description						
H.vulgaris mRNA for Hyp1 protein.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4804632_c1_116	3036	8258	389	1170	197	8.8e-13
Protein name			Locus Name			Acc#
conserved hypothetical protein TP0931			pir:D71264			D71264
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4876556...f3...89.....	3037	8259	715	2148	181	1.9e-10
Protein name			Locus Name			Acc#
immunoreactive 53 kD antigen PG123			gp:AF144641			AF144641
Description						
Porphyromonas gingivalis strain W50 immunoreactive 53 kD antigenPG123 gene, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4960760_c1_117.....	3038	8260	487	1464	230	2.4e-21
Protein name			Locus Name			Acc#
			gp:ATAC004411			AC004411
Description						
Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6442905_c3_158	3039	8261	189	570	171	4.9e-12
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein TP0931			pir:D71264		D71264	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6694705_c1_128	3040	8262	180	543		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7126086_f1_32	3041	8263	63	192		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
785882_c1_113	3042	8264	551	1656	110	2.2e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:U96771		U96771	
<u>Description</u>						

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
859452_c1_120	3043	8265	261	786	241	2.5e-20

Protein name Locus Name Acc#
 probable transmembrane protein pir:T34651 T34651

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
897187_c1_127	3044	8266	532	1599	276	1.2e-21

Protein name Locus Name Acc#
 hypothetical protein PAB1002 pir:G75064 G75064

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10035453_c1_59	3045	8267	74	225		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1052188_c3_87	3046	8268	68	207	71	0.028

Protein name Locus Name Acc#
 gp59 gp:BA1242593 AJ242593

Description

Bacteriophage A118 complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13089760_f2_19	3047	8269	77	234		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14650012_c3_92	3048	8270	536	1611		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14664813_c1_64	3049	8271	62	189		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15742327_c2_79	3050	8272	66	201		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16210456_f1_8	3051	8273	107	324	213	9.1e-17
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
conserved hypothetical protein BB0262					pir:F70132	F70132

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16680455_f3_48	3052	8274	138	417		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22946087_f1_9	3053	8275	108	327	70	0.033

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein 62	pir:T31025	T31025

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23554057_f3_35	3054	8276	412	1239		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24219067_f1_5	3055	8277	62	189		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24398917_f3_38	3056	8278	135	408	112	4.2e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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conserved hypothetical protein	pir:G72380	G72380
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25633312_f3_34	3057	8279	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29921938_f1_16	3058	8280	297	894	435	7.0e-41

Protein name

Locus Name

Acc#

sp:YF23_HAEIN

P44243

Description

HYPOTHETICAL PROTEIN HI1523

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30355305_c3_90	3059	8281	271	816	411	2.5e-38

Protein name

Locus Name

Acc#

sp:SOJ_BACSU

P37522

Description

SOJ PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32069806_f3_33	3060	8282	332	999		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33882837_c3_91	3061	8283	97	294	80	0.024

Protein name

Locus Name

Acc#

hypothetical protein F20D10.230

pir:T05638

T05638

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

34181512_f2_31	3062	8284	207	624		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

34182813_f1_7	3063	8285	260	783		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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34407928_f2_20	3064	8286	134	405		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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35267037_f2_23	3065	8287	117	354		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

36562555_c3_86	3066	8288	64	195		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

36613586_c1_56	3067	8289	65	198		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

4182811_f3_40	3068	8290	393	1182		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

831463_c1_67	3069	8291	141	426		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

839217_c3_93	3070	8292	120	363		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

10820311_c2_198	3071	8293	230	693		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11881375_f2_45	3072	8294	177	534	445	6.1e-42

Protein name

Locus Name

Acc#

sp:YACN_BACSU

Q06756

Description

HYPOTHETICAL 17.1 KD PROTEIN IN MECB-GLTX INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12929693_f3_78	3073	8295	261	786	372	3.3e-34

Protein name

Locus Name

Acc#

sp:YAAA_ECOLI

P11288

Description

HYPOTHETICAL 29.6 KD PROTEIN IN THRC-TALB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1357043_f3_81	3074	8296	477	1434	424	1.0e-39

Protein name

Locus Name

Acc#

sp:RLUB_BACSU

P35159

Description

(PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1444087_f2_50	3075	8297	208	627		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14647277_c3_235	3076	8298	337	1014	1216	1.2e-123

Protein name

Locus Name

Acc#

immunoreactive 36 kDa antigen PG14

gp:AF145798

AF145798

Description

Porphyromonas gingivalis strain W50 immunoreactive 36 kDa antigenPG14 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14886027_f3_79	3077	8299	185	558	416	7.3e-39

Protein name

Locus Name

Acc#

sp:MAA_BACSU

P37515

Description

TRANSACETYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19799013_f2_32	3078	8300	138	417		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20312630_f3_80	3079	8301	478	1437	1372	3.6e-140

Protein name

Locus Name

Acc#

adenylosuccinate lyase

gp:LMFP1421

AL132764

Description

Leishmania major Friedlin chromosome 4 PAC P1421.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21679756_c2_180	3080	8302	642	1929	112	2.3e-11

Protein name

Locus Name

Acc#

sp:THIO_HELPY

P56430

Description

THIOREDOXIN (TRX)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23553426_f2_57	3081	8303	344	1035	827	2.0e-82

Protein name

Locus Name

Acc#

sp:ILVE_HAEIN

P54689

Description

B) (BCAT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23989077_f1_17	3082	8304	268	807	379	6.1e-35

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:E72226

E72226

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24023442_f3_85	3083	8305	282	849	603	1.1e-58

Protein name

Locus Name

Acc#

ribosomal protein S2 (rpsB):ribosomal protein
BS1

pir:A69699

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24026561_c1_148	3084	8306	93	282	78	0.0093

Protein name

Locus Name

Acc#

late expression factor 2 homolog lef-2

gp:AF002732

AF002732

Description

Cydia pomonella granulovirus late expression factor 2 homolog lef-2gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24328386_c2_177	3085	8307	239	720	111	0.00037

Protein name

Locus Name

Acc#

sp:YQEF_BACSU

P54451

Description

PRECURSOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24412511_f3_83	3086	8308	160	483	373	2.6e-34

Protein name

Locus Name

Acc#

ribosomal protein L13

pir:F71677

F71677

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24414827_f1_18	3087	8309	252	759	293	7.9e-26

Protein name

Locus Name

Acc#

conserved hypothetical protein ytmQ

pir:B69997

B69997

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24651013_c1_122	3088	8310	486	1461	244	1.0e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
lipase-like protein	pir:A64706	A64706

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2470802_c1_127	3089	8311	420	1263	367	1.1e-33

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical integral membrane protein HP1486	pir:F64705	F64705

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25415626_c3_238	3090	8312	681	2046	371	2.4e-44

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
alpha-glucosidase	gp:BTU66897	U66897

Description

Bacteroides thetaiotaomicron neopullulanase (susA) and alpha-glucosidase (susB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25440900_c1_158	3091	8313	460	1383		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25588962_f3_88	3092	8314	224	675	357	1.3e-32

Protein name

Locus Name

Acc#

hypothetical protein ydiH

pir:A69787

A69787

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26254813_c3_253	3093	8315	290	873	89	0.0016

Protein name

Locus Name

Acc#

splicing regulatory protein SWAP homolog
(alternatively spliced, clone pFL2)

pir:A54037

A54037

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26283262_f2_43	3094	8316	166	501		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26353388_f3_92	3095	8317	411	1236	425	8.1e-40

Protein name

Locus Name

Acc#

probable exodeoxyribonuclease VII large
subunit

pir:C75549

C75549

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26365887_f3_86	3096	8318	335	1008	354	1.1e-41

Protein name

Locus Name

Acc#

sp:EFTS_MYCTU

Q10788

Description

ELONGATION FACTOR TS (EF-TS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26454391_c1_128	3097	8319	272	819		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26600263_f3_84.....	3098	8320	130	393	318	1.8e-28

Protein name

Locus Name

Acc#

sp:RS9_MYCTU

006259

Description

30S RIBOSOMAL PROTEIN S9

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2756327_c2_209.....	3099	8321	98	297		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29407552_f1_13	3100	8322	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29745386_f1_15	3101	8323	400	1203	624	6.6e-61

Protein name

Locus Name

Acc#

hypothetical protein RP306

pir:E71686

E71686

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30160336_c2_195	3102	8324	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31676510_f3_95	3103	8325	337	1014	680	7.7e-67

Protein name

Locus Name

Acc#

sp:MRP_SYNY3

P53383

Description

MRP PROTEIN HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33398425_f2_72	3104	8326	861	2586	178	4.3e-11

Protein name

Locus Name

Acc#

unknown

gp:AF007381

AF007381

Description

Flavobacterium johnsoniae gliding motility protein (gldA) gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3361250_f2_73	3105	8327	188	567	160	9.7e-12

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33722640_f3_91	3106	8328	153	462	202	6.6e-15

Protein name

Locus Name

Acc#

subtilisin sendai homolog

pir:C69456

C69456

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33847078_f2_51	3107	8329	80	243	72	0.021

Protein name

Locus Name

Acc#

phase-1 flagellin

pir:S33191

S33191

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34105313_c2_179	3108	8330	590	1773	136	4.1e-06

Protein name

Locus Name

Acc#

sp:TONB_HELPY

025899

Description

TONB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34648582_f3_118	3109	8331	319	960	134	3.2e-06

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35312692_f3_74	3110	8332	526	1581		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35625007_c3_245	3111	8333	431	1296		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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35944140_f3_90	3112	8334	301	906		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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36579090_g2_175	3113	8335	347	1044	197	2.7e-13
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Protein name

Locus Name

Acc#

hypothetical protein jhp1380

pir:G71815

G71815

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4095887_f2_56	3114	8336	73	222	79	0.0037
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Protein name

Locus Name

Acc#

exodeoxyribonuclease VII, small chain

pir:JQ0664

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4142762_f1_5	3115	8337	470	1413	1396	1.0e-142
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Protein name

Locus Name

Acc#

sp:SYN_SYNY3

P52276

Description

LIGASE) (ASNRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4379427_c3_240	3116	8338	124	375	131	1.2e-08

Protein name

Locus Name

Acc#

sp:BLAI_STAAU

P18415

Description

REPRESSOR PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4485312_c3_271	3117	8339	746	2241	505	5.9e-47

Protein name

Locus Name

Acc#

sp:NAGH_CLOPE

P26831

Description

(MU TOXIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4883507_c1_152	3118	8340	119	360	181	5.8e-14

Protein name

Locus Name

Acc#

sp:Y546_SYNY3

Q55397

Description

HYPOTHETICAL 11.9 KD PROTEIN SLL0546

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5275292_f3_89	3119	8341	205	618	387	8.6e-36

Protein name

Locus Name

Acc#

isomerase like protein

gp:ATFCA5

Z97340

Description

Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragmentNo. 5.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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5285687_f1_16	3120	8342	93	282		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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78375_f1_3	3121	8343	643	1932	957	3.4e-96
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Protein name

Locus Name

Acc#

sp:BGAL_XANMN

P48982

Description

BETA-GALACTOSIDASE PRECURSOR, (LACTASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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876937_c2_216	3122	8344	64	195		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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10023300_c2_107	3123	8345	105	318		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10603388_c3_138	3124	8346	331	996	341	6.4e-31
Protein name			Locus Name			Acc#
			sp:YEIH_ECOLI			P33019
Description						
HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11882812_f3_64	3125	8347	143	432	130	1.5e-08
Protein name			Locus Name			Acc#
conserved hypothetical protein TP0412			pir:B71327			B71327
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1204010_c2_106	3126	8348	140	423		
Protein name			Locus Name			Acc#
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13065655_c3_123	3127	8349	274	825	1083	1.5e-109
Protein name			Locus Name			Acc#
hypothetical protein			pir:JQ1020			JQ1020
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14730313_f3_59	3128	8350	868	2607	2435	8.2e-253

Protein name

Locus Name

Acc#

sp:CLPB_SYNY3

P74361

Description

CLPB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15641008_c3_132	3129	8351	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c2_116.....	3130	8352	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16989052_f2_27.....	3131	8353	189	570	378	7.7e-35

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_495

pir:E70344

E70344

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
187627_f1_4.....	3132	8354	407	1224	1479	1.6e-151

Protein name

Locus Name

Acc#

hypothetical protein slr0049

pir:S74347

S74347

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19703511_c2_108	3133	8355	105	318	127	3.8e-07

Protein name

Locus Name

Acc#

63 kDa protein

gp:MBU73653

U73653

Description

Mycobacterium bovis 63 kDa protein, 47 kDa protein and clpB gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
197188_c2_95	3134	8356	243	732	113	1.0e-11

Protein name

Locus Name

Acc#

drgA protein:protein slr1719:protein slr1719

pir:S75047

S75047

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2035912_c3_131	3135	8357	210	633	241	2.5e-20

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:D75341

D75341

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c3_140	3136	8358	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23625937_c3_130	3137	8359	116	351	163	4.7e-12

Protein name

Locus Name

Acc#

conserved hypothetical protein yrbF

pir:E69972

E69972

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24500082_f3_67	3138	8360	178	537	200	5.6e-16
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Protein name

Locus Name

Acc#

hypothetical protein SC7H2.05

pir:T35736

T35736

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24640755_f1_22	3139	8361	423	1272	463	7.6e-44
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Protein name

Locus Name

Acc#

glucose/galactose transporter

pir:A71850

A71850

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24640932_f2_30	3140	8362	229	690		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24642312_f1_17	3141	8363	189	570	357	1.3e-32
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Protein name

Locus Name

Acc#

peptidyl-tRNA hydrolase

pir:B72229

B72229

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24803942_f3_51	3142	8364	361	1086	1595	8.4e-164

Protein name

Locus Name

Acc#

sp:RECA_BACFR

P22841

Description

RECA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24881300_c2_111	3143	8365	199	600		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26594010_c2_94.....	3144	8366	234	705	330	9.4e-30

Protein name

Locus Name

Acc#

gp:AB024531

AB024531

Description

Enterococcus seriolicida SA2F01-1, -2, -3 genes, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30271025_c3_146.....	3145	8367	287	864	214	6.2e-17

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:D75333

D75333

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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30519457_f2_29	3146	8368	196	591		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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31417187_c1_81	3147	8369	261	786		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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33401011_c1_80	3148	8370	71	216		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4010927_c2_105	3149	8371	340	1023	103	0.022
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Protein name

Locus Name

Acc#

hypothetical protein ybbR

pir:A69745

A69745

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
426337_f1_7	3150	8372	113	342	106	6.0e-06

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4720311_f3_48	3151	8373	198	597		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4806587_c3_124.....	3152	8374	280	843	217	1.7e-17

Protein name

Locus Name

Acc#

sp:YJJU_ECOLI

P39407

Description

HYPOTHETICAL 39.8 KD PROTEIN IN OSMY-DEOC INTERGENIC REGION (O357)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4878506_f3_49.....	3153	8375	221	666	101	0.017

Protein name

Locus Name

Acc#

KIAA0636 protein

gp:AB014536

AB014536

Description

Homo sapiens mRNA for KIAA0636 protein, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4973765_f1_8	3154	8376	114	345	124	9.4e-08
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
SigG	gp:AF121849				AF121849	
<u>Description</u>						
Synechococcus PCC7002 SigG (sigG) and hypothetical protein genes, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5281562_c3_126	3155	8377	542	1629	186	1.1e-09
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative secreted protein	gp:SC4A7				AL133423	
<u>Description</u>						
Streptomyces coelicolor cosmid 4A7.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
812533_c2_112.....	3156	8378	302	909	372	3.3e-34
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
transcription regulator LysR family	pir:F70356				F70356	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
907137_c2_104.....	3157	8379	338	1017	171	2.1e-12
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
N utilization substance protein B			pir:D72212		D72212	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
976536_f3_65	3158	8380	202	609	208	8.0e-17

Protein name

Locus Name

Acc#

probable ribosomal protein L25

pir:H71665

H71665

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
995461_c1_90.....	3159	8381	108	327	80	0.036

Protein name

Locus Name

Acc#

dihydrofolate reductase, / thymidylate synthase,

pir:T01684

T01684

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10735002_c2_18.....	3160	8382	195	588	177	1.5e-13

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12395950_f2_2.....	3161	8383	132	399	107	2.2e-05

Protein name

Locus Name

Acc#

hypothetical protein F14F9.5

pir:T33774

T33774

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12689712_f3_9	3162	8384	612	1836	588	1.2e-57

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20524150_f2_3	3163	8385	385	1158	144	3.0e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable phosphoesterase, yvnB	pir:C70044	C70044

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4100877_f3_8	3164	8386	338	1017	117	0.00031

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transmembrane sensor	gp:AF051691	AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31726567_c1_11	3165	8387	96	291	450	1.8e-42

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
mobilization protein C	gp:AF118243	AF118243

Description

Bacteroides fragilis mobilization protein C (mobC) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5135158_c1_10	3166	8388	101	306	464	6.0e-44

Protein name

Locus Name

Acc#

mobilization protein C

gp:AF118243

AF118243

Description

Bacteroides fragilis mobilization protein C (mobC) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7112683_f3_6	3167	8389	216	651	1024	2.7e-103

Protein name

Locus Name

Acc#

mobilization protein B

gp:AF118242

AF118242

Description

Bacteroides fragilis mobilization protein B (mobB) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10972160_f3_194.....	3168	8390	439	1320	241	1.3e-17

Protein name

Locus Name

Acc#

sp:HLYD_PASHA

P16534

Description

LEUKOTOXIN SECRETION PROTEIN D

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10973751_f3_179.....	3169	8391	441	1326	670	8.8e-66

Protein name

Locus Name

Acc#

sp:DINF_ECOLI

P28303

Description

DNA-DAMAGE-INDUCIBLE PROTEIN F

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1173187_c3_347	3170	8392	115	348	90	0.011

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein, MAL1P3.07	gp:PFMAL1P3	AL031746

Description

Plasmodium falciparum MAL1P3, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1178325_c2_265	3171	8393	418	1257		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11926083_c3_337.....	3172	8394	103	312		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12501567_f1_55.....	3173	8395	261	786	276	5.0e-24

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

ligase	pir:A70351	A70351
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
134687_c1_221	3174	8396	105	318	304	5.4e-27

Protein name

Locus Name

Acc#

sp:THIM_PEA

Description

THIOREDOXIN M-TYPE, CHLOROPLAST PRECURSOR (TRX-M)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13946017_c3_360	3175	8397	443	1332	481	9.4e-46

Protein name

Locus Name

Acc#

hypothetical protein slr2013

pir:S75346

S75346

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14256505_f2_120.....	3176	8398	288	867	148	5.5e-07

Protein name

Locus Name

Acc#

gp:U93872

U93872

Description

Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNA replication protein, glycoprotein, DNA replication protein, FLICE inhibitory protein and v-cyclin genes, complete cds, and tegument protein gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14460760_f3_196.....	3177	8399	240	723	369	1.2e-32

Protein name

Locus Name

Acc#

hypothetical protein mexF

pir:T30830

T30830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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14657131_f1_33	3178	8400	662	1989		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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15032952_f2_122.....	3179	8401	931	2796		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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15760268_f2_101.....	3180	8402	441	1326	343	4.0e-31
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Protein name

Locus Name

Acc#

YvrN protein

gp:BS43KBDNA

AJ223978

Description

Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16836055_f2_102.....	3181	8403	245	738	170	2.8e-11
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Protein name

Locus Name

Acc#

hypothetical protein Rv3695

pir:H70792

H70792

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16898412_f2_98	3182	8404	602	1809	114	0.00099

Protein name

Locus Name

Acc#

sp:YREC_SYNP2

P19737

Description

HYPOTHETICAL 28.7 KD PROTEIN IN RECA 3'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
17009642_c3_357	3183	8405	236	711	239	4.1e-20

Protein name

Locus Name

Acc#

rprY protein

pir:S33662

S33662

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19589387_f3_190.....	3184	8406	251	756	113	0.00018

Protein name

Locus Name

Acc#

pX02-46

gp:AF188935

AF188935

Description

Bacillus anthracis plasmid pX02, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20508312_f1_39.....	3185	8407	365	1098	206	3.1e-14

Protein name

Locus Name

Acc#

acriflavin resistance protein AcrE

pir:A70361

A70361

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
213340_c3_358	3186	8408	353	1062	114	0.00085

Protein name

Locus Name

Acc#

sp:Y876_METJA

Q58286

Description

PUTATIVE ABC TRANSPORTER PERMEASE PROTEIN MJ0876

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21494031_f2_111	3187	8409	96	291		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21676532_f3_180.....	3188	8410	242	729	653	5.6e-64

Protein name

Locus Name

Acc#

sp:PYRH_ECOLI

P29464

Description

(UMP KINASE) (SMBA PROTEIN)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21769782_f3_135.....	3189	8411	469	1410		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22666577_c1_234	3190	8412	207	624	76	0.024

Protein name

Locus Name

Acc#

sp:E311_ADE03

P11317

Description

EARLY E3 9.0 KD GLYCOPROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2343876_f1_32	3191	8413	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23551325_f3_183.....	3192	8414	165	498		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23625177_f1_61.....	3193	8415	190	573	433	1.1e-40

Protein name

Locus Name

Acc#

ribosome recycling factor

pir:C75386

C75386

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23626561_f3_188	3194	8416	433	1302	118	0.00066

Protein name

Locus Name

Acc#

gp:VCU47542

U47542

Description

Vibrio cholerae ADP-L-glycero-D-mannoheptose-6-epimerase (rfad) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23650288_f1_68	3195	8417	361	1086	327	2.0e-29

Protein name

Locus Name

Acc#

cation efflux system (czcB-like)

pir:C70415

C70415

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23937750_c2_282	3196	8418	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
239665_f1_57	3197	8419	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24015635_f2_126	3198	8420	116	351		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

24016077_f1_38	3199	8421	186	561	129	1.9e-08
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Protein name

Locus Name

Acc#

sp:Y793_METJA

Q58203

Description

HYPOTHETICAL PROTEIN MJ0793

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

24097562_c3_345	3200	8422	270	813	283	2.6e-40
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Protein name

Locus Name

Acc#

DNA polymerase

gp:AF083949

AF083949

Description

Treponema denticola DNA gyrase subunit B (gyrB) and chromosomal replication initiator protein (dnaA) genes, complete cds; and DNA polymerase (dnaE) gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24261627_c1_239	3201	8423	418	1257		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24396877_f3_161	3202	8424	220	663	95	0.0025

Protein name

Locus Name

Acc#

sp:Y794_METJA

Q58204

Description

HYPOTHETICAL PROTEIN MJ0794

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24406886_c3_320	3203	8425	105	318		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24413127_f2_100.....	3204	8426	101	306		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24417812_f1_6.7.....	3205	8427	740	2223	931	1.9e-93

Protein name

Locus Name

Acc#

heterocyst differentiation protein HetC

pir:T31072

T31072

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24423426_c3_338	3206	8428	445	1338	149	7.7e-08

Protein name

Locus Name

Acc#

laminarinase

gp:AF047003

AF047003

Description

Rhodothermus marinus strain ITI278 laminarinase (lamR) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24489377_f3_175	3207	8429	149	450	134	5.5e-09

Protein name

Locus Name

Acc#

hypothetical protein SC2E1.19 SC2E1.19

pir:T34787

T34787

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24640642_f3_176	3208	8430	120	363	168	1.4e-12

Protein name

Locus Name

Acc#

MmcQ

gp:AF127374

AF127374

Description

Streptomyces lavendulae LinA homolog, cytochrome P450 hydroxylase ORF4, cytochrome P450 hydroxylase ORF3, MitT (mitT), MitS (mitS), MitR (mitR), MitQ (mitQ), MitP (mitP), MitO (mitO), MitN (mitN), MitM (mitM), MitL (mitL), MitK (mitK), MitJ (mitJ), MitI (mitI), MitH (mitH), MitG (mitG), MitF (mitF), MitE (mitE), MitD (mitD), MitC (mitC), MitB (mitB), MitA (mitA), MmcA (mmcA), MmcB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648427_c3_339	3209	8431	232	699	118	0.00012

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:A72220

A72220

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24883260_f2_130	3210	8432	690	2070	897	7.8e-90

Protein name

Locus Name

Acc#

acriflavin resistance protein D (acrD) RP170

pir:F71727

F71727

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24884633_c1_240	3211	8433	186	561	359	7.0e-32

Protein name

Locus Name

Acc#

immunoreactive 89kD antigen PG87

gp:AF175722

AF175722

Description

Porphyromonas gingivalis strain W50 immunoreactive 89kD antigenPG87 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25501562_f2_125	3212	8434	525	1578	117	0.00071

Protein name

Locus Name

Acc#

beta-1,4-galactosyltransferase IV

gp:AB024436

AB024436

Description

Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25548463_f1_30	3213	8435	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26370888_f3_148	3214	8436	155	468	239	4.1e-20

Protein name

Locus Name

Acc#

conserved hypothetical protein ydiB

pir:C69786

C69786

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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26594677_f2_121	3215	8437	531	1596	644	3.9e-73
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Protein name

Locus Name

Acc#

sp:DNAK_HALMA

Q01100

Description

DNAK PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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26660812_f1_60	3216	8438	417	1254	115	0.0012
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Protein name

Locus Name

Acc#

enterotoxin

gp:AF192766

AF192766

Description

Bacillus cereus strain Ael0 enterotoxin mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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29511526_c1_220	3217	8439	1072	3219	1446	1.3e-170
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Protein name

Locus Name

Acc#

sp:DP3A_BORBU

O51526

Description

DNA POLYMERASE III, ALPHA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31837701_f1_18	3218	8440	273	822	563	1.9e-54

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein MTH606	pir:E69180	E69180

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32141338_c2_260.....	3219	8441	86	261		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32297293_c2_274.....	3220	8442	149	450	444	7.8e-42

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

gp:PGPGAAGEN	X95938
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Description

P.gingivalis rnhB & pgaA genes & orfs 150, 197, 202 & 199.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33876067_c3_359.....	3221	8443	430	1293		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34254387_c1_219	3222	8444	88	267		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34492925_c3_340	3223	8445	84	255		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36120842_c3_369	3224	8446	65	198	107	7.7e-05
Protein name			Locus Name		Acc#	
immunoreactive 89kD antigen PG87			gp:AF175722		AF175722	
Description						

Porphyromonas gingivalis strain W50 immunoreactive 89kD antigenPG87 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36219693_f2_83	3225	8447	92	279		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36525287_f3_186	3226	8448	311	936	546	1.2e-52

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein	pir:A72219	A72219

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3937775_c2_311	3227	8449	1065	3198	468	4.9e-83

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3944150_f2_82	3228	8450	143	432		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
39663590_c1_241	3229	8451	73	222	133	1.3e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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immunoreactive 89kD antigen PG87	gp:AF175722	AF175722
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Description

Porphyromonas gingivalis strain W50 immunoreactive 89kD antigenPG87 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4031501_c2_281	3230	8452	66	201		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4116566_f3_158	3231	8453	240	723		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
422157_f3_177	3232	8454	451	1356	100	0.00074
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
microbial collagenase, precursor:Cog protein				pir:JC4393		JC4393
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4492787_c3_362	3233	8455	339	1020	212	4.6e-17
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:APX_STRGR		P80561
<u>Description</u>						

AMINOPEPTIDASE, (SGAP)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4725938_f3_171	3234	8456	239	720	229	4.8e-19

Protein name

Locus Name

Acc#

sp:PSS_HELPY

Description

(PHOSPHATIDYLSELINE SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4869802_f3_170	3235	8457	231	696	372	3.3e-34

Protein name

Locus Name

Acc#

unknown

gp:NGU34760

U34760

Description

Neisseria gonorrhoeae UvrA (uvrA) and ORF259 genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4964782_c2_303	3236	8458	503	1512	1227	8.3e-125

Protein name

Locus Name

Acc#

immunoreactive 89kD antigen PG87

gp:AFI75722

AF175722

Description

Porphyromonas gingivalis strain W50 immunoreactive 89kD antigenPG87 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5332187_c1_236	3237	8459	303	912	759	3.3e-75

Protein name

Locus Name

Acc#

hypothetical protein PH0776

pir:B71126

B71126

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
547525_c2_291	3238	8460	339	1020	311	9.7e-28

Protein name

Locus Name

Acc#

hypothetical protein slr1478

pir:S75694

S75694

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
831250_c1_242	3239	8461	892	2679		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
988762_c3_356	3240	8462	474	1425	282	2.2e-23

Protein name

Locus Name

Acc#

RprX

gp:S59000

S59000

Description

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11020692_c2_101	3241	8463	213	642	233	7.0e-18

Protein name

Locus Name

Acc#

hypothetical protein

pir:A75613

A75613

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11754512_f3_67	3242	8464	98	297		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

11907801_c2_106	3243	8465	524	1575		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

19531885_f3_63	3244	8466	118	357		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

20422162_f1_9	3245	8467	597	1794	428	5.6e-39
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Protein name

Locus Name

Acc#

VicK protein

gp:EFA012050

AJ012050

Description

Enterococcus faecalis vic operon and flanking genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

2113812_f2_36	3246	8468	323	972		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22063410_c2_108	3247	8469	632	1899	1362	4.1e-139

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:S76152	S76152

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22438768_c1_89.....	3248	8470	284	855		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648563_c1_88.....	3249	8471	129	390		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26360263_f3_66.....	3250	8472	582	1749	171	1.8e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:MMSAG	X84710

Description

M.mazei surface antigen genes orf492, orf375 and orf783.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

29804754_c2_93	3251	8473	413	1242		
----------------	------	------	-----	------	--	--

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

34087632_f2_38	3252	8474	702	2109	155	4.5e-12
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Protein name

Locus Name

Acc#

sp:BTUB_ECOLI

P06129

Description

VITAMIN B12 RECEPTOR PRECURSOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

35706417_f2_43	3253	8475	483	1452		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

4173751_f3_55	3254	8476	239	720	473	6.6e-45
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Protein name

Locus Name

Acc#

response regulator DrrA

pir:D72228

D72228

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

4878387_c3_122	3255	8477	400	1203		
----------------	------	------	-----	------	--	--

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

4954691_c1_92	3256	8478	270	810	213	2.4e-17
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Protein name

Locus Name

Acc#

sp:HIS9_SCHPO

014059

Description

PROBABLE HISTIDINOL-PHOSPHATASE,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

9921885_c1_81	3257	8479	472	1419	142	9.4e-06
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Protein name

Locus Name

Acc#

hypothetical protein

pir:A75613

A75613

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

10351381_c1_216	3258	8480	409	1230	517	1.4e-49
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Protein name

Locus Name

Acc#

sp:GLUP_BRUAB

Q44623

Description

GLUCOSE/GALACTOSE TRANSPORTER

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
110683_f2_111	3259	8481	301	903	146	1.0e-09

Protein name

Locus Name

Acc#

gp:PVPVA1

X92485

Description

P.vivax pval gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12506407_c2_261	3260	8482	254	765	185	2.8e-17

Protein name

Locus Name

Acc#

sp:GPH_ECOLI

P32662

Description

PHOSPHOGLYCOLATE PHOSPHATASE, (PGP)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12923212_c2_232.....	3261	8483	144	435	72	0.028

Protein name

Locus Name

Acc#

sp:DBHA_SALTY

P15148

Description

DNA-BINDING PROTEIN HU-ALPHA (NS2) (HU-2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13127090_f2_102.....	3262	8484	140	423	112	6.0e-06

Protein name

Locus Name

Acc#

RNA-directed DNA polymerase,, msDNA
specific:DNA nucleotidyltransferase
(RNA-directed):reverse transcriptase:revertase

pir:S19248

S19248

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14226625_f1_1	3263	8485	187	564	220	4.3e-18

Protein name

Locus Name

Acc#

sp:YG77_METJA

Q59071

Description

HYPOTHETICAL PROTEIN MJ1677

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14958557_c1_200	3264	8486	430	1293	1219	5.9e-124

Protein name

Locus Name

Acc#

sp:XAPB_ECOLI

Description

XANTHOSINE PERMEASE (XANTHOSINE TRANSPORTER)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15627161_c1_189.....	3265	8487	239	720	202	3.5e-16

Protein name

Locus Name

Acc#

transcription regulator Crp/Fnr family

pir:A70344

A70344

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15644206_c1_207.....	3266	8488	251	756	601	1.8e-58

Protein name

Locus Name

Acc#

sp:KDSA_CHLPS

Q46225

Description

8-PHOSPHATE SYNTHETASE) (KDO 8-P SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16203213_c3_314	3267	8489	328	987	584	1.1e-56

Protein name
 probable tRNA
 delta(2)-isopentenylpyrophosphate transferase
 (miaA)

Locus Name
 pir:B71301

Acc#
 B71301

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16439662_c1_208	3268	8490	943	2832	2224	1.9e-230

Protein name
 immunoreactive 106 kDa antigen PG115

Locus Name
 gp:AF153767

Acc#
 AF153767

Description

Porphyromonas gingivalis strain W50 immunoreactive 106 kDa antigenPG115
 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16836063_c3_325.....	3269	8491	91	276	298	2.3e-26

Protein name
 50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27)

Locus Name
 sp:RK27_TOBAC

Acc#
 P30155

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
17084637_c3_281.....	3270	8492	370	1113		

Protein name
 NO-HIT

Locus Name
 NO-HIT

Acc#
 NO-HIT

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19569032_c2_268	3271	8493	340	1023	232	2.9e-17

Protein name

Locus Name

Acc#

sp:GLGA_BACST

008328

Description

SYNTHASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21893753_f3_136	3272	8494	88	267		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22470938_c3_311.....	3273	8495	195	588	238	5.3e-20

Protein name

Locus Name

Acc#

sp:YODE_MYCTU

Q50604

Description

HYPOTHETICAL 18.1 KD PROTEIN RV1829

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23617062_c2_250.....	3274	8496	398	1197	668	1.4e-65

Protein name

Locus Name

Acc#

Hypothetical protein

gp:D90734

Description

Escherichia coli genomic DNA. (22.0 - 22.3 min).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24025302_c2_264	3275	8497	763	2292	1140	1.4e-115

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glutamate synthase, beta subunit	pir:H72230	H72230

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24257807_c1_221	3276	8498	507	1524		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24431587_f2_104	3277	8499	305	918	893	2.1e-89

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

sp:YPGA_PORGI	Q51834
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Description

HYPOTHETICAL 33.6 KD PROTEIN IN RNHB-PGAA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648542_f2_106	3278	8500	159	480		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24803137_c3_340	3279	8501	232	699	272	1.3e-23

Protein name

Locus Name

Acc#

sp:Y03M_MYCTU

Q10647

Description

HYPOTHETICAL 25.7 KD PROTEIN CY130.22

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24821094_c2_231	3280	8502	263	792	391	1.6e-35

Protein name

Locus Name

Acc#

putative vicilin storage protein

gp:ATAC006135

AC006135

Description

Arabidopsis thaliana chromosome II BAC F24H14 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25423461_c1_205.....	3281	8503	406	1221	77	0.046

Protein name

Locus Name

Acc#

hypothetical protein aq_125

pir:B70312

B70312

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25506557_f2_90.....	3282	8504	389	1170		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25589087_c3_322	3283	8505	176	531	267	4.5e-23

Protein name

Locus Name

Acc#

sp:SPR_ECOLI

Description

LIPOPROTEIN SPR PRECURSOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26204662_f3_113	3284	8506	466	1401	593	1.3e-57

Protein name

Locus Name

Acc#

sp:AMY_METJA

Q59006

Description

PUTATIVE ALPHA-AMYLASE,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26287593_f2_66.....	3285	8507	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26359703_c2_263.....	3286	8508	121	366	206	1.3e-16

Protein name

Locus Name

Acc#

sp:RL21_HAEIN

P44359

Description

50S RIBOSOMAL PROTEIN L21

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26449224_c1_169	3287	8509	158	477	266	5.7e-23

Protein name

Locus Name

Acc#

hypothetical protein C11G6.3

pir:T19201

T19201

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26600050_f2_103.....	3288	8510	599	1800	2475	4.7e-257

Protein name

Locus Name

Acc#

heme uptake protein A and B

gp:AF143945

AF143945

Description

Porphyromonas gingivalis heme uptake protein A and B gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29316930_f2_110.....	3289	8511	646	1941	416	1.2e-35

Protein name

Locus Name

Acc#

sensory transduction histidine kinase
slr2098:protein slr2098:protein slr2098

pir:S75130

S75130

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30585005_c2_256.....	3290	8512	218	657	227	7.7e-19

Protein name

Locus Name

Acc#

Vexp2

gp:AF140784

AF140784

Description

Streptococcus pneumoniae Vexp1 (vex1), Vexp2 (vex2), Vexp3 (vex3), and P28 (pep27) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30743760_f2_100	3291	8513	740	2223		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33397137_f2_93.....	3292	8514	320	963	780	1.9e-77
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

thioredoxin reductase

gp:AF124757

AF124757

Description

Zymomonas mobilis fosmid clone 43D2, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33476540_c2_248.....	3293	8515	237	714	107	0.00080
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

hypothetical protein SC66T3.28c

pir:T35385

T35385

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34261093_c3_276.....	3294	8516	302	909	394	7.7e-36
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

putative vicilin storage protein

gp:ATAC006135

AC006135

Description

Arabidopsis thaliana chromosome II BAC F24H14 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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35595442_f1_55	3295	8517	176	531		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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35739643_c3_308.....	3296	8518	74	225		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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36132943_c1_170.....	3297	8519	133	402	203	3.1e-15
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Protein name

Locus Name

Acc#

gp:SCYKL202W

Description

S.cerevisiae chromosome XI reading frame ORF YKL202w.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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36225250_f3_112.....	3298	8520	431	1296	363	4.3e-40
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Protein name

Locus Name

Acc#

probable lipopolysaccharide
N-acetylglucosaminyltransferase, rfbU

pir:F64500

F64500

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3913411_c3_298	3299	8521	819	2460	1108	1.4e-119
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
beta-N-acetylglucosaminidase	gp:AF072374				AF072374	
<u>Description</u>	Pseudoalteromonas sp. S9 beta-N-acetylglucosaminidase (chiQ) gene, complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4004010_f1_51	3300	8522	85	258		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4022790_f1_2.....	3301	8523	649	1950	236	1.4e-27
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
glycogen debranching enzyme-related protein	pir:H75549				H75549	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4085937_c2_241.....	3302	8524	745	2238	3767	0.0
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:GLNA_BACFR				P15623	
<u>Description</u>						
GLUTAMINE SYNTHETASE, (GLUTAMATE--AMMONIA LIGASE) (GS)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4104687_c2_260	3303	8525	238	717	343	4.0e-31

Protein name

Locus Name

Acc#

abc transporter, ATP-binding protein PAB1696

pir:H75077

H75077

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4115892_c3_326.....	3304	8526	427	1284	879	6.3e-88

Protein name

Locus Name

Acc#

sp:SYS_AQUAE

O66647

Description

SERYL-TRNA SYNTHETASE, (SERINE--TRNA LIGASE) (SERRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4117177_c2_254.....	3305	8527	232	699	208	8.0e-17

Protein name

Locus Name

Acc#

sp:YGGJ_HAEIN

P44627

Description

HYPOTHETICAL PROTEIN HI0303

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4408537_c1_209.....	3306	8528	496	1491		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4490927_c2_238	3307	8529	264	795	624	6.6e-61

Protein name

Locus Name

Acc#

sp:YABN_BACSU

P37556

Description

HYPOTHETICAL 56.1 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4798203_f1_45	3308	8530	216	651	108	0.0012

Protein name

Locus Name

Acc#

sp:Y687_METJA

Q58100

Description

HYPOTHETICAL PROTEIN MJ0687

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4876507_f1_57	3309	8531	884	2655	1890	4.6e-195

Protein name

Locus Name

Acc#

valine--tRNA ligase,

pir:D72206

D72206

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4895087_c3_315	3310	8532	317	954	289	2.1e-25

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:F72386

F72386

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4897750_c2_255	3311	8533	526	1581		
Protein name					Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4944011_f2_105.....	3312	8534	191	576	218	7.0e-18
Protein name					Locus Name	Acc#

RNA polymerase sigma-E factor

pir:B72234

B72234

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5110962_c2_249.....	3313	8535	218	657	230	1.3e-17
Protein name					Locus Name	Acc#

DNA helicase 1

pir:T14895

T14895

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5350265_f1_52.....	3314	8536	287	864	209	2.2e-34
Protein name					Locus Name	Acc#

sp:RT65_MYXXA

P23071

Description

TRANSCRIPTASE) (MX65-RT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
657555_f1_44	3315	8537	838	2517	1042	9.7e-108

Protein name

Locus Name

Acc#

sp:SP3E_BACSU

Description

STAGE III SPORULATION PROTEIN E

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
819075_f1_8	3316	8538	134	405	342	5.0e-31

Protein name

Locus Name

Acc#

PanD protein

gp:WSAJ3049

AJ003049

Description

Wolinella succinogenes hydD, hydE, panD and ispA genes; orf102 andorf341.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
822750_f3_116	3317	8539	310	933	593	1.3e-57

Protein name

Locus Name

Acc#

pantoate--beta-alanine ligase

pir:E72296

E72296

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10552012_c3_265	3318	8540	288	867	151	2.0e-08

Protein name

Locus Name

Acc#

PobR

gp:RLU40388

U40388

Description

Rhizobium leguminosarum positive regulator of pobA (pobR) gene, complete cds, and 4-hydroxybenzoate hydroxylase (pobA) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10597812_c2_233	3319	8541	323	972	249	3.6e-21

Protein name

Locus Name

Acc#

hypothetical protein PAB0040

pir:B75194

B75194

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10728380_c3_284	3320	8542	269	810	138	5.6e-07

Protein name

Locus Name

Acc#

sp:YA52_HAEIN

P45008

Description

HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI1052

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10815938_f3_136	3321	8543	165	498		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11928462_f2_82	3322	8544	291	876		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12557692_c3_288	3323	8545	430	1293	791	1.3e-78

Protein name

Locus Name

Acc#

hypothetical protein HP0513

pir:A64584

A64584

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12968877_f1_13	3324	8546	283	852	204	2.1e-16
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:FPG_LACLC				P42371	
<u>Description</u>						
GLYCOSYLASE)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12978802_c2_218	3325	8547	338	1017	502	5.6e-48
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
OprM					gp:AB011381	AB011381
<u>Description</u>						
Pseudomonas aeruginosa gene for OprM, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13711378_c1_183.....	3326	8548	560	1683	1603	1.2e-164
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
probable pyrophosphate--fructose 6-phosphate 1-phosphotransferase, beta subunit	pir:C71312				C71312	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13867937_c3_254.....	3327	8549	968	2907	149	1.5e-05
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
KIAA0738 protein	gp:AB018281				AB018281	
<u>Description</u>	Homo sapiens mRNA for KIAA0738 protein, complete cds.					

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14644032_f1_19	3328	8550	176	531	140	1.3e-09

Protein name	Locus Name	Acc#
arsenate reductase	pir:B70360	B70360

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14867837_c3_255	3329	8551	62	189		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
156306_c2_231	3330	8552	395	1188	802	9.1e-80

Protein name	Locus Name	Acc#

sp:TRKH_ECOLI

Description

TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
156376_c3_253	3331	8553	250	753		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16603380_c2_247	3332	8554	316	951	546	1.2e-52

Protein name	Locus Name	Acc#

hypothetical protein jhp0462	pir:C71929	C71929
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f2_84	3337	8559	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23445387_c1_197	3338	8560	194	585		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23598385_f3_135.....	3339	8561	205	618	319	1.4e-28

Protein name

Locus Name

Acc#

hypothetical protein ydeA

pir:C69777

C69777

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24025292_c1_178.....	3340	8562	1126	3381	455	3.8e-73

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24227211_f1_30	3341	8563	102	309	229	4.8e-19

Protein name

Locus Name

Acc#

sp:YGBA_ECOLI

P25728

Description

HYPOTHETICAL 13.9 KD PROTEIN IN PHLA-MUTS INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24257786_f2_114	3342	8564	89	270	91	0.0032

Protein name

Locus Name

Acc#

hypothetical protein pX01-90

pir:B59102

B59102

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24406506_t2_97	3343	8565	96	291	131	1.2e-08

Protein name

Locus Name

Acc#

unknown

gp:LLU80410

U80410

Description

Lactococcus lactis cremoris phosphopentomutase (deoB) and purinenucleoside phosphorylase (deoD) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24647562_c2_223	3344	8566	287	864	488	1.7e-46

Protein name

Locus Name

Acc#

sp:YEGX_ECOLI

Description

HYPOTHETICAL 32.0 KD PROTEIN IN FBAB-THID INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24647760_c3_287	3345	8567	137	414	157	2.0e-11
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
probable general stress protein 26			pir:D75431			D75431
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24648567_c1_180	3346	8568	302	909	129	0.00044
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein SC3A7.16c			pir:T29435			T29435
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26257937_f1_15	3347	8569	360	1083		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26384687_c3_258	3348	8570	88	267	129	1.9e-08
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein APE0900			pir:D72685			D72685
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26447312_f1_40	3349	8571	73	222		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26597066_c1_214	3350	8572	234	705	445	6.1e-42
Protein name			Locus Name		Acc#	
cell division ATP-binding protein ftsE			pir:E70919			
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26694091_f3_125.....	3351	8573	69	210	102	1.4e-05
Protein name			Locus Name		Acc#	
hypothetical protein			gp:SSU18930		Y18930	
Description						

Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29406301_c2_230.....	3352	8574	128	387	97	0.00048
Protein name			Locus Name		Acc#	
TRK potassium uptake system protein (trkH) homolog			pir:G69354		G69354	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29417562_f2_81.....	3353	8575	257	774		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32125280_f3_154	3354	8576	61	186		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33229628_f3_163	3355	8577	65	198		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33369017_c3_286	3356	8578	274	825	109	2.5e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable araC family transcription regulator			pir:T35902		T35902	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33789127_c1_212	3357	8579	244	735	455	5.4e-43
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
phosphoribosylformimino-5 aminoimidazole			gp:AB008676		AB008676	
<u>Description</u>						

Escherichia coli 0157 DNA, map position at 46 min., complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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34084407_f3_158	3358	8580	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3928385_c1_179	3359	8581	639	1920		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4098430_f1_35	3360	8582	395	1188	656	2.7e-64
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Protein name

Locus Name

Acc#

putative membrane transport protein.

gp:SCC75A

AL133220

Description

Streptomyces coelicolor cosmid C75A.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4101550_c1_202	3361	8583	105	318	208	8.0e-17
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Protein name

Locus Name

Acc#

hypothetical protein ysdA

pir:G69983

G69983

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4175305_f2_72	3362	8584	81	246		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
42700_f1_17	3363	8585	247	744		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4414677_c2_249	3364	8586	206	621	540	5.3e-52
Protein name			Locus Name		Acc#	
			sp:HIS2_KLEPN		024714	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4459456_c3_268	3365	8587	407	1224	152	3.9e-07
Protein name			Locus Name		Acc#	
chromosome assembly protein homolog			pir:B70356		B70356	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4723450_f1_8	3366	8588	68	207	79	0.017
Protein name			Locus Name		Acc#	
hypothetical protein YHR167w			pir:S52609		S52609	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4875287_c1_211	3367	8589	199	600	440	2.1e-41

Protein name

Locus Name

Acc#

sp:HIS5_ECOLI

P10375

Description

AMIDOTRANSFERASE HISH,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4878126_c2_251	3368	8590	390	1173	700	5.8e-69

Protein name

Locus Name

Acc#

diaminopimelate decarboxylase,

pir:C70404

C70404

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4885942_c2_250	3369	8591	377	1134	538	8.6e-52

Protein name

Locus Name

Acc#

precursor monofunctional aspartokinase

gp:AF135862

AF135862

Description

Glycine max precursor monofunctional aspartokinase mRNA, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4901562_c2_224	3370	8592	446	1341	378	1.8e-39

Protein name

Locus Name

Acc#

cell division inhibitor:protein
slr1223:protein slr1223

pir:S77404

S77404

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5177305_f1_18	3371	8593	320	963	738	5.5e-73

Protein name

Locus Name

Acc#

sp:YBIN_ECOLI

P75782

Description

HYPOTHETICAL 34.2 KD PROTEIN IN DING-GLNQ INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5329811_f2_96	3372	8594	303	912	190	2.8e-13

Protein name

Locus Name

Acc#

transcription regulator AraC/XylS family
homolog ydeE

pir:G69777

G69777

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5875817_c2_240	3373	8595	256	771	162	6.5e-12

Protein name

Locus Name

Acc#

mutator protein mutT:hypothetical protein
sll1045:hypothetical protein sll1045

pir:S74508

S74508

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
631558_f2_95	3374	8596	319	960	226	9.9e-19

Protein name

Locus Name

Acc#

sp:YT29_MYCTU

P71564

Description

PUTATIVE OXIDOREDUCTASE RV0945,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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800677_c1_184	3375	8597	572	1719		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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9792715_c2_236.....	3376	8598	1242	3729	194	2.7e-23
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Protein name

Locus Name

Acc#

chromosome assembly protein homolog

pir:B70356

B70356

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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9820893_c1_216.....	3377	8599	68	207		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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12583432_c1_57.....	3378	8600	111	336	146	3.0e-10
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Protein name

Locus Name

Acc#

gp:AB006709

AB006709

Description

Vibrio alginolyticus rpoN gene for RNA polymerase sigma factor N,partial and complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14508412_c3_77	3379	8601	174	525	158	1.6e-11
Protein name			Locus Name			Acc#
			sp:RL10_BACSU			P42923
Description						
(VEGETATIVE PROTEIN 300) (VEG300)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19627151_f1_16	3380	8602	196	591	383	2.3e-35
Protein name			Locus Name			Acc#
hypothetical protein RP516			pir:F71655			F71655
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22462765_f3_47	3381	8603	593	1782	1077	6.6e-109
Protein name			Locus Name			Acc#
aminopeptidase P			gp:DME131920			AJ131920
Description						
Drosophila melanogaster Aminopep-p gene, partial.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23710302_c2_65	3382	8604	399	1200	2049	6.5e-212
Protein name			Locus Name			Acc#
			sp:EFTU_BACFR			P33165
Description						
ELONGATION FACTOR TU (EF-TU)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24407752_c2_67	3383	8605	151	456	442	1.3e-41

Protein name

Locus Name

Acc#

sp:RL11_MYCTU

P96931

Description

50S RIBOSOMAL PROTEIN L11

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
274030_f1_12	3384	8606	95	288	108	3.2e-06

Protein name

Locus Name

Acc#

hypothetical protein PH1485

pir:H71023

H71023

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2985637_c1_59	3385	8607	114	345	93	0.00012

Protein name

Locus Name

Acc#

SecE protein

pir:JE0331

JE0331

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34120287_c3_76	3386	8608	76	231	168	1.4e-12

Protein name

Locus Name

Acc#

sp:RL1_HAEIN

P44342

Description

50S RIBOSOMAL PROTEIN L1

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36222568_c2_60	3387	8609	410	1233	390	4.1e-36

Protein name

Locus Name

Acc#

3-deoxy-manno-octulosonic acid transferase

gp:SMU52844

U52844

Description

Serratia marcescens putative glycosyltransferase, putative glycosyltransferase, putative heptosyl III transferase (waaQ), 3-deoxy-manno-octulosonic acid transferase (waaA), glucosyltransferase (waaE), and KdtB (kdtB) genes, complete cds; and Fpg (fpg) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4297002_c2_63	3388	8610	308	927	507	1.7e-48

Protein name

Locus Name

Acc#

tyrosine recombinase XerD

gp:AF093548

AF093548

Description

Staphylococcus aureus tyrosine recombinase XerD (xerD) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4472125_c2_66	3389	8611	190	573	384	1.8e-35

Protein name

Locus Name

Acc#

99% identity over 181 amino acids with E. coli

gp:STYSTMF1

AF170176

Description

Salmonella typhimurium fragment STMF1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5897507_c2_68	3390	8612	180	543	463	7.6e-44

Protein name

Locus Name

Acc#

sp:RL1_STRSQ

Q07976

Description

50S RIBOSOMAL PROTEIN L1

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6839052_c1_56	3391	8613	89	270	138	2.1e-09

Protein name

Locus Name

Acc#

sp:RS21_BORBU

051271

Description

30S RIBOSOMAL PROTEIN S21

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781536_c3_78	3392	8614	138	417	339	1.0e-30

Protein name

Locus Name

Acc#

sp:RL7_HAEIN

P44348

Description

50S RIBOSOMAL PROTEIN L7/L12

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9853461_c2_69	3393	8615	957	2871	1716	1.5e-228

Protein name

Locus Name

Acc#

RNA polymerase B-subunit

gp:AF087812

AF087812

Description

Legionella pneumophila RNA polymerase B-subunit (rpoB) gene, complete cds;
and RNA polymerase B'-subunit (rpoC) gene, partialcds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14650337_f2_2	3394	8616	595	1788	103	1.8e-07

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and
mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415717_f3_4	3395	8617	77	234	146	1.6e-09

Protein name

Locus Name

Acc#

sp:Succ_THEFL

P25126

Description

SUCCINYL-COA SYNTHETASE BETA CHAIN, (SCS-BETA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33324216_f2_1	3396	8618	668	2007	473	2.0e-42

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23617128_c1_25.....	3397	8619	405	1218	734	1.5e-72

Protein name

Locus Name

Acc#

putative hydrolase

gp:SCM11

AL133278

Description

Streptomyces coelicolor cosmid M11.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24317062_f2_14.....	3398	8620	691	2076	220	2.2e-18

Protein name

Locus Name

Acc#

hypothetical protein TM0280

pir:F72395

F72395

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2991276_f3_19	3399	8621	528	1587	165	5.5e-09

Protein name

Locus Name

Acc#

gp:BOU15179

U15179

Description

Bacteroides ovatus arabinosidase (asdII) gene, complete cds andputative transketolase, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31437792_f1_9	3400	8622	244	735		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35837506_c1_20.....	3401	8623	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4039086_c1_24.....	3402	8624	371	1116	102	0.017

Protein name

Locus Name

Acc#

endo-α1,5-arabinanase

gp:PFARBA

Y10458

Description

P.fluorescens arbA gene for endo-α1,5-arabinanase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10751260_f3_9	3403	8625	740	2223	842	2.2e-89

Protein name

Locus Name

Acc#

sp:HLY2_ECOLI

P10089

Description

HEMOLYSIN SECRETION ATP-BINDING PROTEIN, CHROMOSOMAL

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23635937_f1_2	3404	8626	203	612		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644135_f1_1	3405	8627	223	672		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24665831_f3_7	3406	8628	239	720	146	4.8e-08

Protein name

Locus Name

Acc#

glycosyltransferase

gp:AF146532

AF146532

Description

Klebsiella pneumoniae waa gene cluster.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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33442593_f2_6	3407	8629	208	627		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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1347692_f1_1	3408	8630	255	768	557	8.3e-54
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Protein name

Locus Name

Acc#

sp:ATCS_SYNY3

P73241

Description

CATION-TRANSPORTING ATPASE PACS,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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48828124_c1_5	3409	8631	67	204	178	9.6e-13
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Protein name

Locus Name

Acc#

hypothetical protein PFB0225c

pir:E71620

E71620

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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48828124_c2_8	3410	8632	63	192	168	1.2e-11
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Protein name

Locus Name

Acc#

hypothetical protein PFB0225c

pir:E71620

E71620

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
48828124_c3_10	3411	8633	61	186	50	0.0053
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
translation initiation factor eIF-2 beta chain			pir:T17104		T17104	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12587876_c2_118	3412	8634	767	2304	195	2.2e-11
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15040927_c1_80	3413	8635	190	573	203	2.7e-16
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YM67_ARCFU		O28017	
<u>Description</u>						
(EC 1.-.-.-)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15632927_c3_157	3414	8636	240	720		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20336010_f2_50	3415	8637	305	918	132	9.8e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
endo-1,4-beta-xylanase homolog yjeA	pir:G69849	G69849

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23615882_f2_38	3416	8638	671	2016	1649	1.6e-169

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	gp:PAL243361	AJ243361

Description

Prevotella albensis ORF1, isolate M384.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23625277_f3_79	3417	8639	953	2862	2467	3.3e-256

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:S76257	S76257

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23712752_c1_91	3418	8640	737	2214	1460	9.0e-161

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable copper-transporting ATPase, yvgX	pir:E70041	E70041

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24475400_f1_2	3419	8641	214	645	138	6.4e-08
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
response regulator			gp:PPUY18245			Y18245
<u>Description</u>						
Pseudomonas putida todX, todF, todC1, todC2, todB, todA, todD, todE, todG, todI, todH, todS, todT genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24806562_f1_6	3420	8642	132	399		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25525416_f1_12.....	3421	8643	318	957	282	8.7e-24
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:XYNB_BUTFI			P26223
<u>Description</u>						
D-XYLAN XYLANOHYDROLASE B)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25567276_c1_90.....	3422	8644	145	438	115	5.7e-07
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
mercury reductase homolog			pir:I64109			I64109
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26281308_f1_15	3423	8645	106	321		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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29579692_f2_39	3424	8646	282	849	102	0.023
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Protein name

Locus Name

Acc#

gp:AF025396

AF025396

Description

Vibrio anguillarum rfb region, partial sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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30276381_f3_61	3425	8647	467	1404	259	2.6e-19
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Protein name

Locus Name

Acc#

sp:RESE_BACSU

P35164

Description

SENSOR PROTEIN RESE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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31883436_c1_93	3426	8648	282	849	419	3.5e-39
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Protein name

Locus Name

Acc#

lipoate-protein ligase B

gp:AF153678

AF153678

Description

Myxococcus xanthus lipoid acid synthetase precursor, lipoamideacyltransferase, and lipoate-protein ligase B genes, complete cds;and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32218816_f3_78	3427	8649	221	666	370	5.4e-34

Protein name

Locus Name

Acc#

sp:YCBL_ECOLI

P75849

Description

HYPOTHETICAL 23.8 KD PROTEIN IN MUKB-ASPC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33603128_c1_100	3428	8650	129	390	135	4.3e-09

Protein name

Locus Name

Acc#

hypothetical protein PH0362

pir:G71143

G71143

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34173437_f3_68.....	3429	8651	296	891	171	9.1e-11

Protein name

Locus Name

Acc#

regulatory protein

gp:AF036244

AF036244

Description

Azotobacter chroococcum 4-hydroxybenzoate hydroxylase (pobA) gene,partial cds; and regulatory protein (pobR) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3910880_f2_51.....	3430	8652	237	714	230	3.7e-19

Protein name

Locus Name

Acc#

sp:GIDB_BACSU

P25813

Description

GLUCOSE INHIBITED DIVISION PROTEIN B

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
504010_f2_44	3431	8653	134	405	127	3.1e-08
Protein name			Locus Name			Acc#
hypothetical protein APE1455			pir:G72624			G72624
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6351450_f2_35	3432	8654	338	1017	650	1.2e-63
Protein name			Locus Name			Acc#
transcription regulator NtrC family			pir:C70396			C70396
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6647150_c3_138	3433	8655	158	477	101	0.0015
Protein name			Locus Name			Acc#
chitinase IV precursor			gp:AF112966			AF112966
Description						
Triticum aestivum chitinase IV precursor (Cht4) mRNA, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10189063_f1_98	3434	8656	433	1302		
Protein name			Locus Name			Acc#
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1051942_f1_25	3435	8657	266	801	131	5.1e-06
Protein name			Locus Name			Acc#
hypothetical protein AF2299			pir:C69537			C69537
Description						

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PAB0790	pir:H75098	H75098

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10586563.f2.192.....	3437	8659	304	915	90	0.0014

Acc#

D42067

Porphyromonas gingivalis DNA for Fimbrilin, ORF1-4, complete cds.

Protein name	Locus Name	Acc#
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~~NO-HIT~~

Protein name	Locus Name	Acc#
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AE001272

Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
117142_c2_481	3440	8662	326	981	304	5.4e-27

Protein name Locus Name Acc#
 hypothetical protein pir:S76925 S76925

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11834807_c1_346	3441	8663	75	228		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1210252_f2_116	3442	8664	513	1542	1190	7.0e-121

Protein name Locus Name Acc#

conserved hypothetical protein ymdA pir:F69884 F69884

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12110668_c1_418	3443	8665	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12501250_f2_154	3444	8666	251	756	127	3.1e-06

Protein name Locus Name Acc#

hypothetical protein PAB1224 pir:A75022 A75022

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1253425_f1_38	3445	8667	1445	4338	822	2.9e-79

Protein name Locus Name Acc#
DNA helicase related protein pir:H69163 H69163
Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12612930_c2_546.....	3446	8668	343	1032	146	1.6e-07

Protein name Locus Name Acc#
transmembrane sensor gp:AF051691 AF051691
Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor (fiuI), transmembrane sensor (fiuR), and hydroxamate-type ferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12697702_f1_17.....	3447	8669	63	192		

Protein name Locus Name Acc#
Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12770151_f2_141.....	3448	8670	289	870	128	1.0e-05

Protein name Locus Name Acc#
hypothetical protein gp:PST249385 AJ249385
Description

Pseudomonas stutzeri pilT, pilU, ORF1 (partial) and ORF2 (partial) genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1360802_f3_306	3449	8671	373	1122	100	0.030
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
neurofilament protein H form H2 (repetitive region)			pir:B43427		B43427	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13884627_f1_93	3450	8672	125	378	260	1.7e-21
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:TRA2_BACFR		Q45119	
<u>Description</u>						

TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS21-LIKE

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14344010_c1_391	3451	8673	303	912	610	2.0e-59
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable ion transporter			pir:E75470		E75470	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14501300_f1_43	3452	8674	149	450	71	0.040
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:TXMA_DENPO		P80494	
<u>Description</u>						

MUSCARINIC TOXIN ALPHA (MT-ALPHA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14730202_c3_613	3453	8675	88	267	99	9.4e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein F13D12.3			pir:T20831		T20831	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14955312_c1_369	3454	8676	68	207	78	0.012
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:H5_CHICK		P02259	
<u>Description</u>						

HISTONE H5

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15105287_f2_174	3455	8677	85	258		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16225407_f1_97	3456	8678	138	417		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16407262_f3_222	3457	8679	164	495		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16517037_f2_194	3458	8680	61	186		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16525383_f1_99	3459	8681	119	360		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16923417_f3_221	3460	8682	63	192		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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189032_f2_161	3461	8683	450	1353	1085	9.3e-110
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Protein name

Locus Name

Acc#

O-acetylhomoserine sulphydrylase

pir:D72324

D72324

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
196062_c1_399	3462	8684	227	684	378	7.7e-35

Protein name

Locus Name

Acc#

sp:YHID_ECOLI

P26606

Description

HYPOTHETICAL 23.2 KD PROTEIN IN SLP-HDEB INTERGENIC REGION (ORF-C)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1992011_c1_367	3463	8685	91	276		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20047683_f3_225.....	3464	8686	478	1437	772	1.4e-76

Protein name

Locus Name

Acc#

sp:YKGF_ECOLI

P77536

Description

HYPOTHETICAL 53.1 KD PROTEIN IN EAEH-BETA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20712687_c3_604.....	3465	8687	95	288	75	0.047

Protein name

Locus Name

Acc#

hypothetical protein aq_1680

pir:F70445

F70445

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21534653_c3_651	3466	8688	150	453	79	0.0047
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein Rv0603			pir:F70909		F70909	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21995337_c2_469	3467	8689	543	1632	227	5.5e-18
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein PH0142			pir:D71235		D71235	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22052177_c3_568	3468	8690	300	903	90	0.0014
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:PQRA_PROVU		Q52620	
<u>Description</u>						
REGULATORY PROTEIN PQRA						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22548450_f2_172	3469	8691	63	192		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23445887_f2_152	3470	8692	281	846	107	0.0025
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
sensory transduction histidine kinase sll1475:protein sll1475:protein sll1475			pir:S76818		S76818	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23476512_c1_344.....	3471	8693	519	1560	1712	3.4e-176
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
propionyl-CoA carboxylase			gp:AB007000		AB007000	
<u>Description</u>						

Myxococcus xanthus MxppcB gene for propionyl-CoA carboxylase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23635902_c1_445.....	3472	8694	351	1056	94	0.038
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ORF188			gp:AB000109		AB000109	
<u>Description</u>						

Dictyostelium discoideum mitochondrial DNA, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23838137_c2_547.....	3473	8695	1094	3285	300	1.0e-47
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
receptor antigen (RagA)			gp:PGI130872		AJ130872	
<u>Description</u>						

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
241542_f1_86	3474	8696	98	297		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24219077_c1_439.....	3475	8697	179	540	404	1.4e-37

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24225006_c3_666.....	3476	8698	769	2310	1773	1.2e-182

Protein name

Locus Name

Acc#

hypothetical protein b2463

pir:F65021

F65021

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24225326_f2_189.....	3477	8699	317	954	122	7.2e-06

Protein name

Locus Name

Acc#

sp:EXSA_PSEAE

P26993

Description

EXOENZYME S SYNTHESIS REGULATORY PROTEIN EXSA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24255332_f1_87	3478	8700	770	2313	504	8.9e-48

Protein name

Locus Name

Acc#

sp:YBAL_ECOLI

Description

HYPOTHETICAL 59.4 KD PROTEIN IN GSK-FSR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24258385_c1_412	3479	8701	121	366	285	5.5e-25

Protein name

Locus Name

Acc#

arsenate reductase homolog yusI

pir:B70021

B70021

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24260885_c3_570.....	3480	8702	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24328338_c1_444.....	3481	8703	277	834	110	0.00067

Protein name

Locus Name

Acc#

sp:EBA2_FLAME

P36912

Description

(ENDOGLYCOSIDASE F2)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24407150_f2_170	3482	8704	296	891	157	4.0e-09
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
pobR regulator			sp:PSEY18527			Y18527
<u>Description</u>						
Pseudomonas sp. pobA, pobR, pcaQ, pcaH and pcaG genes.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24413137_f2_118	3483	8705	194	585	122	2.0e-12
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:PFS_BACSU			O32028
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24414711_c1_333.....	3484	8706	394	1185	521	5.4e-50
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:PNCB_ECOLI			P18133
<u>Description</u>						
NICOTINATE PHOSPHORIBOSYLTRANSFERASE, (NAPRTASE)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24417062_f3_291.....	3485	8707	228	687	124	2.3e-06
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
isochorismatase homolog ywoC			pir:F70064			F70064
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24494000_f1_20	3486	8708	182	549	251	2.2e-21

Protein name

Locus Name

Acc#

sp:YGCF_HAEIN

P45097

Description

HYPOTHETICAL PROTEIN HI1189

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24633462_c3_630	3487	8709	366	1101	971	1.1e-97

Protein name

Locus Name

Acc#

sp:YE55_HAEIN

P45213

Description

HYPOTHETICAL PROTEIN HI1455

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640885_f1_21	3488	8710	248	747	488	1.7e-46

Protein name

Locus Name

Acc#

hypothetical protein SCF43A.05

pir:T36428

T36428

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24641512_f2_187	3489	8711	405	1218	132	6.1e-08

Protein name

Locus Name

Acc#

gp:YP102KB

AL031866

Description

Yersinia pestis 102 kbases unstable region: from 1 to 119443.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24645932_c2_477	3490	8712	477	1434	511	6.2e-49

Protein name

Locus Name

Acc#

sp:YLCB_ECOLI

P77211

Description

PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648387_f3_234	3491	8713	320	963	578	4.9e-56

Protein name

Locus Name

Acc#

sp:YNBB_ECOLI

Description

HYPOTHETICAL 33.1 KD PROTEIN IN MAOC-ACPD INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24650187_f2_131	3492	8714	443	1332	1119	2.3e-113

Protein name

Locus Name

Acc#

sp:YICE_ECOLI

P27432

Description

HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24806512_f2_117	3493	8715	252	759	569	4.4e-55

Protein name

Locus Name

Acc#

CGI-32 protein

gp:AF132966

AF132966

Description

Homo sapiens CGI-32 protein mRNA, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24870957_f2_200	3494	8716	291	876	104	0.0042
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:VG77_BPML5			Q05292
<u>Description</u>						
GENE 77 PROTEIN (GP77)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24897892_f2_120	3495	8717	200	603	119	1.2e-05
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein HP0137			pir:A64537			A64537
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25422952_f1_94	3496	8718	165	498		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26257687_f3_254	3497	8719	505	1518	107	0.0052
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
fibroin heavy chain PG-2'			pir:B61615			B61615
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26260191_c1_421	3498	8720	60	183		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26287817_f2_146	3499	8721	78	237		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26369387_f3_244	3500	8722	128	387	83	0.013
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Protein name

Locus Name

Acc#

putative integral membrane protein

gp:SC51A

AL121596

Description

Streptomyces coelicolor cosmid 51A.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26439037_c1_370	3501	8723	80	243		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26815936_f1_60	3502	8724	373	1122		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26853838_f2_114	3503	8725	138	417	93	0.00012
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
vacuolar type ATP synthase subunit	gp:D63799				D63799	
<u>Description</u>	Thermus thermophilus genes, Operon of Vacuolar type ATPsyntasesubunit, complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2931593_f2_126	3504	8726	390	1173	202	9.2e-13
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein	pir:JC6027				JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29390682_f2_140.....	3505	8727	311	936	117	0.00023
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
unknown	gp:AF175293				AF175293	
<u>Description</u>						
Enterococcus faecium strain N97-330 vanD glycopeptide resistancegene cluster, complete cds; and unknown gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29486512_f1_49.....	3506	8728	552	1659	360	1.2e-32
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
cation efflux system protein	pir:C71831				C71831	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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30275287_c3_674	3507	8729	394	1185		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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30351687_f1_76	3508	8730	511	1536	1766	6.4e-182
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Protein name

Locus Name

Acc#

sp:IMDH_TRIFO

P50097

Description

DEHYDROGENASE) (IMPDH) (IMPD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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30470408_f2_171	3509	8731	110	333	196	1.5e-15
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Protein name

Locus Name

Acc#

hypothetical protein SC5F2A.08c

pir:T35250

T35250

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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31914013_f1_36	3510	8732	435	1308	544	2.0e-52
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Protein name

Locus Name

Acc#

hypothetical protein MTH1458

pir:B69061

B69061

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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32110150_c1_438	3511	8733	82	249		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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32422050_f2_130	3512	8734	246	741		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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32507687_c3_639	3513	8735	703	2112	196	1.9e-26
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Protein name

Locus Name

Acc#

sp:Y634_METJA

Q58051

Description

HYPOTHETICAL PROTEIN MJ0634

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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33600625_c1_426	3514	8736	134	405	217	8.9e-18
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Protein name

Locus Name

Acc#

sp:YBAN_ECOLI

Description

HYPOTHETICAL 14.8 KD PROTEIN IN PRIC-APT INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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33767187_f2_191	3515	8737	404	1215	96	0.016
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Protein name

Locus Name

Acc#

probable glycine-rich secreted protein

pir:T36291

T36291

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33789067_c2_486	3516	8738	777	2334	95	4.6e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein AF1017			pir:A69377		A69377	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33875836_c3_609	3517	8739	316	951		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34173188_c3_577	3518	8740	170	513	149	1.4e-14
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
methylmalonyl-coa decarboxylase gamma chain PAB1771			pir:F75135		F75135	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34179812_c1_436	3519	8741	449	1350	2234	1.6e-231
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:DHE4_BACTN		P94598	
<u>Description</u>						
(NAD(P)H-DEPENDENT GLUTAMATE DEHYDROGENASE)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34254662_c2_488	3520	8742	294	885	129	1.2e-05

Protein name

Locus Name

Acc#

microfilarial sheath protein SHP3

gp:LSU54556

U54556

Description

Litomosoides sigmodontis microfilarial sheath protein SHP3a (shp3a) and microfilarial sheath protein SHP3 (shp3) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34495216_c1_355	3521	8743	936	2811	1593	1.4e-163

Protein name

Locus Name

Acc#

acriflavin resistance protein acrf:protein slr2131:protein slr2131

pir:S75508

S75508

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36132761_f2_115.....	3522	8744	102	309	83	0.0014

Protein name

Locus Name

Acc#

sp:YGFE_ECOLI

P45580

Description

HYPOTHETICAL 12.6 KD PROTEIN IN PEPP-SSR INTERGENIC REGION (O109)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
364445812_c3_605.....	3523	8745	185	558		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36525343_f3_309	3524	8746	96	291		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3928885_c1_354.....	3525	8747	142	429	336	3.7e-29

Protein name

Locus Name

Acc#

CeoB

gp:BCU97042

U97042

Description

Burkholderia cepacia CeoA (ceoA) and CeoB (ceoB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3946052_c3_586.....	3526	8748	374	1125	392	2.5e-36

Protein name

Locus Name

Acc#

SmeA

gp:AF173226

AF173226

Description

Stenotrophomonas maltophilia multidrug efflux system SmeR (smeR), SmeS (smeS), SmeA (smeA), SmeB (smeB), and SmeC (smeC) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3949052_f1_35.....	3527	8749	61	186	95	7.5e-05

Protein name

Locus Name

Acc#

histone H1-like protein

pir:JH0658

JH0658

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3961641_f3_308	3528	8750	226	681		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4064375_f2_190	3529	8751	411	1236	157	2.4e-08
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Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4100342_f2_193	3530	8752	65	198		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4100917_c2_537	3531	8753	393	1182	144	8.7e-14
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Protein name

Locus Name

Acc#

hypothetical protein RP338

pir:D71690

D71690

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4103438_c2_465	3532	8754	507	1524	1314	5.0e-134

Protein name

Locus Name

Acc#

sp:ACCC_METJA

Q58626

Description

CARBOXYLASE,) (ACC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4105152_c3_583	3533	8755	110	333		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4115925_c1_405.....	3534	8756	462	1389	1234	1.5e-125

Protein name

Locus Name

Acc#

sp:ALST_BACSU

Q45068

Description

AMINO ACID CARRIER PROTEIN ALST

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4116561_c2_485.....	3535	8757	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4144005_f1_44	3536	8758	1255	3768	957	2.8e-173
Protein name			Locus Name		Acc#	
cation efflux system (AcrB/AcrD/AcrF family)			pir:G70396		G70396	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4151510_f3_226	3537	8759	293	882	414	1.2e-38
Protein name			Locus Name		Acc#	
pyridoxal kinase (pdxK) homolog			pir:G70195		G70195	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
422962_c1_361	3538	8760	377	1134	145	1.0e-06
Protein name			Locus Name		Acc#	
N-acetylmuramoyl-L-alanine amidase homolog			pir:H70177		H70177	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4337540_f1_57	3539	8761	106	321		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4345932_c1_331	3540	8762	62	189		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4494016_c2_501	3541	8763	348	1047	308	2.0e-27
Protein name			Locus Name		Acc#	
conserved hypothetical protein aq_1420			pir:D70423		D70423	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4509682_c2_524	3542	8764	197	594	136	3.4e-09
Protein name			Locus Name		Acc#	
unknown			gp:AF088897			
Description						
Zymomonas mobilis cosmid clone 65G3, partial sequence.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4572126_c2_520	3543	8765	213	642		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4725056_f3_224	3544	8766	117	354	176	2.0e-13
Protein name			Locus Name		Acc#	
conserved hypothetical protein aq_853			pir:A70374		A70374	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
506502_c1_443	3545	8767	551	1656		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5273588_f3_235	3546	8768	226	681	142	1.4e-08
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
2-acylglycerophosphoethanolamine acyltransferase			pir:E70476		E70476	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5937505_c1_345.....	3547	8769	76	231		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
594753_f3_245.....	3548	8770	532	1599	552	3.4e-52
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
DNA helicase related protein			pir:H69163		H69163	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6145427_f2_186.....	3549	8771	69	210		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6845262_c2_527	3550	8772	614	1845	1053	2.3e-106

Protein name

Locus Name

Acc#

sp:YFBK_ECOLI

P76481

Description

HYPOTHETICAL 63.6 KD PROTEIN IN ELAD-NUON INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7034587_f3_305	3551	8773	104	315	81	0.0058

Protein name

Locus Name

Acc#

sp:ZN90_HUMAN

Q03938

Description

ZINC FINGER PROTEIN 90 (ZINC FINGER PROTEIN HTF9) (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9452_f3_236	3552	8774	191	576	174	3.2e-13

Protein name

Locus Name

Acc#

sp:RPSH_PSEAE

Q06198

Description

RNA POLYMERASE SIGMA-H FACTOR (SIGMA-30)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10238542_c3_212	3553	8775	107	324		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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11744515_f2_54	3554	8776	577	1734		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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1270751_c2_173	3555	8777	64	195		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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13675401_c3_218	3556	8778	161	486		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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13875343_f1_29	3557	8779	400	1203		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
156662_f3_62	3558	8780	107	324	201	4.4e-16

Protein name

Locus Name

Acc#

sp:DEH_BACST

Description

DNA-BINDING PROTEIN II (HB) (HU)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
18891_f3_74	3559	8781	612	1839	1158	1.7e-117

Protein name

Locus Name

Acc#

sp:SYR_TREPA

083803

Description

ARGINYL-TRNA SYNTHETASE, (ARGININE--TRNA LIGASE) (ARGRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19633590_f3_94	3560	8782	450	1353		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20360282_c1_111	3561	8783	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22853411_c1_127	3562	8784	366	1101	75	0.037
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein SC6E10.19c			pir:T35506		T35506	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23555312_c2_169	3563	8785	85	258		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23625188_f1_34	3564	8786	608	1827	1638	2.3e-168
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hemolysin erythrocyte lysis protein 2			gp:AF052516		AF052516	
<u>Description</u>						

Prevotella intermedia hemolysin hemolytic protein, hemolysin erythrocyte lysis protein 1, and hemolysin erythrocyte lysis protein 2 genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2364687_c2_175	3565	8787	154	465		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23710877_c2_174	3566	8788	1011	3036	942	1.3e-94
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
protein-export membrane protein	gp:AB022865				AB022865	
<u>Description</u>						
Prevotella ruminicola genes for polygalacturonase, xylosidase, protein-export membrane protein, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23925627_c3_195	3567	8789	82	249		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24023500_f1_33.....	3568	8790	493	1482	193	5.2e-13
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:Y907_METJA				Q58317	
<u>Description</u>						
HYPOTHETICAL PROTEIN MJ0907						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24298390_f2_56.....	3569	8791	126	381		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24398412_c3_207	3570	8792	334	1005		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24415877_c1_119	3571	8793	1003	3012	152	2.2e-07
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Protein name

Locus Name

Acc#

conserved hypothetical protein aq_1896

pir:E70463

E70463

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24429643_c3_206	3572	8794	801	2406	1069	2.5e-141
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Protein name

Locus Name

Acc#

topoisomerase I

gp:AF088896

AF088896

Description

Zymomonas mobilis fosmid clone 42C11, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24642836_c1_120	3573	8795	569	1710		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24650377_f1_31	3574	8796	436	1311		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24650377_f2_57	3575	8797	436	1311		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29346012_f3_97	3576	8798	411	1236	105	0.011
Protein name			Locus Name		Acc#	
rRNA methylase (SpoU family) (OO, TP) PFB0855c			pir:B71604		B71604	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29406680_c1_109	3577	8799	126	381		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
29695387_f3_93	3578	8800	399	1200		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30084687_f2_59	3579	8801	428	1287		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30507138_f1_2	3580	8802	561	1686	112	0.038
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
submaxillary mucin 1			pir:T42233		T42233	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34256561_c3_213	3581	8803	228	687	146	1.5e-21
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
probable glpG protein			pir:D71258		D71258	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35267555_c1_126	3582	8804	309	930	177	3.2e-13
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
probable glpG protein			pir:D71258		D71258	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35582908_c2_182	3583	8805	77	234		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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36207937_f1_1	3584	8806	489	1470		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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395662_c1_118	3585	8807	189	570	151	8.8e-11
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Protein name

Locus Name

Acc#

mutator protein mutT

pir:D64443

D64443

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

4103377_f3_98	3586	8808	207	621	177	4.6e-20
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Protein name

Locus Name

Acc#

lic-1 protein D

pir:E64128

E64128

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

441500_f2_42	3587	8809	77	234		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

4694011_f3_73	3588	8810	99	300	272	1.3e-23
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Protein name

Locus Name

Acc#

sp:DBH_BACST

Description

DNA-BINDING PROTEIN II (HB) (HU)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5260952_f1_32	3589	8811	426	1281		
---------------	------	------	-----	------	--	--

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5860750_f1_27	3590	8812	100	303	73	0.023
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Protein name

Locus Name

Acc#

sp:YM25_YEAST

P40219

Description

HYPOTHETICAL 16.4 KD PROTEIN IN TIF34-SWP1 INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
-----------------	-------------	-------------	------------------	------------------	--------------	--------------------

5937825_f2_38	3591	8813	107	324		
---------------	------	------	-----	-----	--	--

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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6914530_c3_202	3592	8814	69	210		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

7134587_f2_36	3593	8815	1022	3069		
---------------	------	------	------	------	--	--

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

10555337_f1_16	3594	8816	233	702	202	5.1e-16
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Protein name

Locus Name

Acc#

glycosyl transferase

gp:SPAJ6986

AJ006986

Description

Streptococcus pneumoniae type 33F DNA, capsular gene cluster.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

10572281_c1_271	3595	8817	254	765		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

10599062_f2_97	3596	8818	94	285		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10740936_f3_233	3597	8819	627	1884	292	7.6e-24
Protein name			Locus Name		Acc#	
serine/threonine protein kinase related protein			pir:H69064		H69064	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11723437_f2_138	3598	8820	307	924		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11984410_c3_488	3599	8821	258	777	460	1.6e-43
Protein name			Locus Name		Acc#	
hypothetical protein			sp:SAURED		Y09927	
Description						
Staphylococcus aureus glmM gene cluster.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1250280_f1_25	3600	8822	157	474	203	2.7e-16
Protein name			Locus Name		Acc#	
			sp:YOHJ_ECOLI		P33372	
Description						
HYPOTHETICAL 14.6 KD PROTEIN IN PBPG-CDD INTERGENIC REGION						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12538406_f3_242	3601	8823	633	1902	454	6.8e-43

Protein name

Locus Name

Acc#

sp:YFEW_ECOLI

P77619

Description

HYPOTHETICAL 47.8 KD PROTEIN IN UCPA-AMIA INTERGENIC REGION PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12673751_f2_171	3602	8824	110	330		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1351375_c3_464.....	3603	8825	82	249		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13709431_c2_416.....	3604	8826	137	414	150	1.1e-10

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76920

S76920

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13808507_f1_45.....	3605	8827	307	924	177	3.1e-13

Protein name

Locus Name

Acc#

comEA protein-related protein

pir:F72301

F72301

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14257802_F3_240	3606	8828	391	1176	127	2.1e-13
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein			pir:G75375			G75375
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14459691_C2_408.....	3607	8829	237	714	106	0.0065
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
triadin isoform 3			gp:AF165917			AF165917
<u>Description</u>						

Canis familiaris triadin isoform 3 mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14500800_C2_415.....	3608	8830	399	1200		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15681530_C3_444.....	3609	8831	295	888	246	5.7e-31
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:CCSA_TOBAC			P12216
<u>Description</u>						

CYTOCHROME C BIOGENESIS PROTEIN CCSA

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

15713262_c3_456	3610	8832	71	216		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

157788_f2_91	3611	8833	263	792		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

16289086_f3_259	3612	8834	309	930	129	3.4e-05
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Protein name

Locus Name

Acc#

interphotoreceptor retinoid-binding protein

gp:DRRNAIRBP

X85957

Description

Danio rerio mRNA for interphotoreceptor retinoid-binding protein.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

16804510_c3_471	3613	8835	79	240		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19547890_f1_5	3614	8836	370	1113	188	8.2e-17

Protein name

Locus Name

Acc#

sp:OTC_ARCFU

029013

Description

ORNITHINE CARBAMOYLTRANSFERASE, (OTCASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19727333_c3_491	3615	8837	208	627		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20134428_f3_255.....	3616	8838	139	420		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20312527_f2_165.....	3617	8839	297	894		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21913177_c3_446	3618	8840	255	768	153	7.6e-11
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
transcription regulator, crp family			pir:F72285			F72285
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21961513_f2_145.....	3619	8841	456	1371	861	5.1e-86
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:YBBC_BACSU			P40407
<u>Description</u>						

(ORF2)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21989375_f2_128.....	3620	8842	443	1332	619	2.2e-60
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:MURF_BACSU			P96613
<u>Description</u>						

(D-ALANYL-D-ALANINE-ADDING ENZYME)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22062501_f3_175.....	3621	8843	287	864	414	1.2e-38
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
glutamate racemase			pir:B70329			B70329
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22136_f2_129	3622	8844	459	1380	948	3.1e-95
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
sodium-dependent transporter homolog yocR			pir:D69902		D69902	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22460312_f1_54	3623	8845	1121	3366	461	1.5e-66
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22900257_c2_355	3624	8846	175	528		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>			NO-HIT			

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23484750_f3_257	3625	8847	893	2682	1179	1.0e-119
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>			sp:PARC_BORBU		051066	
TOPOISOMERASE IV SUBUNIT A,						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23721906_c3_472	3626	8848	111	336		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23930318_f3_172.....	3627	8849	839	2520	407	1.9e-38

Protein name

Locus Name

Acc#

outer membrane protein Omp85

gp:AF021245

AF021245

Description

Neisseria meningitidis outer membrane protein Omp85 (omp85) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23932786_f3_258.....	3628	8850	297	894		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23957950_f1_38.....	3629	8851	702	2109	353	1.0e-28

Protein name

Locus Name

Acc#

two component sensor

gp:AF030352

AF030352

Description

Pseudomonas aeruginosa two component sensor (lemA) gene, partialcds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24019053_f2_101	3630	8852	89	270	169	1.1e-12

Protein name

Locus Name

Acc#

DNA repair protein

pir:H72239

H72239

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24025277_f2_100	3631	8853	141	426	189	8.2e-15

Protein name

Locus Name

Acc#

sp:RADC_BACSU

Q02170

Description

DNA REPAIR PROTEIN RADC HOMOLOG (ORF)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24025316_c3_439	3632	8854	184	555	171	1.1e-15

Protein name

Locus Name

Acc#

immunoreactive 30kD antigen PG44

gp:AF175717

AF175717

Description

Porphyromonas gingivalis strain W50 immunoreactive 30kD antigenPG44 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24026552_f1_67	3633	8855	286	861	607	4.2e-59

Protein name

Locus Name

Acc#

sp:YFEU_HAEIN

P44862

Description

HYPOTHETICAL PROTEIN HI0754

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24270327_c3_498	3634	8856	265	798	98	0.019

Protein name unknown Locus Name gp:AF049236 Acc# AF049236

Description

Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein(ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), putative acyl-coA dehydrogenase(AtG6), and calcium dependent protein kinase genes, complete cds;and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415892_c3_489	3635	8857	76	231		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24470300_c3_500	3636	8858	404	1215	1234	1.5e-125

Protein name Locus Name Acc#

acetate kinase pir:H72397 H72397

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24641933_f2_142	3637	8859	490	1473	167	9.9e-10

Protein name Locus Name Acc#

glycosyl transferase PAB0772 pir:B75096 B75096

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648257_f3_205	3638	8860	233	702	449	2.3e-42
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YOHK_ECOLI		P33373	
<u>Description</u>						
HYPOTHETICAL 24.5 KD PROTEIN IN PBPB-GDD INTERGENIC REGION						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24804562_f3_229	3639	8861	341	1026	968	2.3e-97
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
aspartate-semialdehyde dehydrogenase,			pir:B70461		B70461	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25494017_f3_235	3640	8862	470	1413	259	2.1e-24
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
amidase enhancer			gp:AB017194		AB017194	
<u>Description</u>						
Plectonema boryanum ORF270, proline iminopeptidase, ferredoxin andamidase enhancer genes, complete and partial cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26359827_c3_476	3641	8863	242	729	365	1.8e-33
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YGD_L_ECOLI		Q46927	
<u>Description</u>						
HYPOTHETICAL 28.6 KD PROTEIN IN GCVA-MLTA INTERGENIC REGION						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26364591_c3_512	3642	8864	61	186		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26594061_c2_354.....	3643	8865	495	1488	814	4.2e-122
Protein name			Locus Name		Acc#	
			sp:NRFA_HAEIN		P45017	
Description						

CYTOCHROME C552 PRECURSOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26595877_c3_487.....	3644	8866	323	972	707	1.1e-69
Protein name			Locus Name		Acc#	
			sp:YBAS_ECOLI		P77454	
Description						

HYPOTHETICAL 32.9 KD PROTEIN IN USHA-TESA INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26601586_c2_395.....	3645	8867	288	867	553	2.2e-53
Protein name			Locus Name		Acc#	
dihydropteroate synthase			pir:E72425		E72425	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29414003_f2_118	3646	8868	70	213		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29478385_c1_297.....	3647	8869	712	2139	703	3.0e-79
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein					pir:S76532	S76532
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29882802_f1_65.....	3648	8870	969	2910	1636	3.8e-168
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
d-lactate dehydrogenase					pir:A71843	A71843
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30120267_c1_316.....	3649	8871	385	1158		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30261425_f3_231	3650	8872	600	1803	96	1.3e-05

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3156927_c3_499	3651	8873	341	1026	859	8.3e-86

Protein name

Locus Name

Acc#

phosphotransacetylase

gp:TTAJ4870

AJ004870

Description

Thermoanaerobacterium thermosaccharolyticum ptaA and ackA genes, orf1, orf2, orf3, orf4.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31881508_c1_298.....	3652	8874	237	714	541	4.1e-52

Protein name

Locus Name

Acc#

ABC transporter

pir:B70327

B70327

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33211586_c3_506.....	3653	8875	328	987	429	6.3e-45

Protein name

Locus Name

Acc#

sp:DDL_HAEIN

P44405

Description

D-ALANINE--D-ALANINE LIGASE, (D-ALANYLALANINE SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33406262_c3_440	3654	8876	171	516	238	5.3e-20
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
nimB protein			pir:I40183			
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33675253_f2_127	3655	8877	450	1353	186	1.4e-11
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
NorA			gp:AB019536		AB019536	
<u>Description</u>						
Staphylococcus aureus norA23 gene for NorA, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34023425_c3_486	3656	8878	486	1461	1130	1.6e-114
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
glutamate decarboxylase:protein sll1641:protein sll1641			pir:S75150		S75150	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34069067_f2_98	3657	8879	192	579	929	3.2e-93
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:EFP_BACFR		P70889	
<u>Description</u>						
ELONGATION FACTOR P (EF-P)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34095887_c3_501	3658	8880	470	1413	487	5.7e-58
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
alkaline phosphatase			pir:B72410			B72410
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34632811_f3_178.....	3659	8881	376	1131	93	0.038
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein sll0670			pir:S77054			S77054
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35348812_f3_176.....	3660	8882	413	1242	549	5.9e-53
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
glutamate 5-kinase proJ			pir:F69682			F69682
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36345282_c1_330.....	3661	8883	175	528	364	2.4e-33
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:YBC5_CHLVI			O50310
<u>Description</u>						

HYPOTHETICAL 36.7 KD PROTEIN IN BCHI 5'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36365942_c2_400.....	3662	8884	297	894		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3923751_c1_324	3663	8885	114	345	237	6.8e-20
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
conserved hypothetical protein			pir:C75306			C75306
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3937680_c2_409	3664	8886	521	1566	129	0.0015
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
elastic titin			pir:I38346			I38346
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3939462_c3_492	3665	8887	103	312		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3961412_c2_358	3666	8888	424	1275	83	0.013
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
polyprotein			gp:AF206441			AF206441
<u>Description</u>						
Hepatitis C virus isolate 28B polyprotein gene, E1/E2 region,partial cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4063932_f1_2	3667	8889	85	258	68	0.047
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
conserved hypothetical protein aq_340			pir:C70330			C70330
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4101502_c3_494	3668	8890	376	1131		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4101563_f2_150.....	3669	8891	285	858	106	0.0082
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein W06B4.2			pir:T34482		T34482	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4109777_f2_164.....	3670	8892	599	1800	176	1.5e-09
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:S75991		S75991	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4410807_f3_236.....	3671	8893	437	1314	252	4.1e-19
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:HILIC3		X57315	
<u>Description</u>						

Haemophilus influenzae lic3 locus, containing galE and adk genes for UDP-galactose-4-epimerase and adenylate kinase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4535957_f3_177	3672	8894	419	1260	867	1.2e-86
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
gamma-glutamyl phosphate reductase					gp:STPROBA	X92418
<u>Description</u>						
S.thermophilus proB and proA genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4554687_c1_329	3673	8895	184	555	382	2.9e-35
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:YBC5_CHLVI				050310	
<u>Description</u>						
HYPOTHETICAL 36.7 KD PROTEIN IN BCHI 5' REGION						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4563927_c3_441.....	3674	8896	202	609	338	1.3e-30
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
small subunit of cytochrome c nitrite reductase	gp:WSU245540				AJ245540	
<u>Description</u>						
Wolinella succinogenes mreB gene (partial), nrfH, nrfA, nrfI, andnrfJ genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
46933_c3_495.....	3675	8897	642	1929		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4718961_c2_413	3676	8898	217	654	151	1.3e-08
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
protein kinase homolog			pir:T42077			T42077
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4723376_f1_59	3677	8899	1027	3084		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4744062_c2_397	3678	8900	87	264		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4782761_f3_207	3679	8901	342	1029	109	0.0020
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein PAB0896			pir:G75045			G75045
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4876563_c2_403	3680	8902	105	318		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5272813_f1_63	3681	8903	313	942		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5907312_c1_332	3682	8904	249	750		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6022312_c2_388	3683	8905	164	495	92	0.0068
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein SPAC11E3.10			pir:T37538		T37538	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6109552_c1_317	3684	8906	63	192		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
657811_f3_206	3685	8907	323	972	451	1.4e-42
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein jhp0277			pir:H71950		H71950	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6754515_f1_77	3686	8908	455	1368		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6.7.7088_c2_412.....	3687	8909	112	339		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6.8.3393_f2_162.....	3688	8910	64	195	58	0.0087
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NADH dehydrogenase 1

gp:AF069183 AF069183

Lipolexis gracilis NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6.9.17183_c2_378.....	3689	8911	62	189		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
797255_f3_173	3690	8912	168	507	160	9.7e-12
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
automembrane protein H			sp:YEOMPH		Y12468	
<u>Description</u>						
Y.enterocolitica ompH gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
815626_f2_104	3691	8913	447	1344		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
84812_f1_56	3692	8914	404	1215	632	9.4e-62
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YBBC_BACSU		P40407	
<u>Description</u>						
(ORF2)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
859637_f2_140	3693	8915	494	1485	411	2.5e-38
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:S75887		S75887	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
892000_f3_174	3694	8916	188	567	117	1.8e-06
Protein name			Locus Name			Acc#
periplasmic protein			gp:PLU236920			AJ236920
Description						
Photorhabdus luminescens yaeL (partial), firA (partial), oma and ompH genes.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
969077_c1_264	3695	8917	521	1566	873	4.8e-121
Protein name			Locus Name			Acc#
glycine--tRNA ligase, glyS:glycyl-tRNA synthetase:glycyl-tRNA synthetase			pir:B70146			B70146
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
978432_c1_314	3696	8918	357	1074		
Protein name			Locus Name			Acc#
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9843876_f2_99	3697	8919	196	591		
Protein name			Locus Name			Acc#
Description						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9940957_c1_325	3698	8920	260	783	233	1.8e-19

Protein name

Locus Name

Acc#

sp:YBBF_HAEIN

P44046

Description

HYPOTHETICAL PROTEIN HI0735

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10337833_c2_266	3699	8921	123	372	116	7.8e-06

Protein name

Locus Name

Acc#

sp:FAS_PNECA

P29251

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10625043_c3_280.....	3700	8922	336	1011	329	1.2e-29

Protein name

Locus Name

Acc#

hemin permease

gp:YEHEMSTUV

X77867

Description

Y.enterocolitica hemS, hemT, hemU and hemV genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12616700_c2_253.....	3701	8923	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12629665_c1_202	3702	8924	350	1053		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12713383_f1_3	3703	8925	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13102149_c1_172	3704	8926	199	600	421	2.1e-39

Protein name

Locus Name

Acc#

sp:YLCA_ECOLI

P77380

Description

PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN YLCA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1350942_f1_20	3705	8927	90	273		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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14179057_f1_44	3706	8928	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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14494061_f3_166.....	3707	8929	236	711	228	6.1e-19
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Protein name

Locus Name

Acc#

precorrin-2 methyltransferase, :protein
slr1879:protein slr1879

pir:S77131

S77131

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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14502316_c2_234.....	3708	8930	60	183	49	0.046
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Protein name

Locus Name

Acc#

sp:Y031_TREPA

O83074

Description

HYPOTHETICAL PROTEIN TP0031

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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15078450_c2_270.....	3709	8931	492	1479	829	1.2e-82
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Protein name

Locus Name

Acc#

putative efflux pump component MtrF

gp:AF176820

AF176820

Description

Neisseria gonorrhoeae strain FA19 putative efflux pump componentMtrF (mtrF) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16839502_c2_250	3710	8932	240	723	251	2.2e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PAB0910	pir:B75048	B75048

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16853403_c3_279	3711	8933	73	222		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19553813_f2_91	3712	8934	163	492	376	1.3e-34

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

sp:PYRI_PYRAB	P77919
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Description

ASPARTATE CARBAMOYLTRANSFERASE REGULATORY CHAIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20428526_f3_152	3713	8935	198	597	186	1.7e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

hypothetical protein PH0856	pir:D71136	D71136
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20839062_f3_157	3714	8936	682	2049	310	7.4e-25

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

histidine kinase sensor protein (barA) RP229	pir:B71677	B71677
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Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21978425_f3_150	3715	8937	310	933	92	0.00087

Protein name

Locus Name

Acc#

gp:D42067

D42067

Description

Porphyromonas gingivalis DNA for Fimbrillin, ORF1-4, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22272061_f3_131	3716	8938	317	954	783	9.4e-78

Protein name

Locus Name

Acc#

sp:KPRS_HELPY

P56184

Description

PYROPHOSPHATE SYNTHETASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22375437_f2_90	3717	8939	94	285		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22539002_c1_177	3718	8940	388	1167	269	9.3e-22

Protein name

Locus Name

Acc#

sp:Y878_METJA

Q58288

Description

HYPOTHETICAL PROTEIN MJ0878

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22656925_c1_218	3719	8941	789	2370	459	5.7e-76

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
penicillin binding protein 1A	pir:F70355	F70355

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23456506_f1_22	3720	8942	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23473387_f1_2	3721	8943	208	627	115	0.00026

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

hypothetical protein BBI16	pir:G70241	G70241
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23652250_c3_301	3722	8944	198	597		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24410937_f3_118	3723	8945	137	414	169	1.1e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

structural protein P5	gp:AF155037	AF155037
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Description

Alteromonas phage, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24495875_f2_93	3724	8946	259	780		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24626325_c3_315.....	3725	8947	1496	4491	157	5.2e-08

Protein name

Locus Name

Acc#

putative histidine kinase

gp:AF036964

AF036964

Description

Lactobacillus sake putative response regulator (rrp1) and putative histidine kinase (hpk1) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640875_c1_219.....	3726	8948	329	990	234	5.4e-18

Protein name

Locus Name

Acc#

processing proteinase sll2009:protein
sll2009:protein sll2009

pir:S77156

S77156

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640938_f2_85.....	3727	8949	318	957	829	1.2e-82

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF088897

Description

Zymomonas mobilis cosmid clone 65G3, partial sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24642257_f1_35	3728	8950	238	717		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644067_c1_180	3729	8951	344	1035	469	1.8e-44

Protein name

Locus Name

Acc#

ferric enterobactin transport ATP-binding

gp:U67531

Description

Methanococcus jannaschii section 73 of 150 of the complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24647032_c3_294	3730	8952	725	2178		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24647186_f1_34	3731	8953	428	1287	1159	1.3e-117

Protein name

Locus Name

Acc#

sp:GLYA_ECOLI

P00477

Description

(SHMT)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2519010_f1_31	3732	8954	467	1404	110	0.0040
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
53kDa major outer membrane protein			gp:D31835		D31835	
<u>Description</u>						
Porphyromonas gingivalis DNA for 53kDa major outer membraneprotein, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25429811_c3_274	3733	8955	468	1407	334	1.5e-31
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
LisK			gp:AF139908		AF139908	
<u>Description</u>						
Listeria monocytogenes lisR/lisK gene locus, complete sequence.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25970057_f1_33	3734	8956	312	939	838	1.4e-83
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:PYRE_VIBS2		P96174	
<u>Description</u>						
TRANSCARBAMYLASE) (ATCASE)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26370312_f3_162	3735	8957	300	903	345	2.4e-31
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable dTDP-4-dehydrorhamnose reductase APE1179			pir:G72588		G72588	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26595887_c1_224	3736	8958	244	735	166	2.3e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable two-component system response transcription regulator	pir:T36499	T36499

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26680261_f3_161	3737	8959	181	546		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
27175_c2_236	3738	8960	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
287518_f2_87	3739	8961	75	228		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29789211_f3_146	3740	8962	72	219		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3008468_f3_116	3741	8963	318	957		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31439062_f1_21.....	3742	8964	447	1344	97	0.010

Protein name

Locus Name

Acc#

VirM

gp:ATTIA6NC1

AF039888

Description

Agrobacterium tumefaciens plasmid pTIA6NC VirM (virM) and VirL(virL) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31667587_f2_81.....	3743	8965	451	1356		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32228437_g3_285.....	3744	8966	706	2121	171	2.4e-15

Protein name

Locus Name

Acc#

unknown

gp:AF007381

AF007381

Description

Flavobacterium johnsoniae gliding motility protein (gldA) gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32229687_c1_217	3745	8967	160	483	91	0.00022

Protein name

Locus Name

Acc#

sp:IHFA_HAEIN

P43723

Description

INTEGRATION HOST FACTOR ALPHA-SUBUNIT (IHF-ALPHA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33465_c3_275	3746	8968	233	702	187	1.3e-14

Protein name

Locus Name

Acc#

sp:YVBG_BACSU

O32244

Description

HYPOTHETICAL 22.6 KD PROTEIN IN OPUCA-ENO INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34163936_f1_43	3747	8969	536	1611	440	2.1e-41

Protein name

Locus Name

Acc#

RprX

gp:S59000

S59000

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34275760_c3_310	3748	8970	135	408	147	2.2e-09

Protein name

Locus Name

Acc#

processing proteinase:protein slr1331:protein
slr1331

pir:S75528

S75528

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36040712_c3_292	3749	8971	107	324	101	8.5e-05

Protein name

Locus Name

Acc#

Hypothetical protein HI1452

gp:D90724

Description

Escherichia coli genomic DNA. (19.4 - 19.8 min).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
37575_c2_244	3750	8972	570	1713	1579	4.2e-162

Protein name

Locus Name

Acc#

sp:FTHS_CLOAC

P13419

Description

SYNTHETASE) (FHS) (FTHFS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4007776_f2_84	3751	8973	1095	3288	475	9.6e-78

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4409550_c2_249	3752	8974	74	225	125	5.0e-08

Protein name

Locus Name

Acc#

hypothetical protein PH0719

pir:H71118

H71118

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4484812_c2_267	3753	8975	407	1224	549	5.9e-53

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein slr1485	pir:S74454	S74454

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4727126_f3_117	3754	8976	112	339		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4860263_f2_113	3755	8977	154	465		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4882187_c3_316	3756	8978	390	1173	276	7.8e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

transposase	gp:AF038866	AF038866
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Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4957677_f3_160	3757	8979	266	801		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

5116285_f2_112	3758	8980	585	1758	258	2.8e-21
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Protein name

Locus Name

Acc#

sp:PA1G_HUMAN

Q15102

Description

SUBUNIT) (PAF-AH GAMMA SUBUNIT)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

546942_c3_293	3759	8981	79	240		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

6538182_c1_179	3760	8982	106	321	183	8.2e-14
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Protein name

Locus Name

Acc#

sp:BTUC_ECOLI

Description

VITAMIN B12 TRANSPORT SYSTEM PERMEASE PROTEIN BTUC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6679652_f2_78	3761	8983	288	867	338	1.3e-30

Protein name

Locus Name

Acc#

sp:KDSB_HAEIN

P44490

Description

SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9881327_f3_145	3762	8984	704	2115		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
191552_f1_2	3763	8985	159	477	222	1.2e-17

Protein name

Locus Name

Acc#

probable phospho-sugar mutase 2

pir:E71082

E71082

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19812812_c1_4	3764	8986	136	408		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

3957142_f1_1	3765	8987	76	231		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

10322187_f1_86	3766	8988	219	660		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	-----------	-----------	-------	-------------

1054553_g2_428	3767	8989	360	1083	368	8.9e-34
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Protein name

Locus Name

Acc#

conserved hypothetical protein aq_1630

pir:F70440

F70440

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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10557192_f1_32	3768	8990	78	237		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11726391_c3_547	3769	8991	154	465	538	8.6e-52

Protein name

Locus Name

Acc#

putative UDP-GlcNAc:undecaprenylphosphate

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1178127_f1_9	3770	8992	374	1125	972	8.8e-98

Protein name

Locus Name

Acc#

sp:AROC_SYNY3

P23353

Description

PHOSPHOLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1226412_f2_170.....	3771	8993	370	1113	160	6.6e-09

Protein name

Locus Name

Acc#

GumF protein

pir:S67855

S67855

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12363467_f2_195.....	3772	8994	158	477		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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13009675_c3_590	3773	8995	913	2742		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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14548187_c2_452	3774	8996	376	1131	136	2.0e-08
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Protein name

Locus Name

Acc#

sp:VAPI_BACNO

Q46560

Description

VIRULENCE-ASSOCIATED PROTEIN I

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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14645152_f1_111	3775	8997	64	195		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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14728887_f2_213	3776	8998	412	1239	835	2.9e-83
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Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:H72377

H72377

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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14938777_c2_427	3777	8999	213	642		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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156500_c1_372	3778	9000	122	369	205	1.7e-16
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Protein name

Locus Name

Acc#

ribosomal protein S06

pir:G70305

G70305

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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15650915_f2_210	3779	9001	510	1533	311	4.2e-36
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Protein name

Locus Name

Acc#

hypothetical protein TM1421

pir:B72256

B72256

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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16446002_c3_545	3780	9002	801	2406	901	1.0e-101
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Protein name

Locus Name

Acc#

hypothetical protein Rv0584

pir:G70934

G70934

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16603388_c2_447	3781	9003	181	546	402	2.2e-37

Protein name

Locus Name

Acc#

BsaA

gp:AB013377

AB013377

Description

Bacillus halodurans C-125 comGB and bsaA genes and tRNA-His, Ala,Arg, Gly and Tyr genes, complete and partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
17010942_c1_337	3782	9004	787	2364	1111	1.6e-112

Protein name

Locus Name

Acc#

beta-galactosidase, :lactase

pir:JC5618

JC5618

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
176561_c1_416.....	3783	9005	359	1080	600	2.3e-58

Protein name

Locus Name

Acc#

hypothetical protein slr1772

pir:S74628

S74628

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
191552_c3_532.....	3784	9006	471	1416	687	1.4e-67

Protein name

Locus Name

Acc#

probable phospho-sugar mutase 2

pir:E71082

E71082

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20192257_f1_105	3785	9007	304	915	281	1.5e-24

Protein name

Locus Name

Acc#

gp:STALYTS

L42945

Description

Staphylococcus aureus lytS and lytR genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2031317_f1_99	3786	9008	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20509682_f1_82	3787	9009	293	882	162	1.3e-09

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-type ferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20523966_f2_208	3788	9010	369	1110	240	9.8e-18

Protein name

Locus Name

Acc#

sp:YEHU_ECOLI

Description

HYPOTHETICAL 62.1 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20704802_c1_402	3789	9011	465	1398	465	4.7e-44

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:G72220

G72220

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2110137_c1_359	3790	9012	118	357		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22114756_f1_31	3791	9013	532	1599	512	4.9e-49

Protein name

Locus Name

Acc#

hypothetical protein jhp1110

pir:A71849

A71849

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22300006_f1_33	3792	9014	169	510	81	0.0040

Protein name

Locus Name

Acc#

DbhB

gp:AF110185

AF110185

Description

Burkholderia pseudomallei strain 1026b DbhB (dbhB), general secretory pathway protein D (gspD), general secretory pathway protein E (gspE), general secretory pathway protein F (gspF), GspC (gspC), general secretory pathway protein G (gspG), general secretory pathway protein H (gspH), general secretory pathway protein I (gspI), general secretory pathway protein J

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22910052_f3_310	3793	9015	145	438	290	3.2e-24

Protein name

Locus Name

Acc#

sp:HELA_LEGPN

Q48815

Description

HELA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22915938_c1_408	3794	9016	240	723	86	0.0040

Protein name

Locus Name

Acc#

hypothetical protein APE0978

pir:B72695

B72695

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23470135_f3_270.....	3795	9017	779	2340	695	7.6e-108

Protein name

Locus Name

Acc#

sp:HEXA_PORGI

P49008

Description

(BETA-NAHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23538425_f3_285.....	3796	9018	580	1743	561	1.4e-62

Protein name

Locus Name

Acc#

long-chain-fatty-acid CoA ligase

pir:D70386

D70386

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23601701_f3_289	3797	9019	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23625912_f3_280.....	3798	9020	477	1434	127	2.8e-07

Protein name

Locus Name

Acc#

gp:YPI02KB

AL031866

Description

Yersinia pestis 102 kbases unstable region: from 1 to 119443.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23627187_c1_420.....	3799	9021	423	1272	158	1.0e-08

Protein name

Locus Name

Acc#

sp:FECD_ECOLI

P23485

Description

FECD PROTEIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23945430_c3_604.....	3800	9022	743	2232	228	1.0e-27

Protein name

Locus Name

Acc#

conserved hypothetical protein ylbK

pir:H69874

H69874

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24072712_c3_613	3801	9023	196	591	138	2.1e-09

Protein name

Locus Name

Acc#

hypothetical protein sll0687

pir:S74416

S74416

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24391562_t3_272.....	3802	9024	437	1314	327	2.0e-29
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Protein name

Locus Name

Acc#

N-acetylmuramoyl-L-alanine amidase

pir:G70445

G70445

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24398402_c3_564.....	3803	9025	98	297	225	1.3e-18
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Protein name

Locus Name

Acc#

sp:RS18_BACST

P10806

Description

30S RIBOSOMAL PROTEIN S18 (BS21)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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24407802_c3_617.....	3804	9026	447	1344	164	1.0e-08
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Protein name

Locus Name

Acc#

sp:NANH_MICVI

Q02834

Description

SIALIDASE PRECURSOR, (NEURAMINIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24615811_f1_10	3805	9027	458	1377	1028	1.0e-103
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ArgE/DapE/Acy1 family protein			pir:E75324		E75324	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24645311_f1_52.....	3806	9028	299	900	147	6.9e-08
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein aq_1533			pir:A70433		A70433	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648437_f1_103.....	3807	9029	297	894	211	1.0e-15
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
acriflavin resistance protein AcrE			pir:A70361		A70361	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24650287_c3_534.....	3808	9030	400	1203		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24660412_f3_325.....	3809	9031	350	1053	609	2.6e-59
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein TM1269			pir:D72274		D72274	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24706575_c2_496	3810	9032	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24707287_c1_376.....	3811	9033	349	1050	894	1.6e-89

Protein name

Locus Name

Acc#

gp:PGU60208

U60208

Description

Porphyromonas gingivalis orf1, orf2 and orf3 genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24804187_f2_179.....	3812	9034	76	231	91	0.0011

Protein name

Locus Name

Acc#

sodium channel protein

gp:DVU26718

U26718

Description

Drosophila virilis sodium channel protein (para) gene, exons1,2,3,4, and optional segment i, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24806501_f2_190.....	3813	9035	146	441	71	0.038

Protein name

Locus Name

Acc#

hypothetical protein BBA32

pir:H70210

H70210

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2533590_f2_196	3814	9036	82	249	68	0.034

Protein name

Locus Name

Acc#

cellulose synthase

pir:I39714

I39714

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25431562_c1_371.....	3815	9037	237	714	1212	3.2e-123

Protein name

Locus Name

Acc#

rprY protein

pir:S33662

S33662

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25520626_c1_375.....	3816	9038	449	1350	776	5.2e-77

Protein name

Locus Name

Acc#

sp:YQEV_BACSU

P54462

Description

HYPOTHETICAL 51.7 KD PROTEIN IN DNAJ-RPSU INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25674157_c1_378.....	3817	9039	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25975012_c1_393.....	3818	9040	311	936	158	4.8e-09

Protein name

Locus Name

Acc#

sodium-dependent transporter homolog yocS

pir:E69902

E69902

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2626655_c2_462	3819	9041	159	480		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26306507_c3_607.....	3820	9042	633	1902	1817	2.5e-187
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

sp:MUTB_PORGI Q59676

Description

METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT, (MCM-ALPHA)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26366555_f3_326.....	3821	9043	476	1431	1177	1.7e-119
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

hypothetical protein TM1267

pir:B72274 B72274

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26370302_f2_152.....	3822	9044	449	1350	1232	2.5e-125
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

sp:G6PA_BACST P13375

Description

ISOMERASE A)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26642932_c2_450	3823	9045	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2864693_f3_306.....	3824	9046	442	1329	340	3.5e-62

Protein name

Locus Name

Acc#

sp:QUEA_ECOLI

P21516

Description

(QUEUOSINE BIOSYNTHESIS PROTEIN QUEA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29423910_c2_522.....	3825	9047	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31260938_f3_261.....	3826	9048	591	1776	1242	2.1e-126

Protein name

Locus Name

Acc#

sp:SYK_BACSU

P37477

Description

LYSYL-TRNA SYNTHETASE, (LYSINE--TRNA LIGASE) (LYSRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31289536_f2_164	3827	9049	110	333	83	0.0014

Protein name

Locus Name

Acc#

cytochrome oxidase I

gp:AF072662

AF072662

Description

Exoneurella eremophila cytochrome oxidase I gene, mitochondrial gene encoding mitochondrial protein, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31428541_f3_292	3828	9050	183	552	126	5.7e-06

Protein name

Locus Name

Acc#

sp:YHA2_EIKCO

P35649

Description

HYPOTHETICAL 66.3 KD PROTEIN IN HAG2 5' REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31755000_f1_29	3829	9051	567	1704	1079	4.0e-109

Protein name

Locus Name

Acc#

sp:YIDE_HAEIN

P44472

Description

HYPOTHETICAL PROTEIN HI0035

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31808567_c3_568	3830	9052	311	936	160	3.1e-09

Protein name

Locus Name

Acc#

probable lipid A biosynthesis acyltransferase

pir:H71954

H71954

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33397175_c2_529	3831	9053	633	1902		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33787877_c1_358.....	3832	9054	354	1065	122	0.00032
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

MutS-like protein

gp:SATRXA

AJ223480

Description

Staphylococcus aureus trxA and uvrC genes and partial mutS and dhsCgenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3385890_c3_587.....	3833	9055	161	486	99	0.0018
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

hypothetical protein C56G2.15

pir:T15873

T15873

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34165912_f3_307.....	3834	9056	177	534	175	2.5e-13
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

probable isomerase

pir:B70986

B70986

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34406303_f1_87.....	3835	9057	191	576		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34411051_f3_300	3836	9058	728	2187	134	5.3e-07

Protein name

Locus Name

Acc#

gp:PGU60208

U60208

Description

Porphyromonas gingivalis orf1, orf2 and orf3 genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34417142_c1_414	3837	9059	717	2154	3088	0.0

Protein name

Locus Name

Acc#

sp:MUTA_PORGI

Q59677

Description

METHYLMALONYL-COA MUTASE BETA-SUBUNIT, (MCB-BETA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35661441_f3_251.....	3838	9060	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36134657_f1_90.....	3839	9061	201	606	300	1.4e-26

Protein name

Locus Name

Acc#

hypothetical protein PAB0910

pir:B75048

B75048

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
37562_c2_530	3840	9062	912	2736	506	5.4e-56

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
37785_c3_611.....	3841	9063	264	795	107	0.00081

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein SCE39.30	pir:T36240	T36240

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3944087_c2_451.....	3842	9064	392	1179	153	4.9e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein c0115	pir:S74051	S74051

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4068777_c2_463.....	3843	9065	578	1737	801	6.8e-84

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:EFG_THETH	P13551

Description

ELONGATION FACTOR G (EF-G)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4078910_c3_614	3844	9066	1175	3528	519	8.8e-60
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
receptor antigen (RagA)			gp:PGI130872		AJ130872	
<u>Description</u>						
Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
41562_c3_571	3845	9067	66	201		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
426657_c3_612.....	3846	9068	144	435	268	8.6e-22
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
proline/pyrroline-5-carboxylate dehydrogenase			pir:B71980		B71980	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4329428_f3_265.....	3847	9069	245	738	255	8.4e-22
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:YFBT_ECOLI				P77625	
<u>Description</u>						
HYPOTHETICAL 23.7 KD PROTEIN IN LRHA-ACKA INTERGENIC REGION						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4378530_f1_21	3848	9070	485	1458	468	2.2e-44

Protein name

Locus Name

Acc#

probable glycosyl hydrolase

pir:T36467

T36467

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4532885_c3_593	3849	9071	171	516	96	0.0057

Protein name

Locus Name

Acc#

putative outer surface protein

gp:BBU80960

Description

Borrelia burgdorferi strain CA12 putative outer membrane protein(ospE) gene, complete cds and putative outer surface protein (ospF)gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4551635_f1_102	3850	9072	1285	3858	1850	1.7e-192

Protein name

Locus Name

Acc#

czrA protein

gp:PACZR

Y14018

Description

Pseudomonas aeruginosa czrR, czrC, czrB, czrA genes, ORF5 andpartial ORF6.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4698910_f3_275	3851	9073	892	2679	476	3.4e-78

Protein name

Locus Name

Acc#

ribonucleoside-diphosphate reductase, large chain nrd

pir:G69457

G69457

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4704675_f2_169	3852	9074	905	2718	1036	2.5e-145

Protein name

Locus Name

Acc#

4-alpha-glucanotransferase homolog T20B5.4

pir:T00748

T00748

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4804537_f1_65	3853	9075	149	450	197	1.2e-15
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Protein name

Locus Name

Acc#

sp:FOLB_BACSU

P28823

Description

DIHYDRONEOPTERIN ALDOLASE, (DHNA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4867188_c1_415	3854	9076	719	2160	883	2.4e-88
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Protein name

Locus Name

Acc#

sp:TOP3_HAEIN

P43704

Description

DNA TOPOISOMERASE III,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4882287_f2_188	3855	9077	385	1158	599	2.9e-58
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Protein name

Locus Name

Acc#

coproporphyrinogen oxidase, III,
oxygen-independent hemN

pir:B69640

B69640

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4892261_c2_466	3856	9078	155	468	271	1.7e-23

Protein name Locus Name Acc#
 ribosomal protein L09 pir:B70475 B70475

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4897125_f3_262.....	3857	9079	334	1005	403	1.7e-37

Protein name Locus Name Acc#
 sp:GPDA_BACSU P46919

Description

DEPENDENT DIHYDROXYACETONE-PHOSPHATE REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4975625_f1_91.....	3858	9080	128	387		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5117763_c1_389.....	3859	9081	261	786	287	3.4e-25

Protein name Locus Name Acc#
 probable reductase APE1044 pir:E72703 E72703

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5859380_f3_288	3860	9082	173	522	136	3.4e-09

Protein name

Locus Name

Acc#

unknown

gp:AF095748

AF095748

Description

Burkholderia cepacia principal sigma factor (sigA), phthalatedioxygenase reductase (ophA1), putative phthalate permeaseN-terminal region, putative phthalate permease C-terminal region(ophD), 4,5-dihydroxyphthalate decarboxylase (ophC),phthalate-inducible quinolinate phosphoribosyl transferase (ophE),transposase (tnp), phthalate dihydrodiol dehydrogenase

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5866512_c3_531	3861	9083	226	681		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6031717_c1_370	3862	9084	154	465	321	6.3e-28

Protein name

Locus Name

Acc#

translation elongation factor G

pir:H72227

H72227

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6136675_c3_561	3863	9085	527	1584	2624	7.7e-273

Protein name

Locus Name

Acc#

RprX

gp:S59000

S59000

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
625087_f1_53	3864	9086	488	1467	700	8.9e-78
Protein name			Locus Name			Acc#
			sp:DNAA_BACSU			P05648
Description						
CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6447131_f1_44	3865	9087	221	666	669	1.1e-65
Protein name			Locus Name			Acc#
			sp:UNG_HUMAN			P13051
Description						
URACIL-DNA GLYCOSYLASE PRECURSOR, (UDG)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6454837_c2_477	3866	9088	176	531	352	4.4e-32
Protein name			Locus Name			Acc#
methylglyoxal synthase			pir:G72284			G72284
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6829387_f2_189	3867	9089	189	570	176	2.0e-13
Protein name			Locus Name			Acc#
probable RNA polymerase sigma-24 factor (rpoE)			pir:E71368			E71368
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6837762_c2_502	3868	9090	179	540	167	1.8e-12

Protein name

Locus Name

Acc#

sp:Y778_METJA

Q58188

Description

HYPOTHETICAL PROTEIN MJ0778

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
954787_f1_43	3869	9091	375	1128	828	1.6e-82

Protein name

Locus Name

Acc#

sp:ASNA_HAEIN

P44338

Description

ASPARTATE--AMMONIA LIGASE, (ASPARAGINE SYNTHETASE A)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9782217_f2_145.....	3870	9092	211	636	84	0.047

Protein name

Locus Name

Acc#

sp:Y804_HAEIN

P44053

Description

HYPOTHETICAL PROTEIN HI0804

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11720063_c3_96.....	3871	9093	519	1560	695	2.0e-68

Protein name

Locus Name

Acc#

alpha galactosidase precursor

gp:AF061331

AF061331

Description

Saccharopolyspora erythraea alpha galactosidase precursor (melA) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12688787_f3_50	3872	9094	167	504	215	1.4e-17
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
cytidine deaminase			gp:BCA237979			AJ237979
<u>Description</u>						
Bacillus caldolyticus cdd gene for cytidine deaminase.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12773337_c1_77	3873	9095	426	1281	142	1.1e-06
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
conserved hypothetical protein yknZ			pir:E69858			E69858
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13845217_f3_57	3874	9096	81	246		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14569175_f3_55	3875	9097	329	990	401	2.8e-37
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
unknown			gp:AF083252			AF083252
<u>Description</u>						
Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilinbiosynthetic protein (fimL) gene, complete cds; and unknown gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21665630_f2_34	3876	9098	213	642	448	3.0e-42

Protein name

Locus Name

Acc#

sp:YKGB_HAEIN

P44577

Description

HYPOTHETICAL PROTEIN HI0219

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22144041_f2_33	3877	9099	287	864	233	1.8e-19

Protein name

Locus Name

Acc#

PobR protein

gp:PPU251792

AJ251792

Description

Pseudomonas putida pobR gene for PobR protein and pobA gene forPobA protein.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22305443_c3_94	3878	9100	478	1437	123	0.00026

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase,B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2379442_f1_13	3879	9101	467	1404	970	1.4e-97

Protein name

Locus Name

Acc#

sp:YKGC_ECOLI

P77212

Description

INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24095327_c3_106	3880	9102	299	900	627	3.2e-61
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hemagglutinin	gp:AF017417				AF017417	
<u>Description</u>						
Prevotella intermedia hemagglutinin (phg) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24642687_c1_66	3881	9103	300	903	547	9.5e-53
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:DCHS_CLOPE				P04194	
<u>Description</u>						
HISTIDINE DECARBOXYLASE PROENZYME PRECURSOR, (PI CHAIN)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24719017_c3_95	3882	9104	156	471		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2587908_c3_109	3883	9105	430	1293	182	4.2e-11
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
YvrN protein	gp:BS43KBDNA				AJ223978	
<u>Description</u>						
Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26595051_c3_108	3884	9106	417	1254	184	1.7e-11
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein aq_294			pir:H70326			H70326
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30504157_f2_35	3885	9107	531	1596	779	2.5e-77
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
putative ABC transporter ATP-binding protein			gp:SCF56			AL133424
<u>Description</u>						

Streptomyces coelicolor cosmid F56.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36462776_c1_64	3886	9108	112	339		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4306268_f3_61	3887	9109	63	192	72	0.020
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
ORF MSV147 hypothetical protein			gp:AF063866			AF063866
<u>Description</u>						

Melanoplus sanguinipes entomopoxvirus, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
676677_c3_93	3888	9110	194	585	159	3.0e-10
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
receptor antigen (RagA)	gp:PGI130872				AJ130872	
<u>Description</u>						
Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
975050_c1_78	3889	9111	160	480		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1197324_c1_98.....	3890	9112	155	468	267	8.0e-23
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
endo-beta-galactosidase	gp:AF083896				AF083896	
<u>Description</u>						
Flavobacterium keratolyticus endo-beta-galactosidase gene, completecds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11975307_c3_184.....	3891	9113	71	216	230	3.7e-19
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
rubredoxin	pir:H72348				H72348	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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14354208_c3_195	3892	9114	423	1272		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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15712683_f2_69.....	3893	9115	66	201		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16617135_c3_177.....	3894	9116	70	213		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16914077_f3_94.....	3895	9117	262	789	147	4.3e-10
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Protein name

Locus Name

Acc#

ORF8

gp:D78257

D78257

Description

Enterococcus faecalis plasmid pYI17 genes for BacA, BacB, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21660966_c2_163	3896	9118	140	423	112	2.4e-05
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
unknown	gp:AF116463				AF116463	
<u>Description</u>						
Streptomyces lincolnensis putative regulatory protein WdIA (wdIA) gene, complete cds; and unknown gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21756552_f2_67	3897	9119	217	654		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22270327_c2_130.....	3898	9120	304	915	332	5.8e-30
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein slr1534	pir:S75855				S75855	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22360900_c1_124.....	3899	9121	64	195		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23446055_c1_116	3900	9122	610	1833		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23697132_f2_49	3901	9123	646	1941		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24275380_c2_167	3902	9124	188	567	483	5.8e-46
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
phosphoribosylaminoimidazole carboxylase (pure) PAB1077			pir:B75013		B75013	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24407530_f1_8	3903	9125	157	474		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24409383_f1_31	3904	9126	214	645	234	1.4e-19
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical 23.5K protein (glnA-fdhE intergenic region):hypothetical protein o206			pir:S40829			
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2461693_f1_18.....	3905	9127	612	1839	127	1.6e-13
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein SC6C5.12c SC6C5.12c			pir:T35483		T35483	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648516_c1_114.....	3906	9128	559	1680	1192	4.3e-121
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
uridine kinase-related protein			pir:B72341		B72341	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24666412_f2_64.....	3907	9129	333	1002	527	1.3e-50
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
riboflavin kinase			pir:D70313		D70313	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25682030_f1_1	3908	9130	185	558	310	1.2e-27
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:F72424		F72424	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29861251_c1_115	3909	9131	526	1581	224	1.1e-15
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
sensor histidine kinase			pir:A72383		A72383	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30126500_f2_63	3910	9132	562	1689	664	2.4e-64
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:ATC1_DICDI		P54678	
<u>Description</u>						

CATION-TRANSPORTING ATPASE PAT1,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30509632_f1_28	3911	9133	575	1728	568	3.1e-54
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
sensory transduction histidine kinase slr2104:protein slr2104:protein slr2104			pir:S75136		S75136	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31674158_f1_17	3912	9134	90	273		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31835967_f2_47	3913	9135	515	1548	411	1.1e-50

Protein name Locus Name Acc#
 aminopeptidase gp:AF041033 AF041033

Description
 Shigella flexneri aminopeptidase (pepP) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32219042_c3_196	3914	9136	496	1491	496	2.4e-47

Protein name Locus Name Acc#
 sp:RP54_ACICA P33983

Description
 RNA POLYMERASE SIGMA-54 FACTOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33390937_f3_95	3915	9137	80	243	267	4.5e-23

Protein name Locus Name Acc#
 transcription regulator homolog yozG pir:C69931 C69931

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33992212_c3_199	3916	9138	490	1473	665	3.0e-65

Protein name Locus Name Acc#
 gcpe protein pir:E72087 E72087

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34486592_f2_51	3917	9139	224	675		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35441251_c1_99.....	3918	9140	389	1170	190	2.6e-12
Protein name			Locus Name		Acc#	
			sp:QPCT_HUMAN			
Description						

(GLUTAMINYL-TRNA CYCLOTRANSFERASE) (GLUTAMINYL CYCLASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36413327_f1_30.....	3919	9141	348	1047	538	2.7e-64
Protein name			Locus Name		Acc#	
calcium motive P-type ATPase			gp:AF145282		AF145282	
Description						

Trichomonas vaginalis calcium motive P-type ATPase (CA-2) gene,partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4328175_c1_100.....	3920	9142	145	438	251	2.2e-21
Protein name			Locus Name		Acc#	
			sp:YE19_SYNY3		P74523	
Description						

HYPOTHETICAL 17.7 KD PROTEIN SLR1419

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4334562_c3_198	3921	9143	130	393	339	1.0e-30

Protein name

Locus Name

Acc#

sp:GCSH_ECOLI

P23884

Description

GLYCINE CLEAVAGE SYSTEM H PROTEIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4475705_f1_14	3922	9144	180	543		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4724062_c3_197	3923	9145	235	708	157	2.0e-11

Protein name

Locus Name

Acc#

sp:Y61A_METJA

P81310

Description

HYPOTHETICAL PROTEIN MJ0611.1

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
81887_c1_128	3924	9146	230	693	356	4.6e-36

Protein name

Locus Name

Acc#

hypothetical protein gcpe

pir:E71562

E71562

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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9782828_f2_52	3925	9147	145	438		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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9929832_f3_89	3926	9148	565	1698	739	4.3e-73
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Protein name

Locus Name

Acc#

conserved hypothetical integral membrane protein TP0771

pir:H71283

H71283

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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10003452_c3_632	3927	9149	551	1656	338	1.2e-27
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Protein name

Locus Name

Acc#

sp:YICI_ECOLI

Description

HYPOTHETICAL 88.1 KD PROTEIN IN GLTS-SELC INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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100400_c2_481	3928	9150	108	327		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10188427_f3_266	3929	9151	72	219	103	8.7e-05

Protein name	Locus Name	Acc#
transposase	gp:AF038866	AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10291393_f1_12	3930	9152	464	1395	800	1.5e-79

Protein name	Locus Name	Acc#
	sp:Y260_SYNY3	P74409

Description

HYPOTHETICAL 49.2 KD PROTEIN SLL0260

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10719385_f3_318.....	3931	9153	97	294		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10739387_f3_330.....	3932	9154	469	1410	263	2.1e-20

Protein name	Locus Name	Acc#
transposase	gp:AF038866	AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10739526_c1_416	3933	9155	713	2142	837	2.9e-110
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
alpha-glucosidase	gp:BTU66897				U66897	
<u>Description</u>						
Bacteroides thetaiotaomicron neopullulanase (susA) and alpha-glucosidase (susB) genes, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10979675_f1_20	3934	9156	620	1863	174	2.4e-09
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
probable purine NTPase PAB0812	pir:F75103				F75103	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11016386_f1_116.....	3935	9157	74	225		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
112686_f1_13.....	3936	9158	169	510		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1209436_f2_211	3937	9159	391	1176	493	5.0e-47
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
immunoreactive 42kD antigen PG33	gp:AF175715				AF175715	
<u>Description</u>						
Porphyromonas gingivalis strain W50 immunoreactive 42kD antigenPG33 gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12316382_c2_553	3938	9160	167	504	477	2.5e-45
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
O-acetylhomoserine sulfhydrylase	pir:D72324				D72324	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12516930_f3_291.....	3939	9161	60	183		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12582785_f3_281.....	3940	9162	68	207		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12690927_c3_555	3941	9163	332	999	299	4.2e-36
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein F19D11.16:hypothetical protein F14M4.29:hypothetical protein F14M4.29			pir:T02689			
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12897701_c3_642.....	3942	9164	257	774	748	4.8e-74
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
O-acetylhomoserine sulfhydrylase			pir:D72324		D72324	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13835817_f3_315.....	3943	9165	64	195		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14063318_f2_207.....	3944	9166	60	183	129	1.9e-08
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein PH1147			pir:E71056		E71056	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14156287_f3_255	3945	9167	445	1338	168	4.4e-09
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			gp:PGU60208			U60208
<u>Description</u>						
Porphyromonas gingivalis orf1, orf2 and orf3 genes, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14463437_c3_592	3946	9168	234	705	200	5.6e-16
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein ycgF			pir:A69758			A69758
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14745312_f3_290.....	3947	9169	103	312	77	0.013
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
NADH dehydrogenase subunit 2			gp:AF160864			AF160864
<u>Description</u>						
Tetrahymena pyriformis mitochondrial DNA, complete genome.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15079802_f1_100.....	3948	9170	106	321		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15631502_f1_99	3949	9171	442	1329	300	1.2e-33
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:YHCG_ECOLI				P45423	
<u>Description</u>						
HYPOTHETICAL 43.3 KD PROTEIN IN GLTF-NANT INTERGENIC REGION (O375)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15707788_c2_535	3950	9172	268	807	386	1.1e-35
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
transposase	gp:AF038866				AF038866	
<u>Description</u>						
Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16229142_c2_509.....	3951	9173	75	228		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16493968_c1_455.....	3952	9174	331	996	204	3.4e-16
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:XYNC_CALSA				P23553	
<u>Description</u>						
ACETYL ESTERASE, (ACETYLXYLOSIDASE)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16594202_f1_73	3953	9175	62	189		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f3_339.....	3954	9176	431	1296	1723	2.3e-177
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
hypothetical protein				pir:JQ1020		JQ1020
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
187826_f3_271.....	3955	9177	746	2241	2313	6.9e-240
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:PFL_CLOPA		Q46266
<u>Description</u>						

FORMATE ACETYLTRANSFERASE, (PYRUVATE FORMATE-LYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1954562_c3_605.....	3956	9178	1111	3336	557	5.9e-55
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
115K outer membrane protein precursor:SusC protein				pir:JC6027		JC6027
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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19617202_c3_559	3957	9179	68	207		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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19706258_c2_541.....	3958	9180	76	231	143	4.0e-09
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Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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1987817_c1_388.....	3959	9181	79	240		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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20039010_c2_537.....	3960	9182	130	393		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20213303_c2_519	3961	9183	394	1185	161	7.1e-16

Protein name

Locus Name

Acc#

ATP-dependent activating enzyme

gp:PFFBSCEAB

Y09356

Description

Pseudomonas fluorescens fbsC, fbsE, fbsA and fbsB genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2031290_f1_25	3962	9184	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20319132_c2_523.....	3963	9185	354	1065	159	3.0e-10

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor (fiuI), transmembrane sensor (fiuR), and hydroxamate-type ferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20353400_f1_107.....	3964	9186	833	2502	801	1.2e-79

Protein name

Locus Name

Acc#

sp:MUS2_BACSU

P94545

Description

MUTS2 PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20801930_c2_505	3965	9187	512	1539	467	3.9e-51
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
amidophosphoribosyltransferase	pir:H69185				H69185	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2125277_f1_113.....	3966	9188	526	1581	2616	5.4e-272
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
alkyl hydroperoxide reductase subunit F	gp:AF129406				AF129406	
<u>Description</u>						

Bacteroides fragilis alkyl hydroperoxide reductase subunit C (ahpC) and alkyl hydroperoxide reductase subunit F (ahpF) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2146927_f1_11.....	3967	9189	282	849	410	3.1e-38
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
transcription regulator yggG	pir:G65078					
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21605288_f2_134.....	3968	9190	874	2625	93	0.0019
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein b2228	pir:B64993				B64993	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21722925_c2_496	3969	9191	95	288		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2187805_c2_507.....	3970	9192	64	195	75	0.019
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
putative transmembrane protein			gp:SCU96107		U96107	
<u>Description</u>						

Staphylococcus carnosus N5,N10-methylenetetrahydromethanopterinreductase homolog, SceB precursor (sceB) and putative transmembraneprotein genes, complete cds, and putative Na⁺/H⁺ antiporter NhaC(nhaC) gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2204407_f1_103.....	3971	9193	322	969	87	0.045
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:PRIM_LISMO		P47762	
<u>Description</u>						

DNA PRIMASE,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22289061_f2_142.....	3972	9194	106	321		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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22539088_c3_593	3973	9195	186	561		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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22689628_f2_204	3974	9196	72	219		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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22860128_f1_106	3975	9197	83	252	64	0.031
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Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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22928812_c1_441	3976	9198	65	198		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23445317_c1_458	3977	9199	310	933	721	3.5e-71
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein BB0682			pir:A70185		A70185	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23609517_c3_613.....	3978	9200	358	1077	508	1.3e-48
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:A00047		A00047	
<u>Description</u>						
E.coli mor gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23634701_c1_424.....	3979	9201	308	927	113	3.4e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
AmpG-signal transducer			gp:ECAMPG3		X82159	
<u>Description</u>						
E.coli ampG3 gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23640675_c1_364.....	3980	9202	165	498	101	0.0025
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein A208R			pir:T17698		T17698	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2378150_c3_595	3981	9203	532	1599	1332	6.2e-136

Protein name

Locus Name

Acc#

sp:RF3_ECOLI

P33998

Description

PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23945263_f3_275	3982	9204	257	774		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24093763_c1_398.....	3983	9205	417	1254	1298	2.5e-132

Protein name

Locus Name

Acc#

sp:PEPT_BACSU

P55179

Description

PEPTIDASE T, (AMINOTRIPEPTIDASE) (TRIPETIDASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24229677_c1_375.....	3984	9206	339	1020	1381	4.0e-141

Protein name

Locus Name

Acc#

class A beta-lactamase CFXA2 precursor

gp:AF118110

AF118110

Description

Prevotella intermedia class A beta-lactamase CFXA2 precursor(cfxA2) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24397187_c3_562	3985	9207	186	561		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24414026_f2_150.....	3986	9208	164	495	390	4.1e-36
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Protein name

Locus Name

Acc#

Dps

gp:AB025779

AB025779

Description

Porphyromonas gingivalis gene for Dps, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24429050_c1_403.....	3987	9209	769	2310	465	1.9e-43
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Protein name

Locus Name

Acc#

sp:YBAL_ECOLI

Description

HYPOTHETICAL 59.4 KD PROTEIN IN GSK-FSR INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24644637_c2_460.....	3988	9210	301	906	168	7.1e-10
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Protein name

Locus Name

Acc#

nucleotide pyrophosphatase homolog T16L4.210

pir:T09933

T09933

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24782792_c3_608	3989	9211	395	1188		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24804817_c3_607.....	3990	9212	246	741	123	3.2e-05
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					sp:EBA2_FLAME	P36912
<u>Description</u>						

(ENDOGLYCOSIDASE F2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24807812_f1_108.....	3991	9213	357	1074	528	9.8e-51
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
divalent cation transport-related protein					pir:H72360	H72360
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24822142_f2_226.....	3992	9214	190	573		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24848928_c1_459	3993	9215	66	201		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24849132_f3_335.....	3994	9216	374	1125		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2500052_c2_513.....	3995	9217	423	1272	376	1.3e-34
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

sp:YIDA_ECOLI

HYPOTHETICAL 29.7 KD PROTEIN IN IBPA-GYRB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25398385_c2_461.....	3996	9218	346	1041	262	1.5e-22
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

hypothetical protein F14F9.5

pir:T33774

T33774

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25422162_f1_5	3997	9219	278	837		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25580212_f1_97.....	3998	9220	76	231	78	0.034
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
HCG-1 protein				gp:AF044219		AF044219
<u>Description</u>						

Drosophila melanogaster HCG-1 protein (HCG-1) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25892062_c2_498.....	3999	9221	111	336	173	4.1e-13
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
thioredoxin-like protein				gp:ATAC010718		AC010718
<u>Description</u>						

Arabidopsis thaliana chromosome I BAC F28016 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25892187_c3_594.....	4000	9222	291	876	593	1.3e-57
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
probable dTDP-L-rhamnose synthase				pir:T31087		T31087
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26359635_c1_409	4001	9223	373	1122	280	1.9e-24
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:ENTC_ECOLI		P10377
<u>Description</u>						
ISOCHORISMATE SYNTHASE ENTC,						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26460003_c3_599	4002	9224	579	1740	454	6.8e-43
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:MEND_HABIN		P44612
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26461680_c3_580.....	4003	9225	351	1056	614	7.6e-60
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
probable zinc-containing dehydrogenase				pir:T36961		T36961
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26600327_c1_393.....	4004	9226	145	438	111	1.5e-06
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
ferric uptake regulation protein				pir:G72213		G72213
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26601677_c1_412	4005	9227	276	831	1012	5.1e-102

Protein name
 naphthoate synthase, menB:DHNA
 synthase: dihydroxynaphthoate
 synthase: dihydroxynaphthoic acid synthetase
Description

Locus Name
 pir:F69656
Acc#

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26604687_f2_133	4006	9228	134	405		

Protein name

Description

Locus Name

Acc#

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26604692_c3_621.....	4007	9229	161	486	239	1.1e-19

Protein name
 transposase
Description

Locus Name
 gp:AF038866
Acc#
 AF038866

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26820341_c3_603.....	4008	9230	331	996	140	9.2e-07

Protein name
 Hyp1 protein
Description

Locus Name
 gp:HVHYP1PRO
Acc#
 Y09797

H. vulgaris mRNA for Hyp1 protein.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29398290_f3_257	4009	9231	64	195	83	0.0053

Protein name Locus Name Acc#
 asparagine-rich protein (clone 28C6) pir:S14470 S14470
Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30079675_c3_583	4010	9232	805	2418	366	1.5e-31

Protein name Locus Name Acc#
 Sensor protein Rcsc (EC 2.7.3.-) gp:D90850
Description

E.coli genomic DNA, Kohara clone #373(49.5-49.9 min.)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30195142_c2_536	4011	9233	924	2775	323	8.8e-25

Protein name Locus Name Acc#
 hypothetical protein pir:C72285 C72285
Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30502255_f2_127	4012	9234	344	1035		

Protein name Locus Name Acc#
Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30572331_c1_430	4013	9235	115	348		

Protein name Locus Name Acc#
Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32478803_c2_552	4014	9236	110	333	80	0.033

Protein name

Locus Name

Acc#

sp:CPE1_BOVIN

018963

Description

CYTOCHROME P450 2E1, (CYP11E1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32523576_f1_82	4015	9237	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3319437_c3_628.....	4016	9238	173	522		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33210936_f1_46.....	4017	9239	214	645	163	4.7e-12

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33400263_c1_423	4018	9240	338	1017		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33786083_f3_338	4019	9241	483	1452	2084	1.3e-215
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
NBU1 mobilization protein mob				pir:A49901		A49901
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34026558_f1_36	4020	9242	65	198		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34509700_c1_422	4021	9243	137	414		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35157050_f2_227	4022	9244	327	984	236	8.6e-20
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
hypothetical protein PAB0040				pir:B75194		B75194
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35161302_c2_524	4023	9245	211	636	158	1.0e-10

Protein name

Locus Name

Acc#

sp:Y350_HAEIN

P24326

Description

HYPOTHETICAL PROTEIN HI0350 (ORF3)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36073591_c1_389	4024	9246	301	906	362	3.8e-33

Protein name

Locus Name

Acc#

sp:YZ09_MYCTU

Q10543

Description

HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE CY31.09,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36207933_c1_413.....	4025	9247	355	1068	175	1.1e-10

Protein name

Locus Name

Acc#

chloromuconate cycloisomerase homolog ykfB

pir:H69855

H69855

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36361002_f3_267.....	4026	9248	169	510		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3944688_f3_349	4027	9249	191	576	983	6.0e-99

Protein name Locus Name Acc#
 alkyl hydroperoxide reductase subunit C gp:AF129406 AF129406

Description
 Bacteroides fragilis alkyl hydroperoxide reductase subunit C (ahpC) and alkyl hydroperoxide reductase subunit F (ahpF) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3947562_c2_534	4028	9250	400	1203	758	4.2e-75

Protein name Locus Name Acc#
 transposase gp:AF038866 AF038866

Description
 Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4094563_f2_137	4029	9251	445	1338	128	5.1e-05

Protein name Locus Name Acc#
 hypothetical protein PH0922 pir:D71082 D71082

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4094687_c1_411	4030	9252	337	1014		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4094800_f3_344	4031	9253	405	1218	698	4.8e-83

Protein name

Locus Name

Acc#

sp:SDHL_STRCO

086564

Description

L-SERINE DEHYDRATASE, (L-SERINE DEAMINASE) (SDH) (L-SD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4504682_c1_402	4032	9254	250	753	131	1.4e-05

Protein name

Locus Name

Acc#

intracellular hyaluronic acid binding protein

gp:AF032862

AF032862

Description

Homo sapiens intracellular hyaluronic acid binding protein (IHABP)mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4719626_c2_508.....	4033	9255	592	1779		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4800926_f3_326.....	4034	9256	512	1539	356	5.6e-31

Protein name

Locus Name

Acc#

sp:GA6S_HUMAN

P34059

Description

(CHONDROITINASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4939000_c2_525	4035	9257	336	1011	1037	1.1e-104
Protein name			Locus Name		Acc#	
conserved hypothetical protein			pir:B72278		B72278	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5081927_c2_504	4036	9258	679	2040	1451	1.5e-148
Protein name			Locus Name		Acc#	
cation-transporting atpase, p-type (pacs) PAB0626			pir:E75141		E75141	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
510937_c1_365	4037	9259	171	516		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5117762_c3_616	4038	9260	422	1269	114	0.00075
Protein name			Locus Name		Acc#	
hypothetical protein F42G9.3			pir:T16348		T16348	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5167037_c3_606	4039	9261	518	1557		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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5273552_c3_639	4040	9262	148	447		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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5363816_c1_386	4041	9263	380	1143	104	0.0047
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Protein name

Locus Name

Acc#

gp:PFMAL3P7

Description

Plasmodium falciparum MAL3P7, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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584700_f3_263	4042	9264	90	273		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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6429643_c3_615	4043	9265	189	570	190	6.5e-15
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Protein name

Locus Name

Acc#

sp:RPOE_HAEIN

P44790

Description

RNA POLYMERASE SIGMA-E FACTOR (SIGMA-24)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6444077_f1_27	4044	9266	241	726	555	1.4e-53

Protein name

Locus Name

Acc#

sp:PFLA_ECOLI

P09374

Description

ACTIVATING ENZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7084675_f1_19	4045	9267	387	1164		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7109407...c3...586.....	4046	9268	135	408	253	1.4e-21

Protein name

Locus Name

Acc#

sp:YEAO_ECOLI

P76243

Description

HYPOTHETICAL 14.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
860927...c2...503.....	4047	9269	348	1047	668	1.4e-65

Protein name

Locus Name

Acc#

sp:YEIH_ECOLI

P33019

Description

HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
975780_f3_333	4048	9270	351	1056	93	0.0034
Protein name			Locus Name		Acc#	
troponin T, cardiac muscle:troponin T2			pir:TPHUTC			
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9927330_c3_627	4049	9271	63	192		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9954757_c3_561	4050	9272	189	570		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9959400_c1_399	4051	9273	367	1104	815	3.8e-81
Protein name			Locus Name		Acc#	
			sp:GCST_BACSU		P54378	
Description						

T PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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22438202_f2_1	4052	9274	74	222		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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10556942_f3_138.....	4053	9275	634	1905	411	5.6e-38
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Protein name

Locus Name

Acc#

inner membrane protein homolog

pir:A70155

A70155

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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11125291_f3_146.....	4054	9276	191	576	137	2.7e-09
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Protein name

Locus Name

Acc#

transcriptional regulator

gp:BSUB0017

Description

Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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12931502_f3_166.....	4055	9277	143	432	222	2.6e-18
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Protein name

Locus Name

Acc#

heat shock protein, class I

pir:D72385

D72385

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13860625_c2_279	4056	9278	113	342	78	0.0048
Protein name			Locus Name			Acc#
conserved hypothetical protein yulD			pir:F70014			F70014
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14564061_c1_196	4057	9279	438	1317	1171	7.2e-119
Protein name			Locus Name			Acc#
coenzyme F390 synthetase II			pir:B69115			B69115
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14648587_c3_286	4058	9280	1033	3102	556	1.2e-50
Protein name			Locus Name			Acc#
sensory transduction histidine kinase slr2098:protein slr2098:protein slr2098			pir:S75130			S75130
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14667192_f2_90	4059	9281	737	2214	623	4.4e-72
Protein name			Locus Name			Acc#
Tri r 4 allergen			gp:AF082514			AF082514
Description						
Trichophyton rubrum Tri r 4 allergen mRNA, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
188135_c2_259	4060	9282	556	1671	264	1.0e-35

Protein name

Locus Name

Acc#

sp:YCLF_BACSU

P94408

Description

HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19709682_c1_235	4061	9283	207	621	549	5.9e-53

Protein name

Locus Name

Acc#

CDP-4-keto-6-deoxy-D-glucose-3-dehydrase

pir:E47070

E47070

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19742217_f1_44	4062	9284	189	570		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19785941_c2_237	4063	9285	476	1431	597	2.6e-103

Protein name

Locus Name

Acc#

sp:YBHF_ECOLI

P75776

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBHF

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1992182_f2_107	4064	9286	112	339		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20195302_f3_161	4065	9287	452	1359	83	0.016
Protein name			Locus Name			Acc#
			sp:YK58_YEAST			P36158
Description						

HYPOTHETICAL 68.3 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20321015_c2_242	4066	9288	61	186		
Protein name			Locus Name			Acc#
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20364090_c3_324	4067	9289	958	2877	331	1.2e-25
Protein name			Locus Name			Acc#
hypothetical protein C26D10.4			pir:T19486			T19486
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20595050_c2_261	4068	9290	409	1230	385	1.4e-35
Protein name			Locus Name			Acc#
hypothetical protein SC5C7.08 SC5C7.08			pir:T35215			T35215
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21522003_c3_318	4069	9291	142	429		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22438202_c1_233.....	4070	9292	172	519	180	7.4e-14

Protein name

Locus Name

Acc#

unknown

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22462760_c2_238.....	4071	9293	367	1104	470	1.4e-44

Protein name

Locus Name

Acc#

sp:YBHS_ECOLI

P75775

Description

HYPOTHETICAL 42.1 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22930450_c2_236.....	4072	9294	179	540	146	1.4e-09

Protein name

Locus Name

Acc#

sp:YH11_ECOLI

P37626

Description

(F355)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23459636_f3_160	4073	9295	117	354		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23516000_c1_213.....	4074	9296	93	282		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23594055_c1_190.....	4075	9297	116	351	90	0.00026
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					sp:Y13B_BPT4	P17308
<u>Description</u>						

HYPOTHETICAL 11.5 KD PROTEIN IN GP31-CD INTERGENIC REGION (ORF B)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23642175_f1_11.....	4076	9298	424	1275		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23926877_c1_214	4077	9299	485	1458		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23986057_f1_22	4078	9300	447	1344	363	6.7e-36
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
damage-inducible protein PAB0243			pir:A75151		A75151	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24225316_c1_197	4079	9301	150	453	284	7.1e-25
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
hypothetical protein MTH1854			pir:A69115		A69115	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24257937_c1_204	4080	9302	363	1092	117	2.1e-06
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
hypothetical protein PAB0603			pir:E75137		E75137	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24400285_f3_156	4081	9303	259	780	132	2.1e-06
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
conserved hypothetical protein			pir:F75328		F75328	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24648876_f2_100	4082	9304	237	714		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24820300_c2_241.....	4083	9305	200	603	122	1.4e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:XERC_SALTY		P55888	
<u>Description</u>						

INTEGRASE/RECOMBINASE XERC

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25429715_c3_323.....	4084	9306	546	1641	935	5.8e-112
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
helicase			gp:RNDNAB		Y13813	
<u>Description</u>						

Rhodothermus marinus dnaB gene.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25601662_c1_189.....	4085	9307	105	318		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26574061_f2_106	4086	9308	244	735	472	8.5e-45
Protein name			Locus Name		Acc#	
sanA protein			pir:D75549		D75549	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26594082_c1_222	4087	9309	192	579	559	5.1e-54
Protein name			Locus Name		Acc#	
Na-translocating NADH-quinone reductase, Nqr5 subunit			pir:A72399		A72399	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26744012_c1_200	4088	9310	943	2832	2616	5.4e-272
Protein name			Locus Name		Acc#	
			sp:UVRA_BACSU		O34863	
Description						
EXCINUCLEASE ABC SUBUNIT A						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26758427_c3_321	4089	9311	202	609	555	1.4e-53
Protein name			Locus Name		Acc#	
Na-translocating NADH-quinone reductase, Nqr4 subunit			pir:H72398		H72398	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2944087_c1_203	4090	9312	115	348	225	1.3e-18
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein SCE20.33c.			gp:SCE20		AL136058	
<u>Description</u>						
Streptomyces coelicolor cosmid E20.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3025037_c3_287	4091	9313	705	2118	220	5.5e-21
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
site-specific recombinase			gp:D86934		D86934	
<u>Description</u>						
Staphylococcus aureus genes, mec region, partial and complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33397127_c2_254.....	4092	9314	116	351		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34022187_c2_272.....	4093	9315	334	1005	766	5.9e-76
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
Na-translocating NADH-quinone reductase, Nqr2 subunit			pir:F72398		F72398	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34179712_f3_154	4094	9316	682	2049	1936	6.2e-200

Protein name

Locus Name

Acc#

sp:UVRB_BACSU

Description

EXCINUCLEASE ABC SUBUNIT B (DINA PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35344626_c1_201	4095	9317	176	531	355	2.1e-32

Protein name

Locus Name

Acc#

sp:EBSC_ENTFA

P36922

Description

EBSC PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36129012_c2_239.....	4096	9318	275	828	312	7.6e-28

Protein name

Locus Name

Acc#

sp:YBHR_ECOLI

P75774

Description

HYPOTHETICAL 41.6 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36350812_f1_25.....	4097	9319	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3940668_f1_45	4098	9320	657	1974	237	8.1e-32

Protein name conserved hypothetical protein ylbK Locus Name pir:H69874 Acc# H69874

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3945187_f3_137	4099	9321	542	1629	1569	4.8e-161

Protein name Locus Name sp:PYRG_BACSU Acc# P13242

Description

CTP SYNTHASE, (UTP--AMMONIA LIGASE) (CTP SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3945301_c3_319	4100	9322	293	882	231	2.9e-19

Protein name Locus Name sp:YDGM_ECOLI Acc# P77223

Description

PUTATIVE FERREDOXIN-LIKE PROTEIN IN ADD-NTH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
39642_c3_327	4101	9323	196	591	841	6.7e-84

Protein name Locus Name gp:AF048749 Acc# AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4069800_c2_246	4102	9324	81	246	100	2.2e-05

Protein name

Locus Name

Acc#

sp:RPC_BPPH1

Description

IMMUNITY REPRESSOR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
424002_f3_165	4103	9325	180	543	178	4.7e-13

Protein name

Locus Name

Acc#

alanine--tRNA ligase,

pir:E72216

E72216

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4328380_c2_282	4104	9326	298	897	1398	6.3e-143

Protein name

Locus Name

Acc#

glucose-1-phosphate thymidyl transferase

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4455000_c1_223	4105	9327	364	1095	864	2.4e-86

Protein name

Locus Name

Acc#

sp:GALE_BACSU

P55180

Description

GALACTOSE 4-EPIMERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4507781_f2_73	4106	9328	277	834	322	6.6e-29

Protein name

Locus Name

Acc#

sp:YABH_BACSU

P37550

Description

HYPOTHETICAL 31.7 KD PROTEIN IN SSPF-PURR INTERGENIC REGION (ORF1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4865687_f3_150	4107	9329	598	1797	156	2.2e-08

Protein name

Locus Name

Acc#

cell wall-binding protein homolog yocH

pir:E69901

E69901

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4876682_c3_320.....	4108	9330	452	1359	986	2.9e-99

Protein name

Locus Name

Acc#

hypothetical protein TM0244

pir:E72398

E72398

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5095262_f3_129.....	4109	9331	423	1272		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6027187_c1_220	4110	9332	279	840	221	3.3e-18

Protein name

Locus Name

Acc#

sp:YDGP_ECOLI

P77285

Description

HYPOTHETICAL 21.9 KD PROTEIN IN ADD-NTH INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
788125_f3_157	4111	9333	548	1647	122	0.00083

Protein name

Locus Name

Acc#

ORF MSV198 MTG motif gene family protein

gp:AF063866

AF063866

Description

Melanoplus sanguinipes entomopoxvirus, complete genome.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
911251_c2_253.....	4112	9334	275	828	155	6.0e-09

Protein name

Locus Name

Acc#

hypothetical protein aq_1273

pir:C70410

C70410

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9680_f3_153.....	4113	9335	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9865837_c3_326	4114	9336	177	534	233	1.8e-19
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
unknown			gp:AF048749			AF048749
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9921876_c3_295	4115	9337	161	486		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9932642_c1_183	4116	9338	106	321	92	0.00016
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			gp:D90716			
<u>Description</u>						
Escherichia coli genomic DNA. (17.6 - 18.0 min).						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11131528_c2_62	4117	9339	60	183		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11133437_f1_3	4118	9340	1168	3507	480	6.8e-42

Protein name Locus Name Acc#
 receptor antigen (RagA) gp:PGI130872 AJ130872

Description
 Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11719042_f1_1	4119	9341	810	2433	1607	4.5e-165

Protein name Locus Name Acc#
 probable polynucleotide nucleotidyltransferase (pnp) pir:C71269 C71269

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13869003_f3_31	4120	9342	538	1617	135	2.9e-05

Protein name Locus Name Acc#
 cell surface antigen-like protein A29L pir:T17519 T17519

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14650277_f1_7	4121	9343	253	762		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26364040_f1_5	4122	9344	86	261		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3907687_f3_28	4123	9345	313	942	115	0.00025

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4104632_c2_56	4124	9346	374	1125	974	5.4e-98

Protein name

Locus Name

Acc#

butyrate kinase

gp:AB016775

AB016775

Description

Clostridium perfringens DNA for butyrate kinase and hydrogenase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4303262_f2_13	4125	9347	189	570	196	1.5e-15

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4305337_f1_4	4126	9348	542	1629		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4765625_c2_73	4127	9349	250	750		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4820378_c2_61	4128	9350	107	324		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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6438187_c1_38	4129	9351	317	954	476	3.2e-45
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Protein name

Locus Name

Acc#

sp:PTB_CLOAB

Q05624

Description

PHOSPHATE BUTYRYLTRANSFERASE, (PHOSPHOTRANSBUTYRYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9923505_f1_6	4130	9352	548	1647		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15834557_f1_1	4131	9353	88	267		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
831550_f1_2	4132	9354	388	1164	452	1.4e-41
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1959377_f2_2	4133	9355	71	216	93	0.0021
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
maturase-like protein			gp:CPESPSBC		AJ222583	
<u>Description</u>						

Euglena spirogyra chloroplast partial psbC gene & complete internalmat2 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24736386_c3_3	4134	9356	62	189		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14241518_c1_63.....	4135	9357	79	240	116	4.5e-07
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
iron(II) transport protein A				pir:C72423		C72423
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15017517_f3_37.....	4136	9358	790	2373	912	2.0e-91
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:PBPC_ECOLI		P76577
<u>Description</u>						

BIFUNCTIONAL PENICILLIN-BINDING PROTEIN 1C PRECURSOR (PBP-1C)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19692186_f1_3.....	4137	9359	442	1329	391	1.1e-43
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
cell cycle protein homolog mesJ				pir:T31465		T31465
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24067651_f1_15.....	4138	9360	182	549	137	2.7e-09
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
vsrD protein				pir:I40540		I40540
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31803882_f2_28	4139	9361	350	1053	635	4.5e-62

Protein name	Locus Name	Acc#
conserved hypothetical protein	pir:H72370	H72370

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32112785_c3_93	4140	9362	93	282		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32228163_c1_64	4141	9363	299	897	371	1.7e-40

Protein name	Locus Name	Acc#

sp:FE0B_METJA	Q57986
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Description

FERROUS IRON TRANSPORT PROTEIN B HOMOLOG

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33785957_f1_14	4142	9364	208	627		

Protein name	Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34183437_f2_29	4143	9365	482	1449	751	2.3e-74

Protein name	Locus Name	Acc#

Na+/H+ antiporter homolog yheL

pir:D69829	D69829
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Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4376056_c1_61	4144	9366	63	192		
Protein name			Locus Name		Acc#	

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4423751_f3_38	4145	9367	394	1185	572	2.1e-55
Protein name			Locus Name		Acc#	

antibiotic resistance protein homolog ydeR

pir:D69779

D69779

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
648382_f1_4	4146	9368	1870	5613	644	1.5e-60
Protein name			Locus Name		Acc#	

hypothetical protein b2520

pir:G65028

G65028

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10603135_f1_6	4147	9369	161	486	162	6.0e-12
Protein name			Locus Name		Acc#	

hypothetical protein CT276

pir:A71535

A71535

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1179767_f1_7	4148	9370	421	1266		
Protein name			Locus Name		Acc#	

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1251313_c1_26	4149	9371	386	1161	1228	6.5e-125
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:SYW_CLOLO			Q46127
<u>Description</u>						
(TRPRS)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20975051_f1_1	4150	9372	399	1200	396	9.6e-37
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
immunoreactive 42kD antigen PG33			gp:AF175715			AF175715
<u>Description</u>						
Porphyromonas gingivalis strain W50 immunoreactive 42kD antigenPG33 gene, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23595253_c1_22	4151	9373	62	189		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24494037_f3_15	4152	9374	304	915		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25516062_f2_10	4153	9375	529	1587	220	1.1e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunogenic 75 kDa protein PG4	gp:AF145800	AF145800

Description

Porphyromonas gingivalis strain W50 immunogenic 75 kDa protein PG4gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30210933_f3_13	4154	9376	332	999	144	4.2e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transposase	gp:AF038866	AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33242837_f2_9	4155	9377	202	609		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4718936_f3_12	4156	9378	1081	3246	3056	0.0

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PYR1_DICDI	P20054

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7140652_c3_50	4157	9379	112	339	82	0.032

Protein name Locus Name Acc#

EntT gp:AF099088 AF099088

Description

Enterococcus faecium enterocin A (entA), EntI (entI), EntF (entF), EntK (entK), EntR (entR), bacteriocin-like protein, EntT (entT), EntD (entD), and protease IV homolog genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10741300_f3_30	4158	9380	191	576		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1210910_f2_18	4159	9381	389	1170	252	8.5e-29

Protein name Locus Name Acc#

proline dipeptidase pir:D75419 D75419

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
135050_f3_22	4160	9382	69	210		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14651386_f3_29	4161	9383	471	1416	2343	4.6e-243

Protein name

Locus Name

Acc#

sp:DHE4_BACFR

P94316

Description

(NAD(P)H-DEPENDENT GLUTAMATE DEHYDROGENASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24251553_c2_40	4162	9384	248	747		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24661587_c2_41	4163	9385	201	606		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24895037_c2_39	4164	9386	994	2985	152	8.9e-06

Protein name

Locus Name

Acc#

probable phosphoenolpyruvate synthase APE0026

pir:E72754

E72754

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26288137_f1_7	4165	9387	81	246	114	1.2e-05

Protein name

Locus Name

Acc#

sp:PPCE_HUMAN

P48147

Description

(PE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3959800_c3_48	4166	9388	274	825		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
164933766_c1_41	4167	9389	104	315		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20510052_f3_39	4168	9390	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23627302_f3_40	4169	9391	336	1011	117	0.00030

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24354562_c3_66	4170	9392	515	1548		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642186_c2_55.....	4171	9393	545	1638	156	3.2e-07

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase,B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24736386_c2_48.....	4172	9394	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26376562_c2_54	4173	9395	452	1359	477	2.9e-44

Protein name Locus Name Acc#
115K outer membrane protein precursor:SusC protein pir:JC6027 JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29462512_f1_12	4174	9396	201	606	182	4.5e-14

Protein name Locus Name Acc#
RNA polymerase sigma factor SigZ-like protein gp:AF137263 AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34171886_c2_51	4175	9397	583	1752	110	1.2e-07

Protein name Locus Name Acc#
unknown gp:U96771 U96771

Description

Prevotella bryantii putative polygalacturonase,B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36442805_c1_43	4176	9398	1128	3387	561	2.1e-86

Protein name Locus Name Acc#
receptor antigen (RagA) gp:PGI130872 AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encodinga major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3929183_c1_47	4177	9399	496	1491		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
831550_c1_46	4178	9400	648	1947	588	3.1e-56

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
831550_c3_61	4179	9401	1140	3423	801	5.2e-88

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
990937_c1_45	4180	9402	591	1776	121	0.00017

Protein name

Locus Name

Acc#

outer membrane protein

gp:BNROMPB

L77614

Description

Bacteroides thetaiotaomicron outer membrane protein (susD) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1208550_f2_43	4181	9403	169	510		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12947287_f3_65	4182	9404	87	264		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13869003_f1_15	4183	9405	161	486	215	1.4e-17
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
unknown					gp:AF048749	AF048749
<u>Description</u>						

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14478901_c2_102	4184	9406	77	234		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15103800_f1_19	4185	9407	94	285	78	0.018

Protein name response regulator Locus Name gp:AF130997 Acc# AF130997

Description
Enterococcus faecium strain BM4339 vanD glycopeptide resistance gene cluster, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15822833_f2_21	4186	9408	76	231	198	5.1e-15

Protein name conserved hypothetical protein yisQ Locus Name pir:H69837 Acc# H69837

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16601633_g2_120.....	4187	9409	85	258		

Protein name Locus Name Acc#

Description
NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16603427_f2_40.....	4188	9410	402	1209	1820	1.2e-187

Protein name UDP-ManNAc dehydrogenase Locus Name gp:AF125164 Acc# AF125164

Description
Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c2_101	4189	9411	431	1296	1723	2.3e-177

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:JQ1020	JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20782802_f3_58.....	4190	9412	81	246		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21672181_c3_137.....	4191	9413	278	837		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22469452_f1_14.....	4192	9414	174	525	174	3.2e-13

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

unknown	gp:AF048749	AF048749
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Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22657551_c1_94	4193	9415	565	1698	539	7.9e-58

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
long-chain-fatty-acid CoA ligase	pir:D70386	D70386

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22658450_f2_46.....	4194	9416	72	219	156	2.7e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
arylsulfotransferase	gp:AF126201	AF126201

Description

Pseudomonas putida strain S-313 sulfate ester desulfurization genelocus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22736336_c2_99.....	4195	9417	103	312		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_g3_125.....	4196	9418	83	252	64	0.031

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SPRC_XENLA	P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22899000_f1_17	4197	9419	114	345	59	0.0024
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
retinoid X receptor alpha homolog			gp:UPU31832		U31832	
<u>Description</u>						
Uca pugilator retinoid X receptor alpha homolog mRNA, DNA bindingdomain region, partial cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24035212_c2_110	4198	9420	129	390		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24242700_c3_140.....	4199	9421	364	1095	569	6.8e-86
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
GDP-L-fucose pathway enzyme	gp:AB008676				AB008676	
<u>Description</u>						
Escherichia coli 0157 DNA, map position at 46 min., complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24806501_c1_95.....	4200	9422	386	1161	153	9.9e-08
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
probable PPE protein			pir:D70604		D70604	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2547261_f2_37	4201	9423	83	252		
Protein name					Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2598842_f1_18	4202	9424	69	210	57	0.041
Protein name					Locus Name	Acc#

gp:F23A5 AC011713

Description

Arabidopsis thaliana chromosome 1 BAC F23A5 sequence, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2742755_f2_47	4203	9425	63	192		
Protein name					Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2969387_f2_41	4204	9426	390	1173	1608	3.5e-165
Protein name					Locus Name	Acc#

UDP-GlcNAc 2-epimerase gp:AF125164 AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31444127_f3_51	4205	9427	673	2022	1578	5.3e-162

Protein name Locus Name Acc#
fructose-bisphosphatase, pir:C69621 C69621

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3314078_f3_71	4206	9428	133	402	125	3.9e-07

Protein name Locus Name Acc#
probable lipopolysaccharide O-side chain biosynthesis protein (O-antigen transpoter) pir:F71152 F71152

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34266886_c3_136	4207	9429	122	369		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35166437_f2_39	4208	9430	89	270		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35343753_c1_77	4209	9431	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36134625_f2_36	4210	9432	296	891	1351	6.0e-138
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
glucose-1-phosphate thymidyl transferase			gp:AF048749			AF048749
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon,complete sequence.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4469002_f3_50	4211	9433	556	1671	955	5.6e-96
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:YIDE_ECOLI			
<u>Description</u>						
HYPOTHETICAL 58.9 KD PROTEIN IN GLVC-IBPB INTERGENIC REGION (ORFA)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4694052_f3_67	4212	9434	343	1032	1134	6.0e-115
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
Cap8E			gp:SAU73374			U73374
<u>Description</u>						
Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4720327_f3_62	4213	9435	187	564	792	1.0e-78
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
dTDP-6-deoxy-D-glucose-3,5 epimerase			gp:AF048749			AF048749
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon,complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4941937_c2_112	4214	9436	374	1125	1219	5.9e-124

Protein name Locus Name Acc#

GDP-mannose dehydratase gp:AF047478

Description

Brucella melitensis strain 16M lipopolysaccharide O side chain biosynthesis gene cluster, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5115927_f2_42	4215	9437	364	1095	475	4.1e-45

Protein name Locus Name Acc#

pleiotropic regulatory protein DegT pir:D69025 D69025

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5878176_f3_68	4216	9438	83	252	76	0.048

Protein name Locus Name Acc#

reverse transcriptase like protein 1, intron-encoded pir:S58503 S58503

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7062750_f2_44	4217	9439	358	1077	334	3.6e-30

Protein name Locus Name Acc#

aspartate aminotransferase (aspb-like1) PAB0774 pir:D75096 D75096

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7314165_f1_11	4218	9440	360	1083	407	6.5e-38

Protein name

Locus Name

Acc#

sp:YA38_HAEIN

P44099

Description

HYPOTHETICAL PROTEIN HI1038

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
828957_f3_64	4219	9441	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10737801_c3_238.....	4220	9442	471	1416	718	7.2e-71

Protein name

Locus Name

Acc#

probable oxidoreductase

gp:SCF11

AL132662

Description

Streptomyces coelicolor cosmid F11.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11877138_c2_215.....	4221	9443	319	960	372	3.3e-34

Protein name

Locus Name

Acc#

shikimate 5-dehydrogenase

pir:F70377

F70377

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11963262_c3_239	4222	9444	263	792	334	3.6e-30

Protein name conserved hypothetical protein Locus Name pir:G72409 Acc# G72409

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12507691_c2_217	4223	9445	274	825	478	2.0e-45

Protein name lemA protein Locus Name pir:F72311 Acc# F72311

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12539091_c2_230	4224	9446	862	2589	493	2.9e-46

Protein name Locus Name sp:ALR2_BACSU Acc# P94494

Description

PUTATIVE ALANINE RACEMASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15051562_c1_181	4225	9447	96	291		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15657052_c2_211	4226	9448	169	510		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15829675_f2_57	4227	9449	525	1578	137	2.3e-05

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16131877_c2_231	4228	9450	272	819	318	1.7e-31

Protein name

Locus Name

Acc#

conserved hypothetical integral membrane protein HP1061

pir:E64652

E64652

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20089042_c2_205	4229	9451	1043	3132	1063	1.2e-194

Protein name

Locus Name

Acc#

beta-galactosidase

pir:F72283

F72283

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20710888_f3_138	4230	9452	100	303	72	0.043

Protein name

Locus Name

Acc#

glutamine-asparagine rich protein

gp:DDU07817

U07817

Description

Dictyostellium discoideum AX3 glutamine-asparagine rich protein gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22147552_c2_232	4231	9453	397	1194	268	8.0e-22
Protein name			Locus Name		Acc#	
3-O-acyltransferase, MdmB:midecamycin biosynthesis enzyme			pir:A42719		A42719	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23492786_c2_228.....	4232	9454	85	258		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23632187_c1_184.....	4233	9455	262	789	536	1.4e-51
Protein name			Locus Name		Acc#	
Description			sp:LPXA_ECOLI			

(EC 2.3.1.129) (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23712776_c2_218.....	4234	9456	389	1170	177	1.1e-23
Protein name			Locus Name		Acc#	
Description			sp:PUR5_METJA Q57656			

(AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23850828_c3_254	4235	9457	86	261		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23867302_c2_222.....	4236	9458	230	693		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24038577_c2_219.....	4237	9459	370	1113	899	4.8e-90

Protein name

Locus Name

Acc#

sp:RF1_COXBU

P47849

Description

PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24119033_c2_227.....	4238	9460	130	393		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24634681_c3_256	4243	9465	462	1389	382	2.7e-44

Protein name

Locus Name

Acc#

sp:LPXC_HAEIN

P45070

Description

(EC 3.5.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24640752_f2_45	4244	9466	417	1254		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24651553_c2_220.....	4245	9467	248	747	404	1.4e-37

Protein name

Locus Name

Acc#

OMP decarboxylase-ototate phosphoribosyl
transferase,

pir:T30520

T30520

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24695302_c3_249.....	4246	9468	251	756	465	4.7e-44

Protein name

Locus Name

Acc#

ubiquinone/menaquinone biosynthesis
methyltransferase

pir:F75277

F75277

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24735830_c3_258	4247	9469	395	1188		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24801442_f2_44	4248	9470	76	231	90	0.0023

Protein name

Locus Name

Acc#

probable glycosyl hydrolase

pir:T36467

T36467

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26211057_f1_36	4249	9471	601	1806	91	0.017

Protein name

Locus Name

Acc#

polygalacturonase precursor

pir:S57806

S57806

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26361438_f2_82	4250	9472	226	681		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29344691_f3_110	4251	9473	703	2112	255	8.9e-21

Protein name

Locus Name

Acc#

histidine kinase

gp:SPAJ6393

AJ006393

Description

Streptococcus pneumoniae rr03 and hk03 genes; two component system03.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31520840_f2_95	4252	9474	80	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33235880_f2_55	4253	9475	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33612762_f2_81	4254	9476	318	957	204	5.2e-16

Protein name

Locus Name

Acc#

hypothetical protein aq_246

pir:E70322

E70322

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34173175_c2_214	4255	9477	318	957	611	1.6e-59

Protein name

Locus Name

Acc#

sp:PUR7_ARATH

P38025

Description

(EC 6.3.2.6) (SAICAR SYNTHETASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34546942_f2_80	4256	9478	399	1200	195	7.7e-15

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:C72361

C72361

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35396062_f1_14	4257	9479	79	240		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35401883_f1_43.....	4258	9480	147	444		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36523452_c2_216.....	4259	9481	316	951	327	2.0e-29
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					sp:YQKD_BACSU	P54567
<u>Description</u>						

HYPOTHETICAL 34.6 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3948392_c3_255.....	4260	9482	349	1050	577	6.3e-56
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					sp:LPXD_RICRI	P32202
<u>Description</u>						

(EC 2.3.1.-) (FIRA PROTEIN) (RIFAMPICIN RESISTANCE PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3956556_c2_223	4261	9483	304	915	525	2.0e-50

Protein name Locus Name Acc#
 tRNA isopentenylpyrophosphate transferase
 miaA pir:G69657 G69657

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
424042_f1_37	4262	9484	264	795	404	1.4e-37

Protein name Locus Name Acc#
 sp:TRUA_BACSU P70973

Description

I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4351562_c3_250	4263	9485	375	1128	255	1.2e-30

Protein name Locus Name Acc#
 conserved hypothetical protein pir:G72311 G72311

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4711562_f3_135	4264	9486	230	693		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4767252_c1_174	4265	9487	340	1023	710	5.1e-70

Protein name

Locus Name

Acc#

gp:BMAJ4829

AJ224829

Description

Bacillus megaterium DSM319 spoIV operon, 5' flanking region, 3' flanking region.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5082512_c3_265	4266	9488	332	999		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6360910_c1_196.....	4267	9489	79	240	155	3.3e-11

Protein name

Locus Name

Acc#

conserved hypothetical secreted protein
HP0320

pir:H64559

H64559

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7126431_c1_185.....	4268	9490	61	186	72	0.020

Protein name

Locus Name

Acc#

leech zinc finger protein

gp:HTDNALZF1

X91396

Description

H.triserialis Lzf1 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
85882_f2_56	4269	9491	135	408	147	2.3e-10

Protein name

Locus Name

Acc#

sp:MECI_STAEP

P26598

Description

METHICILLIN RESISTANCE REGULATORY PROTEIN MECI

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
992787_c2_221	4270	9492	437	1314	498	1.5e-47

Protein name

Locus Name

Acc#

sp:YWFO_BACSU

P39651

Description

HYPOTHETICAL 51.0 KD PROTEIN IN PTA 3'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14922291_c3_55.....	4271	9493	287	864		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22079700_f2_11.....	4272	9494	174	525	362	3.8e-33

Protein name

Locus Name

Acc#

sp:RODA_ECOLI

Description

ROD SHAPE-DETERMINING PROTEIN RODA

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23495336_c3_52	4273	9495	115	348		
Protein name					Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2350306_c2_42	4274	9496	100	303	105	6.6e-06
Protein name					Locus Name	Acc#

hypothetical protein PH0217

pir:G71244

G71244

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23944506_c2_39	4275	9497	63	192	108	3.2e-06
Protein name					Locus Name	Acc#

hypothetical protein PH0219

pir:A71245

A71245

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24417061_c1_33	4276	9498	362	1089	389	5.3e-36
Protein name					Locus Name	Acc#

sp:METF_AQUAE

O67422

Description

5,10-METHYLENETETRAHYDROFOLATE REDUCTASE,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
282708_c3_45	4277	9499	60	183		
Protein name					Locus Name	Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5332506_c2_38	4278	9500	95	288	73	0.034

Protein name

Locus Name

Acc#

hypothetical protein PH0220

pir:B71245

B71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.79667_c2_43	4279	9501	492	1479	418	4.5e-39

Protein name

Locus Name

Acc#

sp:YAAT_BACSU

P37541

Description

HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9.658_c1_34	4280	9502	370	1113	168	1.1e-19

Protein name

Locus Name

Acc#

DNA polymerase III gamma subunit

pir:A70460

A70460

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10838905_c1_26	4281	9503	97	294		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11197928_f1_1	4282	9504	828	2487	649	4.5e-112

Protein name

Locus Name

Acc#

sp:BGLS_AGRTU

P27034

Description

GLUCOSIDE GLUCOHYDROLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12698552_c3_72	4283	9505	325	978	398	5.9e-37

Protein name

Locus Name

Acc#

sp:MMSR_PSEAE

P28809

Description

MMSAB OPERON REGULATORY PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19944466_f1_9	4284	9506	348	1047		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2031705_f1_2	4285	9507	482	1449	847	1.5e-84

Protein name

Locus Name

Acc#

L-arabinose transport (permease) araE

pir:F69587

F69587

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24651537_f2_14	4286	9508	1102	3309	2097	5.4e-217

Protein name

Locus Name

Acc#

sp:YPHG_ECOLI

P76585

Description

HYPOTHETICAL 127.3 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34069436_f1_8	4287	9509	940	2823	261	2.5e-18

Protein name

Locus Name

Acc#

beta-galactosidase

gp:AF055482

AF055482

Description

Thermotoga neapolitana galactose utilization operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15789087_c2_51	4288	9510	224	675	179	9.5e-14

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16131437_f2_20	4289	9511	439	1320	118	0.0015

Protein name

Locus Name

Acc#

BcDNA.GH11973

gp:AF145671

AF145671

Description

Drosophila melanogaster clone GH11973 BcDNA.GH11973 (BcDNA.GH11973) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20895303_f2_21	4290	9512	1227	3684		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
212752_c3_69	4291	9513	814	2445	518	1.2e-46

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24335781_f3_25	4292	9514	140	423	77	0.0064

Protein name

Locus Name

Acc#

sp:NOLP_RHILP

P23717

Description

NODULATION PROTEIN NOLP

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25494062_c2_50	4293	9515	84	255		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26594067_c1_39	4294	9516	320	963	155	1.2e-08

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4103377_f3_30	4295	9517	119	360		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
138.78550_f3_40.....	4296	9518	548	1647	2831	8.9e-295

Protein name

Locus Name

Acc#

neuraminidase precursor

gp:BNRNANASE

D28493

Description

Bacteroides fragilis nanH gene for neuraminidase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
148.76300_c2_90.....	4297	9519	532	1599	139	6.7e-08

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16267638_c2_67	4298	9520	93	282		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21595663_f3_39.....	4299	9521	1083	3252	519	4.8e-84

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC
protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22861562_f2_28.....	4300	9522	861	2586	1101	1.9e-111

Protein name

Locus Name

Acc#

hypothetical protein TM1624

pir:H72228

H72228

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24256587_f2_17.....	4301	9523	549	1650	125	1.5e-06

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and
mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24259683_f2_27	4302	9524	691	2076	331	8.1e-35

Protein name

Locus Name

Acc#

sialic-acid O-acetylerase

gp:MMU40408

U40408

Description

Mus musculus lysosomal sialic acid O-acetylerase mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415877_f3_33	4303	9525	521	1566	107	1.2e-07

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24429036_c1_51	4304	9526	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24640892_f2_23	4305	9527	673	2022		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648937_f3_41	4306	9528	209	630	126	2.6e-06

Protein name

Locus Name

Acc#

sp:PA1B_RAT

035264

Description

ACTIVATING FACTOR ACETYLHYDROLASE ALPHA 2 SUBUNIT) (PAF-AH ALPHA 2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2772937_c2_89	4307	9529	1093	3282	528	3.0e-89

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33243818_f2_13	4308	9530	434	1305	740	1.2e-84

Protein name

Locus Name

Acc#

alpha-L-fucosidase, 1 precursor,
tissue:alpha-L-fucosidase I:alpha-L-fucoside
fucosylhydrolase

pir:HWHUFA

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34416427_f1_11	4309	9531	672	2019	310	9.2e-26

Protein name

Locus Name

Acc#

sp:HEXA_PORGI

P49008

Description

(BETA-NAHASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35351583_c3_124	4310	9532	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4140927_f3_43	4311	9533	518	1557	1139	1.8e-115

Protein name

Locus Name

Acc#

sp:HEXA_PORGI

P49008

Description

(BETA-NAHASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4484687_f3_32	4312	9534	529	1590	119	1.8e-06

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5109392_c1_64	4313	9535	173	522		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781932_f1_4	4314	9536	1118	3357	463	5.9e-82

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781932_f2_16	4315	9537	1102	3309	526	5.1e-83

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781932_f3_31	4316	9538	1120	3363	529	2.6e-79

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
859438_c3_108	4317	9539	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1206500_f1_15	4318	9540	385	1158	465	4.7e-44
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
probable nagA protein			pir:C70845			C70845
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1272677_f3_45	4319	9541	398	1197	384	1.8e-35
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein b1325			pir:H64881			H64881
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14656257_f1_8	4320	9542	451	1356	479	2.7e-48
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein			pir:A72430			A72430
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1959437_f1_18	4321	9543	70	213		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2147656_f2_25	4322	9544	406	1221	225	3.8e-18
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
polysugar degrading enzyme homolog ykfC			pir:A69856			A69856
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26367177_c3_110	4328	9550	439	1320	253	2.2e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sensory protein kinase	pir:T30222	T30222

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2931525_f2_31.....	4329	9551	394	1185	192	3.3e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
clostripain-related protein	pir:B72351	B72351

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30494212_f3_51.....	4330	9552	95	288		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33397186_f1_10.....	4331	9553	301	906	933	1.2e-93

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
SigA	gp:CTU67718	U67718

Description

Chlorobium tepidum SigA (sigA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33398377_f3_43	4332	9554	205	618	384	1.8e-35

Protein name

Locus Name

Acc#

sp:RISA_BACSU

Description

RIBOFLAVIN SYNTHASE ALPHA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33863876_c2_96	4333	9555	527	1584		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35366625_f2_37.....	4334	9556	128	387		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36430393_f3_44.....	4335	9557	189	570	141	4.2e-15

Protein name

Locus Name

Acc#

sp:YDGI_BACSU

P96707

Description

POTATIVE NAD(P)H NITROREDUCTASE YDGI,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36525157_f2_19	4336	9558	125	378	496	2.4e-47

Protein name Locus Name Acc#
phosphate transport ATP binding protein pir:G70390 G70390

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
390826_c1_76.....	4337	9559	451	1356	382	2.9e-35

Protein name Locus Name Acc#
sp:RBN_HAEIN P44608

Description

RIBONUCLEASE BN, (RNASE BN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4881450_c3_112.....	4338	9560	157	474		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6674062_c3_113.....	4339	9561	283	852		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
78158_c1_67	4340	9562	236	711	383	2.3e-35

Protein name

Locus Name

Acc#

sp:PHOP_BACSU

P13792

Description

PHOP

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15103800_c3_56	4341	9563	94	285	78	0.018

Protein name

Locus Name

Acc#

response regulator

gp:AF130997

AF130997

Description

Enterococcus faecium strain BM4339 vanD glycopeptide resistance gene cluster, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
157263_c3_59	4342	9564	385	1158		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c1_38	4343	9565	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f3_33	4344	9566	208	624	710	5.1e-70

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:JQ1020	JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
188967_f3_26.....	4345	9567	91	276		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20087753_c3_63.....	4346	9568	317	954	1426	6.8e-146

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

putative UDP-GlcNAc:undecaprenylphosphate	gp:AF048749	AF048749
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Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2040937_c2_52.....	4347	9569	253	762	207	1.0e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

putative glycosyl transferase	gp:LPN7311	AJ007311
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Description

Legionella pneumophila serogroup 1 lipopolysaccharide biosynthesis gene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20594161_c3_61	4348	9570	91	276		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22658450_c1_34.....	4349	9571	72	219	156	2.7e-10

Protein name

Locus Name

Acc#

arylsulfotransferase

gp:AF126201

AF126201

Description

Pseudomonas putida strain S-313 sulfate ester desulfurization genelocus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c2_49.....	4350	9572	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f1_15.....	4351	9573	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24238263_f1_7	4352	9574	129	390		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26212762_c2_48.....	4353	9575	350	1053	123	9.7e-08

Protein name

Locus Name

Acc#

Cap5J

gp:SAU81973

U81973

Description

Staphylococcus aureus capsule gene cluster Cap5A through Cap5Pgenes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2742755_c1_35.....	4354	9576	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32056392_c1_39.....	4355	9577	69	210	85	0.010

Protein name

Locus Name

Acc#

hypothetical protein, 57.8 kD

gp:POL245436

Description

Pseudomonas putida OCT plasmid alk genes cluster and flanking DNA, strain TF4-1L.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3314078_c2_46	4356	9578	470	1413	252	6.0e-19
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable lipopolysaccharide O-side chain biosynthesis protein (O-antigen transpoter)			pir:F71152		F71152	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33460952_c2_54	4357	9579	171	516	95	9.5e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:DBH5_RHILE		P02348	
<u>Description</u>						
DNA-BINDING PROTEIN HRL53						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35970967_f3_27	4358	9580	62	189	71	0.026
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:HIPB_ECOLI		P23873	
<u>Description</u>						
HIPB PROTEIN						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3907151_f1_11	4359	9581	80	243		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3945302_f1_8	4360	9582	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4103387_c1_36.....	4361	9583	305	918	204	2.1e-16

Protein name

Locus Name

Acc#

probable rhamnosyltransferase

pir:H75596

H75596

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
41293_c3_60.....	4362	9584	87	264		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4176566_c1_40.....	4363	9585	77	234	82	0.023

Protein name

Locus Name

Acc#

unknown

gp:AF134706

AF134706

Description

Sinorhizobium meliloti insertion sequence ISRml4, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4198425_c2_47	4364	9586	327	984	130	1.6e-05

Protein name

Locus Name

Acc#

gp:AB000222

AB000222

Description

Staphylococcus capitis epr gene ,complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4704715_c3_62	4365	9587	338	1017	1447	4.1e-148

Protein name

Locus Name

Acc#

UDP-glucose-4-epimerase/dTDP-glucose-4,6

gp:AF048749

AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon,complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5970193_f1_1	4366	9588	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5978385_c1_37	4367	9589	345	1038		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6725327_c2_51	4368	9590	238	717	296	3.8e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glycosyltransferase	pir:G75596	G75596

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13689660_f3_10.....	4369	9591	267	804	1330	1.0e-135

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ISTB_BACFR	Q45120

Description

INSERTION SEQUENCE IS21-LIKE PUTATIVE ATP-BINDING PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14272692_f3_8.....	4370	9592	333	1002	1671	7.4e-172

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:TRA2_BACFR	Q45119

Description

TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS21-LIKE

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16299062_f3_11.....	4371	9593	592	1779		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22460186_f2_6	4372	9594	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29937943_f2_4	4373	9595	214	645	1109	2.7e-112

Protein name

Locus Name

Acc#

sp:TRA2_BACFR

Q45119

Description

TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS21-LIKE

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30525762_f2_7	4374	9596	123	372		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
100385_f1_32	4375	9597	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12285135_c3_311	4376	9598	752	2259	1461	1.3e-149

Protein name

Locus Name

Acc#

sp:BIOA_HAEIN

P44426

Description

AMINOTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12688437_c3_302	4377	9599	489	1470	578	4.9e-56

Protein name

Locus Name

Acc#

immunoreactive 53 kD antigen PG123

gp:AF144641

AF144641

Description

Porphyromonas gingivalis strain W50 immunoreactive 53 kD antigenPG123 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12947777_f2_99	4378	9600	190	573		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13828450_f3_154	4379	9601	140	423	86	0.019

Protein name

Locus Name

Acc#

sp:FKBA_ECOLI

Description

(EC 5.2.1.8) (PPIASE) (ROTAMASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13835937_f2_100	4380	9602	454	1365	789	2.2e-78

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
dihydrolipoamide dehydrogenase, :2-oxoglutarate dehydrogenase complex chain E3:acetoin dehydrogenase complex	pir:I40794	I40794
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14095406_c1_182	4381	9603	140	423		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>		

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14727331_c1_191.....	4382	9604	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>		

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14737507_c2_221.....	4383	9605	129	390	132	9.2e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein APE1673	pir:E72548	E72548
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15040893_f3_137	4384	9606	1043	3132	729	1.7e-120
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
receptor antigen (RagA)			gp:PGI130872		AJ130872	
<u>Description</u>						
Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f3_155	4385	9607	200	603	762	1.6e-75
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:JQ1020		JQ1020	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1753117_c3_292.....	4386	9608	74	225		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>			NO-HIT			

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
199062_f1_48.....	4387	9609	73	222		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>			NO-HIT			

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20582930_c3_321	4388	9610	522	1569	814	4.9e-81

Protein name

Locus Name

Acc#

Salmonella typhimurium transcriptional

gp:STYSTMF1

AF170176

Description

Salmonella typhimurium fragment STMF1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20750302_f1_44	4389	9611	459	1380	445	6.3e-71

Protein name

Locus Name

Acc#

sp:ODB2_BACSU

P37942

Description

CHAIN TRANSACYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21971036_c2_282.....	4390	9612	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22277_c1_157.....	4391	9613	289	870	298	2.3e-26

Protein name

Locus Name

Acc#

gp:AB023064

AB023064

Description

Listeria monocytogenes DNA for DnaK operon, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f1_52	4392	9614	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23851527_c3_312	4393	9615	405	1218	1026	1.7e-103

Protein name

Locus Name

Acc#

sp:BIOF_HAEIN

P44422

Description

LIGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24432030_f2_88	4394	9616	563	1692	114	1.2e-06

Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24641932_f1_40	4395	9617	555	1668		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644015_c3_296	4396	9618	152	459	204	7.4e-16
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
prolidase			gp:AB014613		AB014613	
<u>Description</u>						
Aureobacterium esteraromaticum gene for prolidase, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24645252_f3_123	4397	9619	441	1326	476	3.2e-45
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
immunoreactive 50kD antigen PG53			gp:AF175720		AF175720	
<u>Description</u>						
Porphyromonas gingivalis strain W50 immunoreactive 50kD antigenPG53 gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648407_c3_301	4398	9620	199	600		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24666005_c3_316	4399	9621	68	207	49	0.036
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein A556L			pir:T18058		T18058	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25448566_f1_18	4400	9622	267	804	564	1.5e-54
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:YF08_METJA		Q58903
<u>Description</u>						
HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ1508						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
255313_c1_163	4401	9623	74	225		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26369006_f2_94.....	4402	9624	515	1548	1829	1.3e-188
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
propionyl-CoA carboxylase				gp:AB007000		AB007000
<u>Description</u>						
Myxococcus xanthus MxppcB gene for propionyl-CoA carboxylase, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26445311_c2_263.....	4403	9625	229	690	502	5.6e-48
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:BID2_HAEIN		P45248
<u>Description</u>						
2) (DTB SYNTHETASE 2) (DTBS 2)						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26461542_f2_95	4404	9626	509	1530	1297	3.2e-132
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
acetyl-CoA carboxylase (biotin carboxylase subunit) accC			pir:A69581		A69581	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26594425_f2_69.....	4405	9627	417	1254	214	5.6e-15
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein aq_294			pir:H70326		H70326	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31281883_f3_134.....	4406	9628	118	357	110	1.9e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein APE1466			pir:B72626		B72626	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32115637_f1_43.....	4407	9629	242	729	336	2.2e-30
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:LPLA_MYCPN		P75394	
<u>Description</u>						
PROBABLE LIPOATE-PROTEIN LIGASE A,						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32116703_c2_268	4408	9630	68	207	136	3.4e-09
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein APE2061			pir:G72510			G72510
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32226550_f3_152.....	4409	9631	174	525	367	1.1e-33
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
flavodoxin			pir:A28670			
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32633411_f3_125.....	4410	9632	810	2433	171	2.0e-09
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
conserved hypothetical protein			pir:G72385			G72385
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33218827_c3_300.....	4411	9633	513	1542		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3370317_f1_38.....	4412	9634	144	435	154	5.8e-14
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
methylmalonyl-coa decarboxylase gamma chain PAB1771			pir:F75135			F75135
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35367263_c2_266	4413	9635	433	1302		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35710811_c1_187.....	4414	9636	502	1509	468	2.2e-44

Protein name

Locus Name

Acc#

sp:BIOC_HAEIN

P45249

Description

PUTATIVE BIOTIN SYNTHESIS PROTEIN BIOC

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3929091_c1_201.....	4415	9637	376	1131	256	6.5e-22

Protein name

Locus Name

Acc#

membrane protein

pir:G64590

G64590

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3948425_f1_3.....	4416	9638	402	1209	856	1.7e-85

Protein name

Locus Name

Acc#

aspartate aminotransferase

pir:D72220

D72220

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4337882_f3_151	4417	9639	695	2088	1022	4.4e-103
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable (pyruvate) oxoisovalerate dehydrogenase alpha and beta fusion			pir:G71526		G71526	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4462535_f1_4	4418	9640	438	1317	283	4.4e-23
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YCFW_ECOLI		P75958	
<u>Description</u>						

HYPOTHETICAL 45.3 KD PROTEIN IN MFD-COBB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4486037_c3_330	4419	9641	415	1248	379	6.1e-35
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein APE1887			pir:G72575		G72575	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4807687_c3_303	4420	9642	503	1512	941	1.7e-94
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
L-lactate permease (lctP) homolog			pir:C70175		C70175	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4953527_f1_51	4421	9643	480	1443	104	1.0e-05

Protein name

Locus Name

Acc#

sp:PRTT_PORGI

P43158

Description

THIOL PROTEASE/HEMAGGLUTININ PRTT PRECURSOR,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4957582_c2_281	4422	9644	281	846	209	7.8e-16

Protein name

Locus Name

Acc#

sp:CHAC_SPHHE

Q59288

Description

(CHONDROITIN SULFATE LYASE) (CHONDROITIN AC ELIMINASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5195132_c2_275	4423	9645	425	1278	289	4.7e-26

Protein name

Locus Name

Acc#

sensor protein p11S

pir:S70528

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
523587_c3_319	4424	9646	434	1305		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
54802_c2_264	4425	9647	456	1371	643	6.4e-63
Protein name			Locus Name		Acc#	
NADH dehydrogenase, :protein slr0851:protein slr0851			pir:S74826		S74826	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
628465_c1_172.....	4426	9648	344	1035	369	6.9e-34
Protein name			Locus Name		Acc#	
			sp:YJV3_YEAST		P40896	
Description						
HYPOTHETICAL 35.9 KD PROTEIN IN HXT8-CRT1 INTERGENIC REGION						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
882912_f1_41.....	4427	9649	395	1188		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
914202_c2_276.....	4428	9650	390	1173	162	2.9e-09
Protein name			Locus Name		Acc#	
EpsG			gp:AF036485			
Description						
Plasmid pNZ4000, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1172330_f1_2	4429	9651	345	1038	1055	1.4e-106
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ketol-acid reductoisomerase			gp:PSP16743		Y16743	
<u>Description</u>						
Piromyces sp. E2 mRNA for ketol-acid reductoisomerase.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20443775_c1_29	4430	9652	644	1935	717	9.2e-71
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein T18E12.6			pir:T02699		T02699	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23448402_f3_16.....	4431	9653	658	1977		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23478512_f1_1.....	4432	9654	198	597		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24017827_f2_12	4433	9655	247	744	184	2.5e-15
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
palmitoyl-acyl carrier protein thioesterase	gp:AF034266				AF034266	
<u>Description</u>						
Gossypium hirsutum palmitoyl-acyl carrier protein thioesterase(FatB1) mRNA, partial cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24331376_f1_9	4434	9656	790	2373	2363	3.5e-245
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:ACON_GRAVE				P49609	
<u>Description</u>						
HYDRO-LYASE) (ACONITASE)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24630192_f2_11	4435	9657	153	462	151	8.8e-11
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
acetolactate synthase	pir:E70459				E70459	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4877202_f1_10	4436	9658	303	909	867	3.9e-98
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
isocitrate dehydrogenase	gp:BIISOCIT				Y13358	
<u>Description</u>						
Bacillus israeli isocitrate dehydrogenase gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12509425_f1_8	4437	9659	191	576	639	1.7e-62

Protein name

Locus Name

Acc#

gp:AB022867

AB022867

Description

Prevotella ruminicola genes for polyA polymerase, D-alanineglycinepermease and cellulase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13837557_c3_73	4438	9660	123	372	113	9.3e-07

Protein name

Locus Name

Acc#

gp:MZECWAB

M36913

Description

Z.mays cell wall protein mRNA, 3' end.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14461002_f2_16.....	4439	9661	299	900	264	3.3e-22

Protein name

Locus Name

Acc#

sp:YEBA_HAEIN

P44693

Description

HYPOTHETICAL PROTEIN HI0409

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14744002_f2_14.....	4440	9662	184	555	317	2.2e-28

Protein name

Locus Name

Acc#

4-methyl-5(b-hydroxyethyl)-thiazole
monophosphate biosynthesis protein (thiJ)
homolog

pir:D70177

D70177

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860927_f1_7	4441	9663	166	501	362	3.8e-33

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable nucleoside-diphosphate kinase,	pir:C71116	C71116

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24098388_c2_56.....	4442	9664	310	933	591	2.1e-57

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:PGPUT	X97228

Description

P.gingivalis gpxJ, put, and yhbG-pg genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26213181_c3_61.....	4443	9665	257	774	992	6.7e-100

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:JQ1020	JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26759387_f2_17.....	4444	9666	444	1335		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29480341_c1_44.....	4445	9667	85	255		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3312913_f3_27	4446	9668	223	672	336	2.2e-30

Protein name

Locus Name

Acc#

conserved hypothetical protein yacM

pir:S66119

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33392202_f2_18.....	4447	9669	267	804	587	5.5e-57

Protein name

Locus Name

Acc#

triosephosphate isomerase

gp:AF043386

AF043386

Description

Clostridium acetobutylicum glyceraldehyde-3-phosphate dehydrogenase(gap), phosphoglycerate kinase (pgk), and triosephosphate isomerase(tpi) genes, complete cds; and 2,3-bpg-independent phosphoglyceratemutase (pgm-i) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33476625_f2_15.....	4448	9670	707	2124	1284	7.6e-131

Protein name

Locus Name

Acc#

sp:RECG_SYNY3

Q55681

Description

ATP-DEPENDENT DNA HELICASE RECG,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34081405_f3_22.....	4449	9671	88	267	110	1.9e-06

Protein name

Locus Name

Acc#

hypothetical protein PHS004

pir:F71245

F71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35205387_f3_26	4450	9672	293	882	256	6.5e-22
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:TONB_NEIGO		006432	
<u>Description</u>						
TONB PROTEIN						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4159587_f3_24	4451	9673	211	636	676	2.0e-66
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
pyridoxal phosphate synthetase			gp:PGPUT		X97228	
<u>Description</u>						
P.gingivalis gpdxJ, put, and yhbG-pg genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4578461_f1_5	4452	9674	149	450	139	1.6e-09
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:TOLR_HAEIN		P43769	
<u>Description</u>						
TOLR PROTEIN						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5087912_c2_59	4453	9675	89	270		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9853312_f3_25	4454	9676	245	738	232	2.3e-19
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein	gp:PST243354				AJ243354	
<u>Description</u>	Pseudomonas stutzeri hyp1 and comA genes and putative tolQ, exbB, tolR and exbD genes.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10137_c2_279	4455	9677	185	558	537	1.1e-51
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
carbonic anhydrase homolog ytiB	pir:F69993				F69993	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10632768_c3_321.....	4456	9678	68	207		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10675680_c2_245.....	4457	9679	74	225		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12600340_f3_137	4458	9680	364	1095		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12676061_f1_4	4459	9681	474	1425		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1353457_f1_34	4460	9682	461	1386	461	1.6e-56
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

AlgI gp:PAU50202 U50202

Pseudomonas aeruginosa alginate gene cluster AlgI (algI), AlgJ (algJ) and AlgF (algF) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13785326_f2_111	4461	9683	68	207		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14541001_f2_82	4462	9684	382	1149	315	3.7e-28
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
thiamin biosynthesis protein homolog			pir:H69260			H69260
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14634500_c2_298.....	4463	9685	455	1368	153	3.7e-07
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
KIAA1275 protein			gp:AB033101			AB033101
<u>Description</u>						

Homo sapiens mRNA for KIAA1275 protein, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14650287_c3_304.....	4464	9686	540	1623	416	6.4e-67
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
outer membrane protein			gp:BNROMPB			L77614
<u>Description</u>						

Bacteroides thetaiotaomicron outer membrane protein (susD) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14712516_c3_359.....	4465	9687	133	402		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14954712_f1_49	4466	9688	150	453	125	5.0e-08

Protein name

Locus Name

Acc#

sp:MEXR_PSEAE

P52003

Description

MULTIDRUG RESISTANCE OPERON REPRESSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16101587_f1_50	4467	9689	359	1080	403	1.7e-37

Protein name

Locus Name

Acc#

sp:EMRA_HAEIN

P44928

Description

MULTIDRUG RESISTANCE PROTEIN A HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c2_285.....	4468	9690	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16905_f2_75.....	4469	9691	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20015643_c3_312	4470	9692	66	201		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20369826_c3_332.....	4471	9693	190	573	240	3.2e-20
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

sp:YM67_ARCFU 028017

Description

(EC 1.-.-.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20509630_c1_184.....	4472	9694	954	2865	345	3.3e-28
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

alpha-amylase, precursor:protein c0620

pir:S73087 S73087

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22287681_f3_174.....	4473	9695	402	1209	152	4.0e-10
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

thiol:disulfide interchange protein homolog
yneN

pir:E69891 E69891

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22459655_c3_360	4474	9696	337	1014	133	4.7e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transmembrane sensor	gp:AF051691	AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22478431_f2_84	4475	9697	397	1194	282	1.1e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YRKO_BACSU	P54442

Description

HYPOTHETICAL 46.4 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22687767_f1_19	4476	9698	421	1266	770	1.9e-113

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
cytosolic phosphoglycerate kinase 1	gp:AB018410	AB018410

Description

Populus nigra PnCytPGK1 mRNA for cytosolic phosphoglycerate kinase1, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c3_340	4477	9699	83	252	64	0.031

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SPRC_XENLA	P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23554563_f2_81	4478	9700	229	690	493	5.0e-47

Protein name

Locus Name

Acc#

endonuclease III

pir:B71919

B71919

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23634703_c2_280.....	4479	9701	69	210	58	0.0059

Protein name

Locus Name

Acc#

sp:ARCD_PSEAE

P18275

Description

ARGININE/ORNITHINE ANTIporter

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24000925_c2_301.....	4480	9702	723	2169	440	4.2e-46

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:Susc protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24016525_c2_259.....	4481	9703	343	1032	1174	3.4e-119

Protein name

Locus Name

Acc#

sp:ALF_TREPA

083668

Description

FRUCTOSE-BISPHOSPHATE ALDOLASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24017303_c1_242	4482	9704	677	2034	2862	4.6e-298
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
pullulanase	gp:BTU67061				U67061	
<u>Description</u>						
Bacteroides thetaiotaomicron pullulanase (pull) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24041626_f3_161	4483	9705	452	1359	141	1.5e-06
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
conserved hypothetical protein MTH83				pir:F69210	F69210	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415877_f3_149.....	4484	9706	131	396		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24417075_f3_158.....	4485	9707	167	504	343	4.0e-31
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein PH0272	pir:A71452				A71452	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24487937_f1_46.....	4486	9708	425	1278	153	6.0e-08
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
conserved hypothetical protein BB0195	pir:C70124				C70124	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24689717_f3_135	4487	9709	443	1332	422	1.7e-39
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
antibiotic resistance protein homolog ywoG	pir:B70065				B70065	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24695316_f2_76	4488	9710	349	1050	788	2.8e-78
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:SYFA_BACSU					
<u>Description</u>						
-TRNA LIGASE ALPHA CHAIN) (PHERS)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25634375_c2_246	4489	9711	97	294		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2595036_c3_358	4490	9712	60	183		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25978377_f2_85	4491	9713	733	2202	228	1.8e-16

Protein name

Locus Name

Acc#

sp:Y798_METJA

Q58208

Description

HYPOTHETICAL PROTEIN MJ0798

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26600187_f2_88	4492	9714	508	1527	499	6.4e-51

Protein name

Locus Name

Acc#

gp:AB019578

AB019578

Description

Microcystis aeruginosa mcyA, mcyB and mcyC genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26756557_f1_28	4493	9715	173	522		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29971007_c3_315	4494	9716	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3125006_c2_257	4495	9717	60	183		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31276925_f1_39	4496	9718	285	858		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31854557_c2_247	4497	9719	246	741	503	4.9e-48
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:Susc protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31876687_f1_33	4498	9720	97	294	102	1.4e-05
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
acyl carrier protein			pir:S28475		S28475	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32620812_f2_108	4499	9721	540	1623	176	4.8e-10
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
VceB			gp:AF012101		AF012101	
<u>Description</u>						
Vibrio cholerae efflux gene A (vceA) and efflux gene B (vceB)multidrug resistance pump genes, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3377027_c1_213	4500	9722	310	933	135	1.3e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:F72216		F72216	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34414052_c3_333.....	4501	9723	175	528	285	5.5e-25
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein aq_2171			pir:D70486		D70486	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35820461_c3_316.....	4502	9724	63	192		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36360000_f2_112	4503	9725	624	1875	121	0.00057

Protein name

Locus Name

Acc#

unknown

gp:AF013216

Description

Myxococcus xanthus Dog (dog), isocitrate lyase (icl), Mls (mls), Ufo (ufo), fumarate hydratase (fhy), and proteosome major subunit (clpP) genes, complete cds; and acyl-CoA oxidase (aco) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
391540_c1_201	4504	9726	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4094816_f3_164.....	4505	9727	620	1863	1365	2.0e-139

Protein name

Locus Name

Acc#

neopullulanase

gp:BTU66897

U66897

Description

Bacteroides thetaiotaomicron neopullulanase (susA) and alpha-glucosidase (susB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4104062_f1_58.....	4506	9728	88	267	242	2.0e-20

Protein name

Locus Name

Acc#

probable ribosomal protein L31

pir:T36353

T36353

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4144002_c1_243	4507	9729	190	573	292	1.0e-25
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
RNA polymerase sigma factor SigZ-like protein			gp:AF137263		AF137263	
<u>Description</u>						
Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4172012_c1_223	4508	9730	283	852	464	6.0e-44
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
endo-beta-galactosidase			gp:AF083896		AF083896	
<u>Description</u>						
Flavobacterium keratolyticus endo-beta-galactosidase gene, completecds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4320313_f2_99	4509	9731	520	1563	1634	6.2e-168
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
methylmalonyl-CoA decarboxylase, alpha chain			pir:A49094		A49094	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4820387_f2_100.....	4510	9732	146	441	242	2.0e-20
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
glutaconyl-CoA decarboxylase gamma subunit	gp:AF030576				AF030576	
<u>Description</u>						
Acidaminococcus fermentans methylmalonyl-CoA decarboxylase alphasubunit (mmdA) gene, partial cds; and glutaconyl-CoA decarboxylasedelta subunit (gcdD), glutaconyl-CoA decarboxylase gamma subunit (gcdC), and glutaconyl-CoA decarboxylase beta subunit (gcdB) genes,complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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492206_f1_35	4511	9733	352	1059		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4945187_c2_248.....	4512	9734	538	1617	92	0.0019
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Protein name

Locus Name

Acc#

outer membrane protein

gp:BNROMPA

L77615

Description

Bacteroides thetaiotaomicron outer membrane protein (susE) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5328165_c2_282.....	4513	9735	210	633	336	2.2e-30
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Protein name

Locus Name

Acc#

sp:MAF_BACSU

Description

MAF PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5330267_c2_299.....	4514	9736	200	603	295	4.8e-26
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Protein name

Locus Name

Acc#

crossover junction endodeoxyribonuclease

pir:B72360

B72360

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5890712_f3_171	4515	9737	118	357		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5900682_f1_42	4516	9738	308	927		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9772930_f2_116	4517	9739	104	315		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9796942_c2_258	4518	9740	363	1092		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9847330_f3_160	4519	9741	353	1062	966	3.8e-97

Protein name Locus Name Acc#

oxaloacetate decarboxylase, beta subunit pir:B72324 B72324

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13134680_f3_49	4520	9742	194	585	126	5.8e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
beta-galactosidase,	pir:T29434	T29434

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14720382_f1_14	4521	9743	83	252		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14845965_f2_35	4522	9744	250	753	138	1.3e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

M-protein	gp:SEU73162	U73162
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Description

Streptococcus equi M-protein (seM) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15899063_c3_109	4523	9745	81	246		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16604818_c1_71	4524	9746	783	2352	200	4.7e-15
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
colicin I receptor			gp:ECOCIR			
<u>Description</u>						
E.coli colicin I receptor gene, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
17069076_f1_15	4525	9747	253	762	257	5.1e-22
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
			sp:YJJG_ECOLI			
<u>Description</u>						
HYPOTHETICAL 25.3 KD PROTEIN IN RIMI-PRFC INTERGENIC REGION						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20784708_f1_1	4526	9748	66	201	81	0.021
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
glutamyl-tRNA reductase			gp:AF080069			
<u>Description</u>						
Chlorobium vibrioforme glutamyl-tRNA reductase (hemA) gene,complete cds; and porphobilinogen deaminase (hemC) gene, partialcds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23595055_c3_94	4527	9749	722	2169	342	1.1e-41
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
115K outer membrane protein precursor:SusC protein			pir:JC6027			JC6027
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24225385_f2_38	4528	9750	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24422505_f1_13.....	4529	9751	287	864	98	0.0043

Protein name

Locus Name

Acc#

hypothetical protein

pir:T10699

T10699

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25504687_c2_84.....	4530	9752	219	660	568	5.7e-55

Protein name

Locus Name

Acc#

thymidine kinase

gp:AF028720

AF028720

Description

Rhodothermus sp. 'IT1 518' thymidine kinase (tdk) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33439010_c1_63.....	4531	9753	947	2844	968	2.3e-97

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34178252_c1_64	4532	9754	537	1614		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36018792_f2_34.....	4533	9755	239	720	568	5.7e-55
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

conserved hypothetical protein

pir:D72343

D72343

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3913937_c3_93.....	4534	9756	507	1524	146	3.9e-14
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3948412_c1_72.....	4535	9757	418	1257		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4351417_c1_68	4536	9758	394	1185	300	1.4e-26
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable permease perM homolog (perM) RP630			pir:E71668		E71668	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4739778_f2_21	4537	9759	195	588		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
474143_f2_24	4538	9760	543	1632	628	2.8e-95
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
endo-1,4-beta-xylanase,			pir:T30909		T30909	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4976501_f1_9	4539	9761	339	1020	242	2.0e-20
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
regulatory protein pchR-2:protein slr1489:protein slr1489			pir:S74456		S74456	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5964205_f3_58	4540	9762	71	216		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6914125_f3_55	4541	9763	242	729	363	3.0e-33

Protein name

Locus Name

Acc#

sp:YVBG_BACSU

032244

Description

HYPOTHETICAL 22.6 KD PROTEIN IN OPUCA-ENO INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
895290_c2_83	4542	9764	189	570	137	7.6e-08

Protein name

Locus Name

Acc#

sp:YN23_YEAST

P53832

Description

PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
909513_c2_78	4543	9765	253	762		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10578415_f2_20	4544	9766	1360	4083	335	2.0e-41

Protein name

Locus Name

Acc#

adenylate cyclase homolog

pir:T17197

T17197

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10737900_f3_43	4545	9767	221	666	140	9.3e-08

Protein name

Locus Name

Acc#

Ansh phosphatase

gp:SCAHBAGC2

AF131879

Description

Streptomyces collinus ansatrienin AHBA biosynthetic gene clusterregion 2, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f2_28	4546	9768	159	477	535	1.8e-51

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f3_32	4547	9769	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19537503_f1_8	4548	9770	188	567		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1960876_f1_2	4549	9771	500	1503	96	0.0095
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative glucosyl hydrolase precursor	gp:AF047839				AF047839	
<u>Description</u>	Pseudoalteromonas sp. S9 putative glucosyl hydrolase precursor and adaptive response regulatory protein (ada) genes, complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19688778_c3_87	4550	9772	301	906	165	6.6e-12
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
MsmR	gp:SPU49397				U49397	
<u>Description</u>						
Streptococcus pyogenes MsmR (msmR) gene, partial cds; LepA (lepA), Cpa (cpa), and Nra (nra) genes, complete cds; SsbA (ssbA) gene,partial cds; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20704052_c3_82	4551	9773	465	1398	380	4.7e-35
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein PAB0790			pir:H75098		H75098	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f1_3.....	4552	9774	83	252	64	0.031
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:SPRC_XENLA				P36378	
<u>Description</u>						
(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f3_49	4553	9775	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24229677_c2_64	4554	9776	225	678		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2507010_f2_13.....	4555	9777	349	1050	213	4.2e-16

Protein name

Locus Name

Acc#

hypothetical protein PH1107

pir:D71051

D71051

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25798155_f3_36.....	4556	9778	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33442_f1_9	4557	9779	390	1173	153	1.5e-16
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
transcription regulator AraC/XylS family homolog ydeE			pir:G69777		G69777	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33625407_c1_50.....	4558	9780	118	357	119	1.6e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
transposase			gp:AF038866		AF038866	
<u>Description</u>						

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35555187_c3_80.....	4559	9781	112	339	111	1.2e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
transposase			gp:AF038866		AF038866	
<u>Description</u>						

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36361510_f1_10.....	4560	9782	157	474	116	4.5e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein MTH628			pir:E69183		E69183	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36523937_c2_72	4561	9783	658	1977	243	4.7e-34

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sialic acid-specific 9-O-acetylesterase	gp:MMAS90A	X98625

Description

M.musculus mRNA for sialic acid-specific 9-O-acetylesterase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4095062_c1_53	4562	9784	514	1545	90	0.00020

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
oligopeptide ABC transporter, ATP-binding protein	pir:D72289	D72289

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4103816_c1_57	4563	9785	70	213		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4110010_f3_47	4564	9786	82	249		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4884682_c2_65	4565	9787	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
548762_f2_21.....	4566	9788	220	663	429	3.0e-40

Protein name

Locus Name

Acc#

sp:YJV8_YEAST

P40892

Description

(EC 2.3.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
587763_f3_41.....	4567	9789	170	513	212	3.0e-17

Protein name

Locus Name

Acc#

hypothetical protein TM0383

pir:G72383

G72383

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6364505_f3_29.....	4568	9790	260	783		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
7031556_f1_11	4569	9791	174	525		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
866537_f3_35	4570	9792	654	1965	354	4.4e-40
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
alpha-glucosidase			gp:BTU66897		U66897	
<u>Description</u>						

Bacteroides thetaiotaomicron neopullulanase (susA) and alpha-glucosidase (susB) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15097187_f3_38	4571	9793	118	357		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
17074063_f2_13	4572	9794	98	297		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
193757_f2_27	4573	9795	788	2367	830	9.8e-83
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20820162_f2_11	4574	9796	597	1794	1587	5.9e-163
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
immunoreactive 87kD antigen PG92			gp:AF175724		AF175724	
<u>Description</u>						

Porphyromonas gingivalis strain W50 immunoreactive 87kD antigenPG92 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22478383_f3_37	4575	9797	188	567	215	1.4e-17
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
RNA polymerase ECF-type sigma factor sigW			pir:H69706		H69706	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22698312_f1_7	4576	9798	359	1080		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24023387_f2_12	4577	9799	839	2520	1103	1.2e-111
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative secreted beta-galactosidase	gp:SCF81				AL133171	
<u>Description</u>	Streptomyces coelicolor cosmid F81.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24219562_f1_9	4578	9800	292	879	338	1.3e-30
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein	pir:S76053				S76053	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25484661_f2_20.....	4579	9801	567	1704	1736	9.6e-179
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
ABC transporter (ATP-binding protein) homolog ykpA	pir:E69861				E69861	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25595943_f2_10.....	4580	9802	68	207		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26306512_c1_56	4581	9803	395	1188	1301	1.2e-132
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
immunoreactive heat shock protein DnaJ				gp:AF145797		AF145797
<u>Description</u>						
Porphyromonas gingivalis strain W50 immunoreactive heat shockprotein DnaJ gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34181503_f1_2	4582	9804	544	1635	130	5.1e-09
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
outer membrane protein				gp:BNROMPB		L77614
<u>Description</u>						
Bacteroides thetaiotaomicron outer membrane protein (susD) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34553375_c2_78.....	4583	9805	83	252		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35797208_f2_14.....	4584	9806	841	2526	407	1.1e-70
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36360255_f2_26	4585	9807	347	1044	261	1.9e-22

Protein name

Locus Name

Acc#

sp:PLC_BACCE

P14262

Description

(PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36540925_f2_25	4586	9808	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4328182_c3_89.....	4587	9809	353	1062	149	5.7e-07

Protein name

Locus Name

Acc#

surface antigen BspA

pir:T31094

T31094

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4879627_f1_8.....	4588	9810	292	879	259	3.1e-22

Protein name

Locus Name

Acc#

probable transmembrane protein

pir:T34651

T34651

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6283150_f1_1	4589	9811	261	786	789	2.2e-78
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
immunoreactive 87kD antigen PG92	gp:AF175724				AF175724	
<u>Description</u>	Porphyromonas gingivalis strain W50 immunoreactive 87kD antigenPG92 gene, complete cds.					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6640682_c1_55	4590	9812	255	768	309	1.6e-27
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:GREP_FRATU				P48204	
<u>Description</u>						
GRPE PROTEIN						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10000261_c3_250.....	4591	9813	297	894	603	1.1e-58
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
integrase	gp:BFU75371				U75371	
<u>Description</u>						
Bacteroides fragilis transposon Tn4555 TnpA (tnpA), integrase(int), TnpC (tnpC), excisionase (xis), mobilization protein (mobA),and beta-lactamase (cfxA) genes, complete cds; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10555153_c3_255.....	4592	9814	573	1722	373	5.3e-34
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein sll0855				pir:S74833		S74833
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1203515_c3_268	4593	9815	60	183		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13750040_c1_159.....	4594	9816	80	243		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13759507_f3_114.....	4595	9817	304	915	159	5.9e-10
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein jhp0651					pir:E71905	E71905
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13782212_f3_105.....	4596	9818	82	249		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13882712_f2_84.....	4597	9819	87	264		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14970628_c1_165	4598	9820	547	1644	355	1.3e-53
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
K+ transport protein homolog			pir:H70430			H70430
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16054635_f2_70	4599	9821	208	627		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16433140_c3_253	4600	9822	76	231		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16695462_f3_104	4601	9823	68	207		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c1_166	4602	9824	431	1296	1723	2.3e-177
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein			pir:JQ1020			JQ1020
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
176875_c1_156	4603	9825	194	585		

Protein name

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
189010_f1_28	4604	9826	1198	3597	111	1.5e-06

Protein name

Description

sp:YY02_METJA Q60301

HYPOTHETICAL PROTEIN MJEC502

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19726387_f1_8	4605	9827	490	1473	2625	6.0e-273

Protein name

Description

sp:CATB_BACFR P45737

CATALASE,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19959762_c2_184	4606	9828	1167	3504		

Protein name

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20101577_f1_50	4607	9829	334	1005	514	3.0e-49

Protein name

Locus Name

Acc#

hemin permease

pir:S54438

S54438

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20110930_f1_14	4608	9830	461	1386	1259	3.4e-128

Protein name

Locus Name

Acc#

tryptophan synthase, subunit beta (trpB-1)
homolog

pir:G69404

G69404

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20312527_c3_266	4609	9831	203	612	203	2.7e-16

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20320177_f2_75	4610	9832	278	837	103	0.0042

Protein name

Locus Name

Acc#

branched-chain amino acid ABC transporter,
ATP-binding protein (braG-4) homolog

pir:D69423

D69423

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20422203_f3_101	4611	9833	305	918	941	1.7e-94

Protein name

Locus Name

Acc#

sp:END4_ECOLI

Description

ENDONUCLEASE IV, (ENDODEOXYRIBONUCLEASE IV)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20517142_f2_74	4612	9834	855	2568		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20706678_c2_177.....	4613	9835	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2115625_c2_207.....	4614	9836	285	858	107	1.1e-06

Protein name

Locus Name

Acc#

sp:YZ35_METJA

Q60291

Description

HYPOTHETICAL PROTEIN MJECL35

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2150262_f1_22	4615	9837	194	585		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21739427_f1_21	4616	9838	161	486		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22386007_c1_160	4617	9839	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22461713_f2_69	4618	9840	82	249	101	3.9e-05

Protein name

Locus Name

Acc#

gp:BP053767

U53767

Description

Bacillus pumilus plasmid pSH1452, Rep gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c2_211	4619	9841	83	252	64	0.031

Protein name

Locus Name

Acc#

sp:SPRC_XENLA

P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23478176_f1_25	4620	9842	124	375	94	0.00045

Protein name

Locus Name

Acc#

TnpC

gp:BFU75371

U75371

Description

Bacteroides fragilis transposon Tn4555 TnpA (tnpA), integrase(int), TnpC (tnpC), excisionase (xis), mobilization protein (mobA), and beta-lactamase (cfxA) genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23628262_f2_86	4621	9843	70	213	53	0.0033

Protein name

Locus Name

Acc#

hypothetical protein BB0404

pir:C70150

C70150

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23992136_f1_7	4622	9844	849	2550	323	4.9e-39

Protein name

Locus Name

Acc#

putative alpha-glucosidase

gp:AAC252161

AJ252161

Description

Alicyclobacillus acidocaldarius maltose/maltodextrine transport gene region (malEFGR genes, cdaA gene and glcA gene).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24020312_c2_221	4623	9845	962	2889	436	2.7e-37
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24237762_c1_176	4624	9846	325	978		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24241377_f3_93	4625	9847	320	963	1564	1.6e-160
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
beta-lactamase, A precursor:cephalosporinase			pir:I40192			
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24329702_c2_182	4626	9848	174	525	79	0.036
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:AF048749		AF048749	
<u>Description</u>						
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415932_f3_107	4627	9849	422	1269	119	0.00030

Protein name

Locus Name

Acc#

sp:Y665_HAEIN

P44033

Description

HYPOTHETICAL PROTEIN HI0665

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648550_f3_109	4628	9850	213	642		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25658441_c2_222.....	4629	9851	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25945152_f2_71.....	4630	9852	1215	3648	93	0.014

Protein name

Locus Name

Acc#

rhoptry protein

pir:T28676

T28676

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26594683_c2_185	4631	9853	728	2187		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26597832_f3_113	4632	9854	679	2040		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3006377_f2_66	4633	9855	98	297	113	4.0e-06
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
AbiEii				gp:LLU36837		U36837
<u>Description</u>						

Lactococcus lactis plasmid pNP40, abortive infection locus, AbiEi,AbiEii, RecA(LP), AbiF genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30128208_c2_206	4634	9856	96	291		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32243757_f1_26	4635	9857	89	270		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34257752_c2_216.....	4636	9858	369	1110	209	7.6e-24

Protein name

Locus Name

Acc#

sp:XYLB_BACOV

P49943

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34578410_c3_254.....	4637	9859	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35665952_f3_95.....	4638	9860	127	384	644	5.0e-63

Protein name

Locus Name

Acc#

hypothetical protein 2

pir:I40233

I40233

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35792967_c2_183.....	4639	9861	660	1983	2579	4.5e-268

Protein name

Locus Name

Acc#

DnaK

gp:AB015879

AB015879

Description

Porphyromonas gingivalis dnaK operon genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3959627_c3_225	4640	9862	196	591	295	4.8e-26

Protein name

Locus Name

Acc#

ORF5

gp:AB015879

AB015879

Description

Porphyromonas gingivalis dnaK operon genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4147126_f1_32	4641	9863	318	957	534	2.3e-51

Protein name

Locus Name

Acc#

5'-nucleotidase

gp:CL1131243

AJ131243

Description

Columba livia mRNA for 5'-nucleotidase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4173530_c2_192	4642	9864	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
42700_c1_167	4643	9865	95	288	163	3.1e-11

Protein name

Locus Name

Acc#

Na+-ATPase chain J:protein slr1509:protein slr1509

pir:S75455

S75455

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4727280_f2_87	4644	9866	396	1191	277	8.9e-23

Protein name

Locus Name

Acc#

sp:Y878_METJA

Q58288

Description

HYPOTHETICAL PROTEIN MJ0878

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4727337_f1_29	4645	9867	536	1611	127	1.4e-13

Protein name

Locus Name

Acc#

hypothetical protein PAB1002

pir:G75064

G75064

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4954832_f2_55.....	4646	9868	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5274003_c1_138.....	4647	9869	724	2175	438	3.0e-52

Protein name

Locus Name

Acc#

otnA protein

pir:S70958

S70958

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9798467_c1_140.....	4648	9870	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
984805_c1_168	4649	9871	233	702	294	6.2e-26

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_1503

pir:G70430

G70430

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1211062_f2_93	4650	9872	84	255	90	0.0068

Protein name

Locus Name

Acc#

CryIA toxin receptor A

gp:AF173552

AF173552

Description

Heliothis virescens CryIA toxin receptor A mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1226510_c1_222	4651	9873	448	1347	319	1.3e-31

Protein name

Locus Name

Acc#

putative putrescine/spermidine binding protein

gp:PSEPAPHP

L49465

Description

Pseudomonas fluorescens hypothetical metabolite transport protein, positive transcriptional regulator (phnR), phosphonoacetatehydrolase (phnA), 2-phosphonopropionate transporter (phnB), putative putrescine/spermidine binding protein, and putativemethionine sulfoxide reductase genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13906285_f1_29	4652	9874	1069	3210	393	1.8e-48

Protein name

Locus Name

Acc#

histidine protein kinase homolog GacS

gp:AF197912

AF197912

Description

Azotobacter vinelandii histidine protein kinase homolog GacS (gacS) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14225953_f3_194	4653	9875	65	198	158	1.6e-11
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein APE2061	pir:G72510				G72510	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14485880_f1_53.....	4654	9876	395	1188	206	4.5e-16
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:TLPA_BRAJA				P43221	
<u>Description</u>						
PROTEIN TLPA)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14539662_f3_160.....	4655	9877	204	615	308	2.0e-27
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein MTH671	pir:D69189				D69189	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14630035_c2_271.....	4656	9878	597	1794	1319	1.5e-134
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
probable V-type ATPase, subunit A (atpA-1)	pir:G71325				G71325	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15712666_f1_24	4657	9879	198	597	222	2.6e-18
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					sp:YJJP_HAEIN	P44520
<u>Description</u>						
HYPOTHETICAL PROTEIN HI0108						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15719042_c2_270	4658	9880	296	891	93	5.1e-06
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein BB0095					pir:G70111	G70111
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16539038_c3_351.....	4659	9881	199	600	427	5.0e-40
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
2-keto-3-deoxygluconate kinase					pir:G72422	G72422
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16610827_f1_37.....	4660	9882	468	1407	753	1.4e-74
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
Na+/H+ antiporter (nhaC-1) homolog					pir:D70179	D70179
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16833455_c2_316	4661	9883	304	915	589	3.4e-57
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
cation efflux system protein			gp:AF203881		AF203881	
<u>Description</u>						
Zymomonas mobilis strain ZM4 clone 43F4, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19687750_c1_228	4662	9884	75	228		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20972755_f3_146.....	4663	9885	85	258	78	0.0019
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:PRS6_MANSE		P46507	
<u>Description</u>						
26S PROTEASE REGULATORY SUBUNIT 6B (ATPASE MS73)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21515678_c3_334.....	4664	9886	865	2598	1621	1.5e-166
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein PH1512			pir:D71027		D71027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22445301_f2_87	4665	9887	231	696	122	2.0e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF125164	AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22454707_f3_161	4666	9888	356	1071	1394	1.7e-142

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RIR2_TREPA	083092

Description

(RIBONUCLEOTIDE REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23595180_c1_266.....	4667	9889	403	1212	268	1.7e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YRKO_BACSU	P54442

Description

HYPOTHETICAL 46.4 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23631627_c1_213.....	4668	9890	444	1335	1018	1.2e-102

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable V-type ATPase, subunit B (atpB-1)	pir:H71325	H71325

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24253311_f3_167	4669	9891	405	1218	213	3.9e-15

Protein name

Locus Name

Acc#

gp:AB016260

Description

Agrobacterium tumefaciens plasmid pTi-SAKURA, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24257692_f1_9	4670	9892	599	1800	649	1.5e-63

Protein name

Locus Name

Acc#

TonB-dependent receptor HmuR

gp:PGU87395

U87395

Description

Porphyromonas gingivalis TonB-dependent receptor HmuR (hmuR) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24347153_c3_330.....	4671	9893	623	1872	559	5.1e-54

Protein name

Locus Name

Acc#

V-type ATPase, subunit I homolog

pir:C70111

C70111

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24509627_c3_350.....	4672	9894	142	429	494	3.9e-47

Protein name

Locus Name

Acc#

2-keto-3-deoxygluconate kinase

pir:G72422

G72422

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24806567_c1_238	4673	9895	119	360	245	9.6e-21

Protein name conserved hypothetical protein MTH1285 Locus Name pir:A69038 Acc# A69038

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25469832_t3_184	4674	9896	252	759	824	4.2e-82

Protein name 30S ribosomal protein S16-like protein Locus Name gp:AF137263 Acc# AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25984388_t1_47	4675	9897	447	1344		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26288442_c3_348	4676	9898	154	465	233	1.8e-19

Protein name conserved hypothetical protein yvbK Locus Name pir:B70030 Acc# B70030

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26365691_c2_287	4677	9899	243	732	184	1.0e-22

Protein name Locus Name Acc#
hypothetical protein pir:B75629 B75629

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
293337830_c1_231	4678	9900	371	1116	214	7.6e-25

Protein name Locus Name Acc#
hypothetical protein pir:H75628 H75628

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29589842_c2_268	4679	9901	65	198		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30493775_c3_332	4680	9902	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31461016_c3_380	4681	9903	515	1548	700	5.8e-69

Protein name Locus Name Acc#
sp:YHCA_BACSU P54585

Description

HYPOTHETICAL 58.3 KD PROTEIN IN GLPD-CSPE INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31833126_f2_86	4682	9904	309	930	106	0.021
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
probable erythrocyte-binding protein MAEBL			pir:T09129			T09129
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32042553_c2_317	4683	9905	61	186		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32234752_f2_91	4684	9906	117	354	73	0.016
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein MTH670			pir:C69189			C69189
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33236050_c3_377	4685	9907	138	417		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33401552_c1_230	4686	9908	211	636	386	1.1e-35
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
peptide chain release factor homolog prfH			pir:E64748			E64748
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33711081_f2_136	4687	9909	99	300	111	2.4e-06
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein			gp:SSU18930			Y18930
<u>Description</u>						
Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3398466_f2_90	4688	9910	1467	4404	687	4.4e-125
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
cobalamin biosynthesis protein N			pir:C69048			C69048
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34065926_c1_265.....	4689	9911	231	696	231	5.8e-26
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein aq_1060			pir:D70391			D70391
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34081405_c1_212.....	4690	9912	88	267	110	1.9e-06
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
hypothetical protein PHS004			pir:F71245			F71245
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34242285_c1_221	4691	9913	269	810	469	1.8e-44
Protein name			Locus Name		Acc#	
spermidine/putrescine ABC transporter, permease protein (potC) homolog			pir:G70179		G70179	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34648557_c2_279	4692	9914	137	414		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35352135_c3_339	4693	9915	417	1254	97	0.038
Protein name			Locus Name		Acc#	
hypothetical protein DKFZp566D1824.1			pir:T14767		T14767	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3926531_f2_94	4694	9916	260	783	257	5.1e-22
Protein name			Locus Name		Acc#	
			sp:YJJP_ECOLI		P39402	
Description						
HYPOTHETICAL 30.5 KD PROTEIN IN DNAT-BGLJ INTERGENIC REGION (F277)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3939211_f2_89	4695	9917	185	558	206	1.4e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
TonB-dependent receptor HmuR	gp:PGU87395	U87395

Description

Porphyromonas gingivalis TonB-dependent receptor HmuR (hmuR) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4069152_c1_241	4696	9918	227	684	262	1.5e-22

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase	pir:F72422	F72422

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4103530_c3_326	4697	9919	199	600	152	6.9e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
V-type ATPase, subunit E homolog	pir:H70111	H70111

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4148892_c1_217	4698	9920	220	663		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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489680_f1_43	4699	9921	130	393		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4900276_f2_92	4700	9922	840	2523	2812	9.2e-293
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Protein name

Locus Name

Acc#

sp:RIR1_TREPA

083972

Description

(RIBONUCLEOTIDE REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4956537_f1_17	4701	9923	234	705	99	0.012
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Protein name

Locus Name

Acc#

conserved hypothetical protein AF1223

pir:F69402

F69402

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4960967_f3_145	4702	9924	79	240		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
501952_c3_336	4703	9925	470	1413	1004	3.6e-101
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
spermidine/putrescine ABC transporter, ATP-binding protein (potA) homolog			pir:A70180		A70180	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5285927_c1_214.....	4704	9926	204	615	231	2.9e-19
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable V-type ATPase, subunit D (atpD-1)			pir:A71326		A71326	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5892183_c3_342.....	4705	9927	439	1320	1009	1.1e-101
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
rtcB protein			pir:D75521		D75521	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5909512_c3_333.....	4706	9928	593	1782	427	4.8e-60
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
UDPGlucose--glycogen glucosyltransferase,, skeletal muscle:glycogen(starch) synthase:glycogen(starch) synthase			pir:A33369			
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6912588_c2_278	4707	9929	268	807	426	6.3e-40
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
spermidine/putrescine ABC transporter, permease protein (potB) homolog			pir:H70179		H70179	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
7072953_c1_243	4708	9930	72	219		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
781561_c3_338	4709	9931	133	402	294	6.2e-26
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
glycine-rich RNA-binding protein (clone A81)			pir:S31443		S31443	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
791537_c1_225	4710	9932	688	2067	55	0.036
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:CPU53466		U53466	
<u>Description</u>						

Cydia pomonella granulosus virus ORF13L gene, partial cds, ORF15L, ORF15R, ORF16L, ORF17L genes, complete cds, ORF17R gene, partialcds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
970262_c2_274	4711	9933	163	492	228	6.1e-19
Protein name			Locus Name		Acc#	
hypothetical protein PH1980			pir:D71214		D71214	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
975186_c3_379	4712	9934	540	1623	749	3.7e-74
Protein name			Locus Name		Acc#	
			sp:YIDE_HAEIN		P44472	
Description						
HYPOTHETICAL PROTEIN HI0035						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11882928_f1_24	4713	9935	65	198		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11929010_f1_30	4714	9936	75	228		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1192950_f1_6	4715	9937	67	204		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12112502_c3_184.....	4716	9938	519	1560		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12535687_f2_39.....	4717	9939	735	2208	580	3.4e-76
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
hypothetical protein TM0280				pir:F72395		F72395
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1282807_c2_129.....	4718	9940	64	195	53	0.017
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:RYL2_YARLI		P41925
<u>Description</u>						

RAS-LIKE GTP-BINDING PROTEIN RYL2

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13066438_f2_54	4719	9941	88	267		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13798552_f2_57	4720	9942	69	210		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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14709701_c1_123	4721	9943	363	1092	521	5.4e-50
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Protein name

Locus Name

Acc#

FuCR

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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187637_c2_130	4722	9944	641	1926		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22353385_f2_44	4723	9945	157	474	313	6.0e-28
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein slr0698			pir:S77038		S77038	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22939206_c1_101	4724	9946	393	1182	908	5.3e-91
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein			pir:H72299		H72299	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23615930_c3_176	4725	9947	696	2091	457	3.1e-41
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:BGAL_THETU		P26257	
<u>Description</u>						
BETA-GALACTOSIDASE, (LACTASE)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23625926_c1_126	4726	9948	390	1173	246	6.8e-19
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:AF141932		AF141932	
<u>Description</u>						
Rhizobium leguminosarum bv. trifolii plasmid PR1e162Y10C rspDEFoperon, partial sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24259438_c1_125	4727	9949	204	615	98	0.026

Protein name Locus Name Acc#
protein kinase,, cGMP-dependent pir:B28269 B28269

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24335301_f2_43	4728	9950	606	1821	1237	7.3e-126

Protein name Locus Name Acc#
sp:LCFH_HAEIN P44446

Description

ACYL-COA SYNTHETASE) (LACS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24626876_f3_63	4729	9951	469	1410		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24640762_c1_95	4730	9952	380	1143		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26595067_f1_15	4731	9953	433	1302	244	3.7e-20

Protein name Locus Name Acc#

hypothetical protein MTH1451 pir:C69060 C69060

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29462801_f1_2	4732	9954	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33729675_f3_65.....	4733	9955	848	2547	313	8.0e-26

Protein name

Locus Name

Acc#

putative alpha-L-arabinofuranosidase

gp:ATAC011708

AC011708

Description

Arabidopsis thaliana chromosome III BAC T7M13 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34178305_f1_14.....	4734	9956	444	1335	146	5.3e-07

Protein name

Locus Name

Acc#

sp:PORP_PSEAE

P05695

Description

PORIN P PRECURSOR (OUTER MEMBRANE PROTEIN D1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34252176_c1_93.....	4735	9957	84	255	116	1.1e-05

Protein name

Locus Name

Acc#

Styrene sensor kinase

gp:PSSTYCATA

AJ000330

Description

Pseudomonas sp. DNA for styrene catabolism genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34406517_c2_127	4736	9958	1119	3360	826	7.2e-97

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34410751_f3_75	4737	9959	860	2583	419	3.1e-37

Protein name

Locus Name

Acc#

unknown

gp:AF007381

AF007381

Description

Flavobacterium johnsoniae gliding motility protein (gldA) gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3907253_f3_66	4738	9960	882	2649	1066	1.1e-127

Protein name

Locus Name

Acc#

hypothetical protein SCF34.07

pir:T36406

T36406

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4176462_c2_128	4739	9961	272	819		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
424193_f3_71	4740	9962	354	1065	697	1.2e-68

Protein name

Locus Name

Acc#

sp:RF2_ECOLI

Description

PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4330312_c1_98	4741	9963	306	921	160	8.0e-13

Protein name

Locus Name

Acc#

hypothetical protein

pir:T33724

T33724

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4689392_f1_1	4742	9964	135	408		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5345192_c1_99	4743	9965	514	1545	705	1.7e-69

Protein name

Locus Name

Acc#

sp:HEXA_PORGI

P49008

Description

(BETA-NAHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13765751_f2_15	4748	9970	299	897	143	3.3e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
cytochrome b			gp:GPA249395		AJ249395	
<u>Description</u>						
Globodera pallida mitochondrial COII, ND4, COIII, ND6, ND1, ND3 andcytb genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13838463_f2_11	4749	9971	69	210		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15709788_f3_17	4750	9972	405	1218		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21646915_f2_8	4751	9973	246	741		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22848775_c1_23	4752	9974	199	600	92	0.00035

Protein name

Locus Name

Acc#

sp:DNU4_RHORU

P15017

Description

PROBABLE TRANSCRIPTIONAL REGULATOR IN ATPASE CF(0) REGION (URF4)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23444088_c1_24	4753	9975	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25834567_e1_1	4754	9976	244	735	75	0.039

Protein name

Locus Name

Acc#

gp:MUSIGKBJ

M13606

Description

Mouse Ig active kappa-chain VJ2 mRNA from HP22.134.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29859506_e2_7	4755	9977	183	552		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34570927_f1_2	4756	9978	329	990		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35142837_c3_40	4757	9979	65	198	78	0.021
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
hypothetical protein C17F3.3				pir:T32879		T32879
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4162818_f2_14	4758	9980	133	402	72	0.021
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
conserved hypothetical protein BBI40				pir:G70244		G70244
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5859640_f2_9	4759	9981	422	1269	88	0.0055
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
unknown				gp:AF033858		AF033858
<u>Description</u>						

Pediococcus pentosaceus strain ATCC43200 plasmid pMD136, complete plasmid sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11769375_c2_42	4760	9982	681	2046	240	4.1e-25

Protein name receptor antigen (RagA) Locus Name gp:PGI130872 Acc# AJ130872

Description
Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16579388_c3_46	4761	9983	190	573	401	2.8e-37

Protein name Locus Name sp:Y4PL_RHISN Acc# P55617

Description
PUTATIVE INSERTION SEQUENCE ATP-BINDING PROTEIN Y4PL

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20265_c1_37	4762	9984	89	267		

Protein name Locus Name Acc#

Description
NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32501380_f3_28	4763	9985	130	393		

Protein name Locus Name Acc#

Description
NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34181512_c2_38	4764	9986	207	624		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36429763_c1_34.....	4765	9987	79	240	66	0.011
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>

gp:ATAC011020 AC011020

Description

Arabidopsis thaliana chromosome I BAC F12B7 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4098562_f1_4.....	4766	9988	92	279	77	0.015
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>

probable sigK protein pir:F70830 F70830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5276442_c3_47.....	4767	9989	156	471		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
85151_c2_41	4768	9990	299	900	436	7.4e-40

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14885458_f2_3	4769	9991	600	1803	563	1.9e-54

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:BGAL_THETU	P26257

Description

BETA-GALACTOSIDASE, (LACTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10837887_c3_30	4770	9992	374	1125	1011	6.5e-102

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
CDP-glucose-4,6-dehydratase	pir:D47070	D47070

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14640675_c3_31	4771	9993	298	894	950	1.9e-95

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
CDP-tyvelose epimerase	gp:YPU29691	U29691

Description

Yersinia pseudotuberculosis group
IVACDP-4-keto-6-deoxy-D-glucose-3-dehydrase (ddhC) gene, partial
cds, CDP-paratose synthetase (prt) and CDP-tyvelose epimerase (tyv) genes,
complete cds, and putative O antigen export protein (wzx) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20312800_c1_22	4772	9994	306	921	225	1.3e-18

Protein name

Locus Name

Acc#

dTDP-glucose 4,6-dehydratase

pir:H69105

H69105

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20507213_c3_29	4773	9995	86	261		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24880278_f2_12	4774	9996	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
391531_f1_5	4775	9997	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
46378150_c1_20	4776	9998	285	858	475	4.1e-45

Protein name

Locus Name

Acc#

glucose-1-phosphate cytidylyltransferase,

pir:C47070

C47070

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13070915_c1_11	4777	9999	845	2538	679	3.4e-66
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4400952_c3_13	4778	10000	264	795	445	8.0e-41
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10635936_f1_15	4779	10001	419	1260		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11829203_c1_283	4780	10002	270	813	132	2.5e-08
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:D86934		D86934	
<u>Description</u>						
Staphylococcus aureus genes, mec region, partial and complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12298437_c2_380	4781	10003	321	966	252	1.7e-21

Protein name

Locus Name

Acc#

sp:YYAM_BACSU

P37511

Description

HYPOTHETICAL 32.9 KD PROTEIN IN TETB-EXOA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13865675_c1_304	4782	10004	312	939	964	6.2e-97

Protein name

Locus Name

Acc#

homoserine O-succinyltransferase

pir:C72324

C72324

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13868955_f3_200.....	4783	10005	111	336		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1407956_c3_406.....	4784	10006	147	444		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14640762_f2_103	4785	10007	86	261		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14657700_c1_301.....	4786	10008	642	1929	155	2.3e-10
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
conserved hypothetical protein			pir:E75439		E75439	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15703215_f3_266.....	4787	10009	61	186		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
159562_f1_41.....	4788	10010	74	225	209	6.3e-17
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:FER_BUTME		P14073
<u>Description</u>						

FERREDOXIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16615912_f3_261	4789	10011	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c2_358.....	4790	10012	431	1296	1723	2.3e-177

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19689075_c1_334.....	4791	10013	867	2604	453	1.5e-39

Protein name

Locus Name

Acc#

hypothetical protein F10M10.30

pir:T04772

T04772

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19710881_f1_89.....	4792	10014	216	651	79	0.012

Protein name

Locus Name

Acc#

gp:TCU64729

U64729

Description

Toxocara canis TcH SLdT.460 mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19770066_c2_351	4793	10015	389	1170	652	7.1e-64
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
potassium-dependent ATPase subunit D'			gp:AF213466		AF213466	
<u>Description</u>						
Anabaena sp. L-31 kdp operon, complete sequence.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20119033_f1_10	4794	10016	191	576	144	4.1e-20
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:PNUC_SALTY		P24520	
<u>Description</u>						
PNUC PROTEIN						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
204687_c2_352	4795	10017	64	195		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22298176_f1_91	4796	10018	62	189		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23632875_c3_403	4801	10023	573	1722	1228	6.5e-125

Protein name

Locus Name

Acc#

potassium-translocating ATPase A chain

gp:AAC243194

AJ243194

Description

Alicyclobacillus acidocaldarius kdpA gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23960013_c3_418	4802	10024	954	2865	935	2.4e-115

Protein name

Locus Name

Acc#

putative secreted protein

gp:SCF41

AL117387

Description

Streptomyces coelicolor cosmid F41.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24007761_c1_297.....	4803	10025	986	2961		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24322063_c2_362.....	4804	10026	333	1002		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24322712_c1_295	4805	10027	1152	3459	754	5.3e-132

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24334692_f3_240	4806	10028	222	669		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24640915_f2_106	4807	10029	209	630	297	3.0e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein jhp1211	pir:C71832	C71832
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642818_f2_187	4808	10030	118	357	98	3.6e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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gp:SSK3MECA1 Y13052

Description

S.sciuri mecA1 gene, strain K3(MM2).

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24804691_c1_298	4809	10031	257	774		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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24820326_c1_322.....	4810	10032	290	873	607	1.2e-58
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Protein name

Locus Name

Acc#

aspartate kinase, / homoserine dehydrogenase,
T16H5.70:protein T16H5.70:protein T16H5.70

pir:T04752

T04752

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
----------	------	------	--------------	--------------	-------	-------------

24866706_c1_293.....	4811	10033	447	1344	423	1.5e-39
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Protein name

Locus Name

Acc#

VicK protein

gp:EFA012050

AJ012050

Description

Enterococcus faecalis vic operon and flanking genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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25277_c3_411.....	4812	10034	798	2397		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2557712_c1_333	4813	10035	208	627	167	1.8e-12

Protein name

Locus Name

Acc#

hypothetical protein sll0687

pir:S74416

S74416

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25835942_c2_385	4814	10036	336	1011	131	7.6e-06

Protein name

Locus Name

Acc#

sp:FECR_ECOLI

P23485

Description

FECR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25945887_c3_417	4815	10037	401	1206	983	6.0e-99

Protein name

Locus Name

Acc#

sp:AAT_BACST

Q59228

Description

ASPARTATE AMINOTRANSFERASE, (TRANSAMINASE A) (ASPAT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29720927_c1_321	4816	10038	527	1584	788	2.8e-78

Protein name

Locus Name

Acc#

sp:AK_METJA

Q57991

Description

PROBABLE ASPARTOKINASE, (ASPARTATE KINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3001402_f3_222	4817	10039	212	639	115	1.9e-06

Protein name

Locus Name

Acc#

gp:SCU40158

U40158

Description

Staphylococcus carnosus response regulator-like protein (orfx)gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30656255_c1_294	4818	10040	193	582	316	2.9e-28

Protein name

Locus Name

Acc#

RNA polymerase sigma factor SigZ-like protein

gp:AF137263

AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30661682_f2_185.....	4819	10041	486	1461	379	8.2e-35

Protein name

Locus Name

Acc#

putative aspartate kinase

gp:ATAC010797

AC010797

Description

Arabidopsis thaliana chromosome III BAC F28J7 genomic sequence,complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30720407_c2_349.....	4820	10042	234	705	359	8.0e-33

Protein name

Locus Name

Acc#

sp:ATKC_MYCTU

P96369

Description

C CHAIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3125011_f3_223	4821	10043	811	2436	253	1.1e-29

Protein name

Locus Name

Acc#

SfTP

gp:AF126201

AF126201

Description

Pseudomonas putida strain S-313 sulfate ester desulfurization genelocus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3132040_f2_120	4822	10044	385	1158	728	6.3e-72

Protein name

Locus Name

Acc#

sp:ASG1_ECOLI

P18840

Description

(L-ASNASE I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32188_f2_186.....	4823	10045	836	2511	971	1.1e-97

Protein name

Locus Name

Acc#

NADH oxidase (noxA-3) homolog

pir:H69299

H69299

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33486502_c3_408.....	4824	10046	340	1023	114	0.00068

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35245635_c3_410	4825	10047	511	1536	129	2.4e-09
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
unknown	gp:U96771				U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36375662_c1_323	4826	10048	451	1356	939	2.8e-94
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:THRC_HAEIN				P44503	
<u>Description</u>						
THREONINE SYNTHASE,						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3912663_f2_122.....	4827	10049	462	1389	1242	2.1e-126
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:RADA_BACSU				P37572	
<u>Description</u>						
DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS HOMOLOG)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3939387_c3_437.....	4828	10050	305	918	551	3.6e-53
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative 30.6 kDa protein	gp:AF037440				AF037440	
<u>Description</u>						
Edwardsiella ictaluri D-3-phosphoglycerate dehydrogenase (serA) gene, partial cds; ribose-5-phosphate isomerase (rpiA), inhibitor of chromosome initiation (iciA), putative 26 kDa protein (yggE), putative 30.6 kDa protein (yggB), and fructose 1,6-bisphosphate aldolase (fda) genes, complete cds; and phosphoglycerate kinase (pgk) gene, partial cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3942202_c2_339	4829	10051	489	1470	267	2.9e-38

Protein name

Locus Name

Acc#

sp:ARSF_HUMAN

P54793

Description

ARYLSULFATASE F PRECURSOR, (ASF)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4078255_c1_281	4830	10052	494	1485	496	2.4e-47

Protein name

Locus Name

Acc#

tripeptidyl aminopeptidase

gp:STMTAPAP

L46588

Description

Streptomyces lividans tripeptidyl aminopeptidase gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4103410_c3_390.....	4831	10053	657	1974		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4414086_c1_289.....	4832	10054	467	1404	859	8.3e-86

Protein name

Locus Name

Acc#

response regulatory protein (rrp-2) homolog

pir:B70195

B70195

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4694087_c2_359	4833	10055	415	1248	1213	2.5e-123

Protein name Locus Name Acc#

GTP cyclohydrolase II, / 3,
4-dihydroxy-2-butanone 4-phosphate synthase,
ribA:ribA protein pir:C70331 C70331

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4881507_c3_439	4834	10056	960	2880	929	3.2e-93

Protein name Locus Name Acc#

115K outer membrane protein precursor:SusC
protein pir:JC6027 JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5173192_c3_419.....	4835	10057	611	1836	1321	9.1e-135

Protein name Locus Name Acc#

sp:YDCP_ECOLI

Description

POTATIVE PROTEASE YDCP PRECURSOR,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5259838_f1_9.....	4836	10058	707	2124	123	3.9e-08

Protein name Locus Name Acc#

heme receptor gp:VIBHUTA L27149

Description

Vibrio cholerae heme receptor (huta) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5272312_c2_350	4837	10059	120	363	88	0.0018

Protein name

Locus Name

Acc#

hypothetical protein Rv0587

pir:F70907

F70907

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5275425_f2_134	4838	10060	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5290912_f3_221	4839	10061	124	375		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5880050_c3_414	4840	10062	111	336		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6366576_f1_13	4841	10063	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6367805_f3_272	4842	10064	212	639	96	0.010

Protein name

Locus Name

Acc#

outer membrane protein 21, Omp21

gp:CAAJ1918

AJ001918

Description

Comamonas acidovorans omp21 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6417192_c3_420	4843	10065	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13757180_f1_23.....	4844	10066	60	183	70	0.033

Protein name

Locus Name

Acc#

hypothetical protein APE1598

pir:A72539

A72539

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16535830_f3_59.....	4845	10067	91	276	69	0.042

Protein name

Locus Name

Acc#

hypothetical protein ORF87

pir:T30436

T30436

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16603402_c2_78	4846	10068	337	1014	943	1.0e-94

Protein name

Locus Name

Acc#

WbnF

gp:AF172324

AF172324

Description

Escherichia coli GalF (galF) gene, partial cds; O-antigen repeatunit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy(wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenaseGnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF)genes, complete cds; and chain length determinant

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21678500_c1_64	4847	10069	474	1425	1297	3.2e-132

Protein name

Locus Name

Acc#

3-isopropylmalate dehydratase, large chain

pir:T29083

T29083

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23631627_c2_74	4848	10070	201	606	462	9.7e-44

Protein name

Locus Name

Acc#

sp:LEUD_HAEIN

P44438

Description

(ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23634425_c1_66	4849	10071	357	1074	1836	2.4e-189

Protein name

Locus Name

Acc#

sp:LEU3_BACFR

P54354

Description

(IMDH) (3-IPM-DH)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24270450_c1_67	4850	10072	528	1587	216	2.0e-14

Protein name

Locus Name

Acc#

unknown

gp:AF036677

AF036677

Description

Salmonella typhimurium putative operon regulated by PmrAB, necessary for 4-aminoarabinose lipid A modification and polymyxin resistance, PmrG (pmrG) gene, partial cds; PmrF (pmrF) gene and 6orf5, complete cds; and PmrD (pmrD) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24335131_f1_25	4851	10073	63	192	106	5.1e-06

Protein name

Locus Name

Acc#

hypothetical protein PH0219

pir:A71245

A71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24337765_c1_68	4852	10074	1032	3096	617	2.6e-86

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
282708_f2_42	4853	10075	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34081405_c2_71	4854	10076	88	267	110	1.9e-06

Protein name

Locus Name

Acc#

hypothetical protein PHS004

pir:F71245

F71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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34407837_c2_73	4855	10077	500	1503	1207	1.1e-122
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Protein name

Locus Name

Acc#

sp:LEU1_HAEIN

P43861

Description

SYNTHASE) (ALPHA-IPM SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4805262_c1_65	4856	10078	512	1539	666	2.3e-65
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Protein name

Locus Name

Acc#

2-isopropylmalate synthase (leuA-1) homolog

pir:E69369

E69369

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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5332506_f1_24	4857	10079	95	288	73	0.034
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Protein name

Locus Name

Acc#

hypothetical protein PH0220

pir:B71245

B71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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5867141_c3_83	4858	10080	218	657	232	2.0e-18
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Protein name

Locus Name

Acc#

lipid A disaccharide synthase

pir:B72014

B72014

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5901877_c2_76	4859	10081	269	810	366	1.4e-33
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
dolichol-phosphate mannosyltransferase			pir:G70463			G70463
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
656551_f3_46	4860	10082	86	261		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10164677_c2_249	4861	10083	154	465	170	1.7e-12
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
proline-rich protein precursor			pir:S23737			S23737
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10241436_f1_8	4862	10084	142	429		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12360002_c2_228	4863	10085	169	510	111	1.4e-05
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
arabinogalactan-like protein			pir:S52994			S52994
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12500183_f2_42	4864	10086	128	387	124	4.4e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein Rv3864	pir:E70656	E70656

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
125037_f1_34	4865	10087	687	2064	439	3.2e-40

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13000040_f3_115	4866	10088	332	999		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13069511_f2_47	4867	10089	121	366		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13956536_c1_183	4868	10090	431	1296		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14587753_c2_217.....	4869	10091	325	978	270	4.5e-22

Protein name

Locus Name

Acc#

sp:TRC4_ECOLI

Description

DNA PRIMASE TRAC, (REPLICATION PRIMASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14727281_f2_72.....	4870	10092	119	360	98	5.8e-05

Protein name

Locus Name

Acc#

sp:DH18_ARATH

P30185

Description

DEHYDRIN RAB18

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15032692_c1_162.....	4871	10093	220	663	101	0.036

Protein name

Locus Name

Acc#

exodeoxyribonuclease V, gamma chain (recC)
homolog

pir:A70179

A70179

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20260_f3_137	4872	10094	589	1770	89	0.041
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:U96771		U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20506501_c2_202	4873	10095	269	810	235	1.1e-19
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein b1488			pir:C64902		C64902	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20594841_f3_117	4874	10096	60	183		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2119013_c1_147	4875	10097	400	1203	115	1.5e-08
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein SC6G4.36c SC6G4.36c			pir:T35587		T35587	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21507338_f1_11	4876	10098	736	2211	559	2.3e-89
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				gp:BFU63096		U63096
<u>Description</u>						
Bacteroides fragilis (bctA) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21578375_c1_197	4877	10099	776	2331	197	3.2e-12
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				gp:AF083424		AF083424
<u>Description</u>						
Ateline herpesvirus 3 complete genome.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22548191_f2_51	4878	10100	177	534	122	5.2e-06
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
hypothetical protein T15B7.3				pir:T32250		T32250
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22906506_c3_309	4879	10101	882	2649	315	5.4e-25
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
mobilization protein C				gp:AF118243		AF118243
<u>Description</u>						
Bacteroides fragilis mobilization protein C (mobC) gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23486336_c1_146	4880	10102	77	234	63	0.0098
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
R07E5.1 protein (clone R07E5)	pir:S43604				S43604	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2350306_c1_144	4881	10103	100	303	111	1.5e-06
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein PH0217	pir:G71244				G71244	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23860937_c2_219	4882	10104	186	561	149	1.4e-10
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:YPSA_BACSU				P50838	
<u>Description</u>						
HYPOTHETICAL 21.1 KD PROTEIN IN COTD-KDUD INTERGENIC REGION						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24265637_f1_12	4883	10105	131	396		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24480382_f1_35	4884	10106	154	465		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24489062_f3_120	4885	10107	286	861		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24504062_f1_14	4886	10108	211	636		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642200_c2_262	4887	10109	192	576		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24693836_c2_230	4888	10110	191	576		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25589017_c1_192	4889	10111	233	702		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25627153_f3_143	4890	10112	74	222		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25878812_f1_10	4891	10113	109	330	85	0.0044

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

antigen 5401	pir:A60643	A60643
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26442203_f3_104	4892	10114	278	837	125	2.0e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

chromosome partitioning ATPase Soj	pir:D75570	D75570
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26752162_f2_60	4893	10115	213	642		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26751652_f2_71	4894	10116	359	1080		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29354192_c2_253	4895	10117	349	1050	79	0.027

Protein name

Locus Name

Acc#

gp:S83195

S83195

Description

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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3136318_c1_189	4896	10118	226	681	108	2.3e-08

Protein name

Locus Name

Acc#

sperm mitochondrial capsule selenoprotein

pir:A37199

A37199

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31423591_f1_17.....	4897	10119	116	351	116	7.5e-06

Protein name

Locus Name

Acc#

major ampullate fibroin protein

pir:A36068

A36068

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31432007_c2_234.....	4898	10120	101	306	118	3.8e-06

Protein name

Locus Name

Acc#

KIAA0775 protein

gp:AB018318

AB018318

Description

Homo sapiens mRNA for KIAA0775 protein, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31836561_c1_166	4899	10121	596	1791	313	3.1e-27

Protein name

Locus Name

Acc#

gp:CBGIDPAB

Y10436

Description

C.burnetii put. genes for encoding glucose inhibited divisionprotein A and B.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33398568_c1_145	4900	10122	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33792215_f2_67.....	4901	10123	457	1374		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34119841_f2_54.....	4902	10124	240	723	111	0.00096

Protein name

Locus Name

Acc#

troponin T

pir:S02708

S02708

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34181583_f3_116	4903	10125	194	585		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34407575_f1_20	4904	10126	155	468		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34413942_f2_55	4905	10127	101	306		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34473416_c2_223	4906	10128	251	756		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34495965_f1_31	4907	10129	110	333		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34652032_f3_107	4908	10130	407	1224	162	3.0e-08
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical 119.5K protein (uvrA region):ORF1 protein			pir:JQ0405		JQ0405	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35239458_c1_179.....	4909	10131	134	405	100	3.5e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
latent nuclear antigen			gp:AF083501		AF083501	
<u>Description</u>						

Macaca mulatta rhadinovirus 17577 R1, dihydrofolate reductase, complement binding protein, ssDNA binding protein, transport protein, glycoprotein B, DNA polymerase, R2, thymidylate synthase, R3, Bcl-2 homolog, capsid protein, tegument protein, thymidine kinase, glycoprotein H, major capsid protein, capsid protein, kinase, alkaline exonuclease, glycoprotein M,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35267567_c3_299.....	4910	10132	476	1431	89	0.0035
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
beta-D-galactosidase			gp:BRPLACZ01		M63097	
<u>Description</u>						

Brugia malayi beta-D-galactosidase (lacZ) mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36067343_c3_308.....	4911	10133	286	861	179	9.1e-12
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
MocB (Tn4399)			pir:B48487		B48487	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36150277_c1_164	4912	10134	65	198		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36442965_c3_270.....	4913	10135	69	210	63	0.014
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
envelope protein				gp:HTVENVHE		M61052
<u>Description</u>						

Human T-cell leukemia virus I (HTLV1) envelope (env) gene, 5' end.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36509443_f3_131.....	4914	10136	684	2055	375	1.7e-31
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
hypothetical protein slr1135				pir:S77439		S77439
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36520337_c1_196.....	4915	10137	132	399		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
400767_c3_284.....	4916	10138	168	507	228	6.1e-19
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
DNA repair protein RadC				pir:C70439		C70439
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4027135_f3_110	4917	10139	337	1014		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
500925_c3_266.....	4918	10140	442	1329	867	1.2e-86

Protein name

Locus Name

Acc#

transposase

gp:AF038866

AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
593752_f1_16.....	4919	10141	104	315	81	6.7e-05

Protein name

Locus Name

Acc#

hypothetical protein

pir:B40505

B40505

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
813902_f3_132.....	4920	10142	112	339	83	0.0034

Protein name

Locus Name

Acc#

putative resolvase

gp:DASOR

Description

Desulfurolobus ambivalens tnpA, tnpB, rfbD and sor genes and ORF2, ORF3, ORF4 and ORF5.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12944067_f2_4	4921	10143	334	1005		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4095192_f1_1	4922	10144	309	930		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1226063_c3_5	4923	10145	174	522		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
183_c1_18	4924	10146	425	1278	1208	8.6e-123
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

sp:KBL_ECOLI

P07912

Description

(GLYCINE ACETYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25783462_f1_7	4925	10147	244	735		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34181515_f2_8	4926	10148	349	1050		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5189062_c2_27	4927	10149	139	420	77	0.018
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH0778					pir:D71126	D71126
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5257762_f2_9	4928	10150	309	930	106	0.0078
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					gp:D42067	D42067
<u>Description</u>						

Porphyromonas gingivalis DNA for Fimbrilin, ORF1-4, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
676887_f1_5	4929	10151	68	207	130	1.5e-08
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:VCH231106		AJ231106	
<u>Description</u>						
Vibrio cholerae z47f gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
785285_f2_11	4930	10152	324	975	570	3.5e-55
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein F08F3.4			pir:T29433		T29433	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10757933_f2_49.....	4931	10153	589	1770	107	3.4e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
unknown			gp:U96771		U96771	
<u>Description</u>						
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10938205_c1_106.....	4932	10154	1060	3183	565	1.8e-57
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
beta-N-Acetylglucosaminidase			gp:AB008771		AB008771	
<u>Description</u>						
Streptomyces thermoviolaceus nagA gene for beta-N-Acetylglucosaminidase, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14657927_f3_70	4933	10155	242	729	563	1.9e-54
Protein name			Locus Name		Acc#	
			sp:Y796_METJA		Q58206	
Description						
HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0796						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
17010202_f2_40	4934	10156	148	447	218	1.5e-17
Protein name			Locus Name		Acc#	
conserved hypothetical protein MTH695			pir:F69192		F69192	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1995305_f3_73	4935	10157	261	786	214	1.8e-17
Protein name			Locus Name		Acc#	
RNA polymerase sigma factor SigZ-like protein			gp:AF137263		AF137263	
Description						
Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19972762_g2_124	4936	10158	1007	3024	566	5.9e-58
Protein name			Locus Name		Acc#	
beta-N-Acetylglucosaminidase			gp:AB008771		AB008771	
Description						
Streptomyces thermoviolaceus nagA gene forbeta-N-Acetylglucosaminidase, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
212757_c1_80	4937	10159	466	1401	247	8.9e-24

Protein name

Locus Name

Acc#

sp:MUTS_THEAQ

Q56215

Description

DNA MISMATCH REPAIR PROTEIN MUTS

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21681502_f3_74	4938	10160	310	933	200	3.2e-14

Protein name

Locus Name

Acc#

transmembrane sensor

gp:AF051691

AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23475053_f1_20	4939	10161	1085	3258	583	1.8e-93

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encodinga major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24072250_c3_154	4940	10162	343	1032	512	4.9e-49

Protein name

Locus Name

Acc#

glucose kinase

gp:BMGLUCKIN

AJ000005

Description

Bacillus megaterium glk gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24651537_f2_41	4941	10163	368	1107	156	3.4e-16
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein slr1207			pir:S77541		S77541	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25557818_f2_42	4942	10164	450	1353	662	6.2e-65
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
immunoreactive 51kD antigen PG52			gp:AF175719		AF175719	
<u>Description</u>						

Porphyromonas gingivalis strain W50 immunoreactive 51kD antigenPG52 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26600932_f1_17	4943	10165	119	360	299	1.8e-26
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:RL19_STRTR		034031	
<u>Description</u>						

50S RIBOSOMAL PROTEIN L19

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
267027_f1_26	4944	10166	117	351	86	0.027
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein BB0794			pir:A70199		A70199	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26750178_c1_104	4945	10167	266	801	199	5.1e-15

Protein name

Locus Name

Acc#

UDP-sugar hydrolase

pir:A72201

A72201

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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3163392_f2_51	4946	10168	724	2175	1095	8.1e-111
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Protein name

Locus Name

Acc#

melibiase

gp:TEMELA

Y08557

Description

T.ethanolicus mela and lacA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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35978253_c2_129	4947	10169	1029	3087	454	2.3e-73
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Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
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4115927_c1_81	4948	10170	202	609		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4305138_f1_22	4949	10171	538	1617	156	9.3e-14
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
alpha-xylosidase	pir:A72394				A72394	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4409540_f2_39	4950	10172	436	1311	305	4.2e-27
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
conserved hypothetical protein yknZ	pir:E69858				E69858	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5086542_f1_19	4951	10173	280	843	226	3.0e-18
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
hypothetical protein	pir:S76946				S76946	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5273438_f3_76	4952	10174	183	552	150	1.8e-09
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative alpha-glucosidase	gp:AAC252161				AJ252161	
<u>Description</u>						

Alicyclobacillus acidocaldarius maltose/maltodextrine transportgene region (malEFGR genes, cdaA gene and glcA gene).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5339381_f3_75	4953	10175	116	351	157	3.1e-10
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
putative alpha-glucosidase	gp:AAC252161				AJ252161	
<u>Description</u>						
Allicyclobacillus acidocaldarius maltose/maltodextrine transportgene region (maleFGR genes, cdaA gene and glcA gene).						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
822127_c1_105	4954	10176	291	876	328	6.1e-29
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
	sp:5NTD_DISOM				P29240	
<u>Description</u>	5'-NUCLEOTIDASE PRECURSOR, (ECTO-NUCLEOTIDASE)					

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10345327_c2_2	4955	10177	114	345	266	1.2e-21
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein				pir:JC6027		JC6027
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13099158_c3_48.....	4956	10178	118	357		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16589717_c2_28	4957	10179	301	906	167	2.2e-09

Protein name

Locus Name

Acc#

gp:MMSAG

X84710

Description

M.mazei surface antigen genes orf492, orf375 and orf783.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24024182_f3_13	4958	10180	311	936		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24068841_c3_46.....	4959	10181	281	846		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25422331_c3_47.....	4960	10182	518	1557		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26370887_c3_45	4961	10183	179	540		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29511635_c3_44	4962	10184	106	321	84	0.0076

Protein name

Locus Name

Acc#

hypothetical protein BB0212

pir:D70126

D70126

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3001566_f3_12	4963	10185	318	957	103	0.024

Protein name

Locus Name

Acc#

probable chitinase

pir:T42071

T42071

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32040953_c1_22	4964	10186	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35143_f3_14	4965	10187	624	1875	371	1.6e-44

Protein name

Locus Name

Acc#

otnA protein

pir:S70958

S70958

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6495337_f1_1	4966	10188	132	399		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13100885_f1_1	4967	10189	316	951	129	2.4e-05
Protein name			Locus Name		Acc#	
hypothetical protein slr1515			pir:S75464		S75464	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1219538_c2_95	4968	10190	508	1527	195	7.9e-17
Protein name			Locus Name		Acc#	
unknown			gp:U96771		U96771	
Description						

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13672753_c2_88	4969	10191	572	1719	613	9.7e-60
Protein name			Locus Name		Acc#	
carboxyl-terminal proteinase			pir:F70369		F70369	
Description						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14492660_c2_98	4970	10192	71	213		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14631626_f3_55.....	4971	10193	149	450		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23548552_c2_90.....	4972	10194	772	2319	3902	0.0
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
beta-glucosidase					gp:AF006658	AF006658
<u>Description</u>						

Bacteroides fragilis beta-glucosidase gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24806576_c2_89.....	4973	10195	948	2847	104	7.9e-05
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
unknown					gp:AF124349	AF124349
<u>Description</u>						

Zymomonas mobilis ZM4 fosmid clone 41A4, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26385883_c3_101	4974	10196	360	1083	419	3.5e-39
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YZ37_SYNY3		Q55480	
<u>Description</u>						
HYPOTHETICAL SUGAR KINASE SLR0537						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33242062_c3_100	4975	10197	824	2475	802	8.8e-82
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein TM0280			pir:F72395		F72395	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33864378_c1_78.....	4976	10198	1009	3030	432	1.3e-92
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
receptor antigen (RagA)			gp:PGI130872		AJ130872	
<u>Description</u>						
Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4413377_c2_97.....	4977	10199	576	1731	136	5.4e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:XYNB_PRERU		P48791	
<u>Description</u>						
1,4-BETA-XYLOSIDASE) (EXO-BETA-(1,4)-XYLANASE)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4961578_c2_86	4978	10200	514	1545		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
984512_c2_96.....	4979	10201	437	1314		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15797080_f3_1.....	4980	10202	113	342		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24806591_c1_2.....	4981	10203	89	267	226	6.0e-18
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

sp:YNHE_ECOLI

P77522

Description

HYPOTHETICAL 56.3 KD PROTEIN IN LPP-AROD INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25815841_c3_4	4982	10204	77	234	223	2.1e-18
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
probable oxidoreductase			pir:T34993		T34993	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11854168_f3_1	4983	10205	187	564	317	2.2e-28
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein (thiJ) homolog			pir:D70177		D70177	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21595663_c2_2	4984	10206	134	402	200	1.3e-14
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10944505_f3_7	4985	10207	70	213		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13707938_f1_1	4986	10208	374	1125	106	0.0014
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
omp85 analog			pir:D72094		D72094	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
17070300_c3_15.....	4987	10209	69	210		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24431268_f2_5.....	4988	10210	187	564		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25786067_f3_8.....	4989	10211	68	207	104	0.00010
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YJDB_ECOLI			
<u>Description</u>						

HYPOTHETICAL 61.7 KD PROTEIN IN BASS-ADIY INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32031466_f1_3	4990	10212	133	402	100	0.00026

Protein name

Locus Name

Acc#

sp:YBIP_ECOLI

P75785

Description

HYPOTHETICAL 59.7 KD PROTEIN IN OMPX-MOEB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10635006_f1_1	4991	10213	107	324		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23475780_c2_2	4992	10214	288	864		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23991662_f1_1	4993	10215	210	633	553	2.2e-53

Protein name

Locus Name

Acc#

mobilization protein A

gp:AF118241

AF118241

Description

Bacteroides fragilis mobilization protein A (mobA) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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12541385_c2_36	4994	10216	104	312		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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20588187_c2_30.....	4995	10217	276	831	91	0.047
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Protein name

Locus Name

Acc#

polymorphic outer membrane protein G family

gp:AB033794

AB033794

Description

Chlamydophila pneumoniae pmp_3.1 gene for polymorphic outermembrane protein G family, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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21914762_c2_32.....	4996	10218	61	186		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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22265701_f2_8.....	4997	10219	495	1488		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24641877_c3_38	4998	10220	115	348		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25597781_c3_40	4999	10221	555	1668		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4110090_c3_37	5000	10222	358	1077	104	0.032

Protein name

Locus Name

Acc#

hypothetical protein Y26D4A.9

pir:T26569

T26569

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5164042_c1_28	5001	10223	209	630		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15911275_c1_24	5002	10224	337	1014		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26368757_c2_29	5003	10225	126	381		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2736657_c2_31	5004	10226	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4900250_f3_17	5005	10227	708	2127	929	3.3e-178

Protein name

Locus Name

Acc#

conserved hypothetical protein ydcI

pir:G69773

G69773

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6054083_c2_36	5006	10228	108	324	75	0.0099

Protein name

Locus Name

Acc#

E3 class 2 protein

pir:B46308

B46308

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6285817_c3_37	5007	10229	277	834		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14882768_f3_29	5008	10230	304	912	587	5.5e-57
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
conserved hypothetical protein yisQ			pir:H69837		H69837	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15042062_f3_25	5009	10231	257	774	213	2.4e-17
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:SPU59236		U59236	
<u>Description</u>						
<p>Synechococcus PCC7942 ribosomal protein S1 of 30S ribosome (rps1), ORF271, ORF231, ORF341, carboxyltransferase alpha subunit (accA), ORF245, ORF227, and GTP cyclohydrolase I (folE) genes, completecds, and ORF205 gene, partial cds.</p>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16829637_f3_23	5010	10232	118	357	213	2.4e-17
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YE8R_EC01			
<u>Description</u>						
HYPOTHETICAL 20.3 KD PROTEIN IN PRC-PPHA INTERGENIC REGION						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24800063_g3_62	5011	10233	66	201		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25943937_f3_28	5012	10234	152	459		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29473527_f1_1	5013	10235	160	483	198	1.8e-14

Protein name

Locus Name

Acc#

two component sensor

gp:AF030352

AF030352

Description

Pseudomonas aeruginosa two component sensor (lemA) gene, partialcds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3398391_f3_27	5014	10236	463	1392	414	1.2e-38

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:G72220

G72220

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3947162_f3_22	5015	10237	583	1752	540	5.3e-52

Protein name

Locus Name

Acc#

2',3'-cyclic-nucleotide 2'-phosphodiesterase, precursor

pir:H64532

H64532

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4477328_f2_13	5016	10238	112	339		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4960936_f1_7	5017	10239	766	2301	252	7.1e-18

Protein name

Locus Name

Acc#

sp:CIRA_ECOLI

P17315

Description

COLICIN I RECEPTOR PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
86037_c1_32	5018	10240	224	675		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13105192_c3_22	5019	10241	653	1962		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26369015_c2_21	5020	10242	840	2520	440	7.4e-74
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein			pir:JC6027		JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4408275_c3_23	5021	10243	62	189		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25832158_f1_1	5022	10244	191	576	475	4.1e-45
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein jhp0042			pir:H71981		H71981	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3382312_f1_1	5023	10245	202	609	127	1.3e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
TonB-dependent receptor HmuR			gp:PGU87395		U87395	
<u>Description</u>						

Porphyromonas gingivalis TonB-dependent receptor HmuR (hmuR) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1038140_f1_2	5024	10246	1095	3288		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10585927_f1_12	5025	10247	89	270		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10979687_c3_125	5026	10248	136	411	330	9.4e-30
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:MSCL_ERWCA		068284
<u>Description</u>						

LARGE-CONDUCTANCE MECHANOSENSITIVE CHANNEL

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11751442_f1_1	5027	10249	93	282		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13017676_c1_85	5028	10250	176	531	133	1.2e-07
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
trsl protein (traI)			gp:AE001272		AE001272	
<u>Description</u>						
Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmidsequence.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13781250_c2_106	5029	10251	67	204	202	3.5e-16
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein 1			pir:I40237		I40237	
<u>Description</u>						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13932825_f3_50.....	5030	10252	721	2166	121	0.00075
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			gp:T7CG			
<u>Description</u>						
Genome of bacteriophage T7.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14315933_c1_75.....	5031	10253	140	423		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16531331_c3_128	5032	10254	292	879	90	0.00059

Protein name

Locus Name

Acc#

ras interacting protein RIPA

gp:AF159241

AF159241

Description

Dictyostelium discoideum ras interacting protein RIPA (ripA) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23636550_f2_25	5033	10255	281	846	154	7.3e-10

Protein name

Locus Name

Acc#

tetracycline resistance element mobilization regulatory protein rteC

pir:A36927

A36927

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23674130_c2_107.....	5034	10256	415	1248	137	5.2e-06

Protein name

Locus Name

Acc#

clostripain-related protein

pir:B72351

B72351

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23954136_c2_119.....	5035	10257	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24641637_c2_103	5036	10258	232	699	485	3.5e-46

Protein name

Locus Name

Acc#

sp:AQPZ_ECOLI

Description

AQUAPORIN Z (BACTERIAL NODULIN-LIKE INTRINSIC PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24645261_c3_132	5037	10259	378	1137	395	1.2e-36

Protein name

Locus Name

Acc#

sp:YHCG_ECOLI

P45423

Description

HYPOTHETICAL 43.3 KD PROTEIN IN GLTF-NANT INTERGENIC REGION (O375)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2537562_c1_69.....	5038	10260	120	363		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26594087_f2_26.....	5039	10261	138	417		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32317217_f1_4	5040	10262	143	432		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32442125_c1_70.....	5041	10263	235	708	170	1.8e-13
Protein name			Locus Name		Acc#	
immunoreactive 42kD antigen PG33			gp:AF175715		AF175715	
Description						

Porphyromonas gingivalis strain W50 immunoreactive 42kD antigenPG33 gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32453507_c1_74.....	5042	10264	91	276	76	0.023
Protein name			Locus Name		Acc#	
elongation factor Ts			gp:AF195952		AF195952	
Description						

Phaeodactylum tricornutum ribulose-1,5-bisphosphatecarboxylase/oxygenase large subunit (rbcL), ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit(rbcS), and elongation factor Ts (EF-Ts) genes, complete cds;chloroplast genes for chloroplast products.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33397331_c3_126.....	5043	10265	87	264		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35292938_f3_53	5044	10266	143	432		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4116262_c2_105.....	5045	10267	98	297	169	1.1e-12
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
DNA-binding protein, HU					pir:H72396	H72396
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4159811_c1_93.....	5046	10268	81	246		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5110942_c2_109.....	5047	10269	546	1641	912	2.0e-91
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
DNA topoisomerase III topB					pir:H69724	H69724
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5250000_c2_108	5048	10270	517	1554	178	4.0e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
high molecular weight glutenin subunit	gp:ASU39229	U39229

Description

Aegilops tauschii high molecular weight glutenin subunit (Glu-1-2)gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5895187_f1_5	5049	10271	165	498		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6525286_f2_30	5050	10272	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13869003_f3_3	5051	10273	163	492	183	3.6e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22469452_f3_2	5052	10274	174	525	174	3.2e-13

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34266886_c1_4	5053	10275	122	369		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
781932_f1_1	5054	10276	308	927	528	9.5e-50

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23631887_c3_5	5055	10277	268	807	151	1.0e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:HOLB_HAEIN	P43748

Description

DNA POLYMERASE III, DELTA' SUBUNIT,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16445326_f3_22	5056	10278	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16603377_f2_15.....	5057	10279	559	1680	122	0.00036

Protein name

Locus Name

Acc#

carboxyl-terminal proteinase
ctpB:hypothetical protein slr0257:hypothetical
protein slr0257

pir:S74579

S74579

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
187540_c2_32.....	5058	10280	171	516		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24412632_c3_35.....	5059	10281	84	255		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648941_c3_41	5060	10282	498	1494	755	8.7e-75

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative TonB-dependent outer membrane receptor	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25785191_c3_34	5061	10283	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29453375_c1_26.....	5062	10284	65	198		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29739375_c1_25.....	5063	10285	931	2796	136	0.00047

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PFB0540w	pir:D71612	D71612

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3145252_c1_24	5064	10286	278	837	139	1.3e-06

Protein name

Locus Name

Acc#

sp:APRF_PSEAE

Q03027

Description

ALKALINE PROTEASE SECRETION PROTEIN APRF

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35194686_f3_23	5065	10287	249	750		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4335962_c3_40.....	5066	10288	228	687	92	0.0096

Protein name

Locus Name

Acc#

putative HSP20

gp:AF072875

AF072875

Description

Mycobacterium smegmatis putative HSP20 (hsp) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4892140_c3_39.....	5067	10289	475	1428	134	2.2e-05

Protein name

Locus Name

Acc#

ORF MSV261 leucine rich repeat gene family

gp:AF063866

AF063866

Description

Melanoplus sanguinipes entomopoxvirus, complete genome.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10429567_f3_3	5068	10290	77	234		

Protein name

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4103575_f3_4	5069	10291	394	1185	514	1.3e-54

Protein name

Description

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10995166_f2_44	5070	10292	63	192		

Protein name

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14665963_f2_30	5071	10293	393	1182	255	4.8e-20

Protein name

Description

conserved hypothetical protein

pir:H72273

H72273

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16676688_f1_1	5072	10294	492	1479	646	3.1e-63

Protein name

Description

conserved hypothetical protein yngK

pir:H69893

H69893

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21521937_c1_70	5073	10295	301	906	231	2.9e-19

Protein name

Locus Name

Acc#

sp:SCRK_SALTY

P26984

Description

FRUCTOKINASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24023457_f3_52	5074	10296	768	2307	373	8.2e-31

Protein name

Locus Name

Acc#

sp:LEMA_PSESY

P48027

Description

SENSOR PROTEIN LEMA,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24298262_c1_74	5075	10297	282	849	752	1.8e-74

Protein name

Locus Name

Acc#

sp:PROW_ECOLI

P14176

Description

GLYCINE BETAINE/L-PROLINE TRANSPORT SYSTEM PERMEASE PROTEIN PROW

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24478388_c2_101	5076	10298	285	858	453	8.7e-43

Protein name

Locus Name

Acc#

glycine-betaine binding permease protein

gp:AF139575

AF139575

Description

Lactococcus lactis BusAA (busAA) and glycine-betaine bindingpermease protein (busAB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644706_c1_71	5077	10299	909	2730	391	2.7e-55
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hybrid histidine kinase			gp:AF029704		AF029704	
<u>Description</u>						
Dictyostelium discoideum hybrid histidine kinase (dhkD) mRNA,complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648432_f1_10	5078	10300	214	645		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24660817_c3_113.....	5079	10301	281	846	1490	1.1e-152
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
fructanase			pir:A36915		A36915	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26597136_c3_114.....	5080	10302	390	1173	268	1.3e-21
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:GLUP_BRUAB		Q44623	
<u>Description</u>						
GLUCOSE/GALACTOSE TRANSPORTER						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2817217_c1_72	5081	10303	124	375	210	4.9e-17

Protein name

Locus Name

Acc#

sp:YBAZ_ECOLI

P75707

Description

HYPOTHETICAL 14.4 KD PROTEIN IN TESB-HHA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30084532_c2_100	5082	10304	412	1239	1028	1.0e-103

Protein name

Locus Name

Acc#

ATPase homolog GbuA

gp:AF039835

AF039835

Description

Listeria monocytogenes ATPase homolog GbuA (gbuA), putative glycinebetaine membrane transport protein GbuB (gbuB), and putative glycine betaine binding protein GbuC (gbuC) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35681308_f1_14	5083	10305	102	309	125	5.0e-08

Protein name

Locus Name

Acc#

hypothetical protein APE2061

pir:G72510

G72510

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
429511_f2_31	5084	10306	192	579	132	9.0e-09

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:G75555

G75555

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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4712825_c1_88	5085	10307	398	1197		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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547752_f1_9	5086	10308	1193	3582	3762	0.0
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Protein name

Locus Name

Acc#

pyruvate ferredoxin oxidoreductase

gp:CPA17727

Y17727

Description

Clostridium pasteurianum genes encoding putative pyruvateferredoxin oxidoreductase (8005 bp).

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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2031461_c2_5	5087	10309	281	846	150	1.8e-08
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Protein name

Locus Name

Acc#

hypothetical protein aq_1477

pir:D70428

D70428

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
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32431880_f2_1	5088	10310	280	843		
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Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21562667_f1_4	5089	10311	617	1854	2041	4.6e-211

Protein name

Locus Name

Acc#

sp:ILVD_HAEIN

P44851

Description

DIHYDROXY-ACID DEHYDRATASE, (DAD)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23712785_f2_10	5090	10312	569	1710	1245	1.0e-126

Protein name

Locus Name

Acc#

acetolactate synthase, large subunit

pir:B72362

B72362

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31908538_f2_7	5091	10313	235	708		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35204656_f1_6	5092	10314	80	240	64	0.0053

Protein name

Locus Name

Acc#

capsid portal protein

gp:B1U32222

Description

Bacteriophage 186, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4822001_f3_12	5093	10315	718	2157	269	2.4e-20
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				gp:AF083424		AF083424
<u>Description</u>						
Ateline herpesvirus 3 complete genome.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6678425_f2_9	5094	10316	397	1194		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23516942_c3_5	5095	10317	305	915		
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25667631_c2_3	5096	10318	83	252	131	1.4e-08
<u>Protein name</u>				<u>Locus Name</u>		<u>Acc#</u>
				sp:Y052_BORBU		051081
<u>Description</u>						
HYPOTHETICAL tRNA/RRNA METHYLTRANSFERASE BB0052,						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2442257_f1_1	5097	10319	80	243		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26289650_f1_3	5098	10320	140	423	257	5.1e-22

Protein name

Locus Name

Acc#

sp:YM64_ARCFU

028020

Description

HYPOTHETICAL PROTEIN AF2264

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31913933_c3_27	5099	10321	304	915		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4164011_f3_8	5100	10322	320	963	377	9.9e-35

Protein name

Locus Name

Acc#

sp:YXEH_BACSU

P54947

Description

HYPOTHETICAL 30.2 KD PROTEIN IN IDH-DEOR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6444402_f2_5	5101	10323	495	1488	1190	7.0e-121
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
cysteinyI-tRNA synthetase			pir:A75368		A75368	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12125931_f2_4	5102	10324	214	645	220	4.3e-18
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase-related protein			pir:H72245		H72245	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12988762_f2_5	5103	10325	62	189		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2813942_f2_3	5104	10326	73	222		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12944677_c2_5	5105	10327	453	1359	302	7.3e-35

Protein name

Locus Name

Acc#

TonB-dependent receptor HmuR

gp:PGU87395

U87395

Description

Porphyromonas gingivalis TonB-dependent receptor HmuR (hmuR) gene, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22850381_c1_4	5106	10328	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14664017_c3_4	5107	10329	210	630	379	9.1e-34

Protein name

Locus Name

Acc#

receptor antigen (RagA)

gp:PGI130872

AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20164665_f1_1	5108	10330	68	207	51	0.0055

Protein name

Locus Name

Acc#

50kDa lectin

gp:BMO50KDAL

D14168

Description

Silk worm mRNA for 50kDa lectin, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2460837_f3_2	5109	10331	614	1845	556	9.9e-54
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
adenylate cyclase homolog	pir:T17197				T17197	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14923563_c1_10.....	5110	10332	145	438		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15742327_f1_2.....	5111	10333	60	183		
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24398917_c1_11.....	5112	10334	193	582	302	8.7e-27
<u>Protein name</u>	<u>Locus Name</u>				<u>Acc#</u>	
conserved hypothetical protein	pir:G72380				G72380	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33772907_c2_15	5113	10335	117	354	71	0.026
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
HdcB			gp:00U58865		U58865	
<u>Description</u>						
Oenococcus oeni histidine decarboxylase (hdca) gene, complete cds;and HdcB (hdcB) gene, partial cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35267037_c2_16	5114	10336	117	354		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16541003_f3_3	5115	10337	64	195		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20500657_f3_4	5116	10338	515	1548	1069	4.6e-108
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
inorganic pyrophosphatase			gp:D88820		D88820	
<u>Description</u>						
Acetabularia mediterranea mRNA for inorganic pyrophosphatase, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10944500_c2_9	5117	10339	299	900	341	6.4e-31

Protein name

Locus Name

Acc#

gp:PIGUFMR

M30284

Description

Pig uteroferrin mRNA, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
834393_f1_1	5118	10340	163	492	407	6.5e-38

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76672

S76672

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1987750_f2_4	5119	10341	333	1002		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23704675_c3_10	5120	10342	300	903	1106	5.5e-112

Protein name

Locus Name

Acc#

heat shock protein 60

gp:BFO6516

AJ006516

Description

Bacteroides forsythus groEL gene, strain ATCC 43037.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4022312_c3_9	5121	10343	93	282	393	2.0e-36

Protein name

Locus Name

Acc#

sp:CH10_PORGI

P42376

Description

10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10394667_f2_16	5122	10344	123	372		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14496030_f1_8	5123	10345	227	684		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15742327_c2_71	5124	10346	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19562800_f2_14	5125	10347	327	984		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19814057_f1_7	5126	10348	224	675		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23438557_f1_13	5127	10349	397	1194		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23554057_f1_10	5128	10350	75	228	71	0.039

Protein name

Locus Name

Acc#

sp:UCRH_YEAST

P00127

Description

(MITOCHONDRIAL HINGE PROTEIN) (COMPLEX III POLYPEPTIDE VI)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24024067_f1_5	5129	10351	810	2433	224	2.5e-28

Protein name

Locus Name

Acc#

gp:BFU63096

U63096

Description

Bacteroides fragilis (bctA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24398917_f3_50	5130	10352	193	582	304	5.4e-27

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:G72380

G72380

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648436_f1_3	5131	10353	204	615		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
253783_c1_64	5132	10354	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25442675_f1_4	5133	10355	140	423		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25633287_f1_9	5134	10356	62	189		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25633312_f3_47	5135	10357	434	1305		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26568908_f3_30	5136	10358	154	465		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26758568_f3_43	5137	10359	283	852	94	0.045
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
H+-transporting ATP synthase, protein 6					pir:T11121	T11121
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26854156_f1_2	5138	10360	548	1647	143	7.1e-06
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
hypothetical protein H02F09.3			pir:T33369		T33369	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32066943_c1_62.....	5139	10361	148	447		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32069681_f3_45.....	5140	10362	204	615	78	0.014
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ATP synthase, subunit F			pir:H69227		H69227	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32229662_f1_6.....	5141	10363	177	534	108	5.4e-05
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:YPI6_CLOPE		P18017	
<u>Description</u>						

HYPOTHETICAL 19.7 KD PROTEIN (ORF6)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4409433_c3_95	5142	10364	151	456	85	0.049
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
ORF MSV223 hypothetical protein			gp:AF063866		AF063866	
<u>Description</u>						
Melanoplus sanguinipes entomopoxvirus, complete genome.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
831463_c1_56	5143	10365	217	654		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>			NO-HIT			

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23612512_c2_5	5144	10366	204	615	141	9.2e-08
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
integrase IntN1			gp:BUU51917		U51917	
<u>Description</u>						
Bacteroides uniformis insertion element NBU1 fragment, integraseIntN1 gene, complete cds.						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24219066_f3_2	5145	10367	71	216	52	0.015
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:G3P_SCHMA		P20287	
<u>Description</u>						
LARVAL SURFACE ANTIGEN) (P-37)						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4103388_c3_9	5146	10368	79	240	62	0.0027
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
neuroendocrine protein 7B2			pir:S03938		S03938	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4960925_c3_10.....	5147	10369	150	450		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5255160_c1_4.....	5148	10370	72	219		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5266880_c2_7.....	5149	10371	205	615	276	1.1e-23
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
methyl transferase			gp:STRMTR		L29323	
<u>Description</u>						

Streptococcus pneumoniae methyl transferase gene cluster, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2812785_c2_6	5150	10372	276	828	286	3.8e-24

Protein name

Locus Name

Acc#

sp:BGAL_HUMAN

P16278

Description

GALACTOSIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5867213_c1_4	5151	10373	217	654		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13085162_f2_14.....	5152	10374	362	1089		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20082962_f2_13.....	5153	10375	205	618	384	1.3e-34

Protein name

Locus Name

Acc#

beta-glucosidase

gp:RAU92808

U92808

Description

Ruminococcus albus beta-glucosidase (gluA) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644575_c1_33	5154	10376	292	879	227	2.6e-18

Protein name

Locus Name

Acc#

sp:YIBP_ECOLI

P37690

Description

HYPOTHETICAL 46.6 KD PROTEIN IN SECB-TDH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4476427_c1_34	5155	10377	1050	3153	334	3.3e-26

Protein name

Locus Name

Acc#

bZIP histidine kinase

gp:PPUY18245

Y18245

Description

Pseudomonas putida todX, todF, todC1, todC2, todB, todA, todD, todE, todG, todI, todH, todS, todT genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5275033_c2_40	5156	10378	301	906	232	2.3e-19

Protein name

Locus Name

Acc#

response regulator DrrA

pir:D72228

D72228

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7129666_f1_1	5157	10379	649	1950	914	1.2e-91

Protein name

Locus Name

Acc#

sp:BGLS_AGRTU

P27034

Description

GLUCOSIDE GLUCOHYDROLASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10251900_c1_94	5158	10380	216	651		
Protein name					Locus Name	Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10662758_f1_22.....	5159	10381	183	552	271	1.7e-23
Protein name					Locus Name	Acc#

gp:ATAC006202 AC006202

Description

Arabidopsis thaliana chromosome II BAC T3B23 genomic sequence, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10962692_c2_116.....	5160	10382	194	585	96	0.0022
Protein name					Locus Name	Acc#

hypothetical protein c04040 pir:S75406 S75406

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12194150_f2_41.....	5161	10383	235	708	131	3.9e-10
Protein name					Locus Name	Acc#

sp:YS29_MYCTU P71786

Description

HYPOTHETICAL 27.1 KD PROTEIN CY277.29C

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12687826_f1_16	5162	10384	413	1242	1308	2.2e-133

Protein name

Locus Name

Acc#

sp:UXUA_HAEIN

P44488

Description

MANNONATE DEHYDRATASE, (D-MANNONATE HYDROLASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14588387_c3_163	5163	10385	93	282		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
178405_f1_19	5164	10386	131	396		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20593760_f3_62	5165	10387	254	765	228	6.2e-28

Protein name

Locus Name

Acc#

dihydrodipicolinate reductase

pir:A72246

A72246

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21897192_f1_24	5166	10388	324	975	215	3.8e-16

Protein name

Locus Name

Acc#

hypothetical protein 7

pir:S20799

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2225275_c2_120	5167	10389	61	186		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22381561_f3_59.....	5168	10390	411	1236		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22851526_f1_6.....	5169	10391	528	1587	1117	3.8e-113
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

hypothetical protein mexF

pir:T30830

T30830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24005316_f1_15.....	5170	10392	284	855	696	1.5e-68
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>

oxidoreductase

gp:NOSHRMA

L37087

Description

Nostoc sp. ATCC 29133 oxidoreductase (hrmU) and HrmA (hrmA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24225682_f1_5	5171	10393	394	1185	493	5.0e-47

Protein name

Locus Name

Acc#

sp:YHIU_ECOLI

P37636

Description

PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24509680_f2_40	5172	10394	312	939	152	7.8e-16

Protein name

Locus Name

Acc#

prokaryotic type I signal peptidase SipF

gp:AF065159

AF065159

Description

Bradyrhizobium japonicum putative arylsulfatase (arsA), putative soluble lytic transglycosylase precursor (sltA), dihydrodipicolinate synthase (dapA), MscL (mscL), SmpB (smpB), BcpB (bcpB), RnpO (rnpO), RelA/Spot homolog (relA), PdxJ (pdxJ), and acyl carrier protein synthase AcpS (acpS) genes, complete cds; prokaryotic type I signal peptidase SipF (sipF) gene, sipF-sipS allele,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24615787_f1_7	5173	10395	491	1476	503	4.4e-48

Protein name

Locus Name

Acc#

OprM

gp:AB011381

AB011381

Description

Pseudomonas aeruginosa gene for OprM, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24651437_f3_60	5174	10396	312	939	247	5.9e-21

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:H72417

H72417

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25820437_f3_56	5175	10397	564	1695	827	9.8e-85
Protein name			Locus Name		Acc#	
hypothetical protein mexF			pir:T30830		T30830	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26360717_c1_109.....	5176	10398	208	627	321	8.5e-29
Protein name			Locus Name		Acc#	
phosphoglycolate phosphatase (gph) homolog			pir:C70184		C70184	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26617128_f2_47.....	5177	10399	171	516	354	2.7e-32
Protein name			Locus Name		Acc#	
polysialic acid capsule expression protein			pir:B70434		B70434	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
266178200_f2_27.....	5178	10400	1030	3093	1827	2.2e-188
Protein name			Locus Name		Acc#	
beta-galactosidase			gp:AF055482		AF055482	
Description						

Thermotoga neapolitana galactose utilization operon, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3001251_c1_93.....	5179	10401	450	1353		
Protein name			Locus Name		Acc#	
Description						
NO-HIT						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33593963_c2_136	5180	10402	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33625658_f2_30	5181	10403	275	828	453	8.7e-43

Protein name

Locus Name

Acc#

sp:LPXA_ECOLI

Description

(EC 2.3.1.129) (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34022832_c3_147	5182	10404	433	1302	508	1.3e-48

Protein name

Locus Name

Acc#

sp:YMXG_BACSU

Q04805

Description

HYPOTHETICAL PROCESSING PROTEASE, (ORFP)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4484712_f1_14	5183	10405	498	1497	173	1.5e-21

Protein name

Locus Name

Acc#

sp:LEP_SALTY

P23697

Description

SIGNAL PEPTIDASE I, (SPASE I) (LEADER PEPTIDASE I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
549091_c3_174	5184	10406	112	339		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6035675_f2_49	5185	10407	371	1116	295	4.8e-26

Protein name

Locus Name

Acc#

protein-tyrosine phosphatase

gp:AB028630

AB028630

Description

Clostridium perfringens hyp27, bach, ptp, cpd genes for hypothetical protein, bacterial hemoglobin, protein-tyrosine phosphatase, 2', 3'-cyclic nucleotide 2'-phosphodiesterase, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6837782_c1_96	5186	10408	214	645		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
84790_f3_73	5187	10409	485	1455	880	4.9e-88

Protein name

Locus Name

Acc#

ATP-dependent RNA helicase homolog ydbr

pir:D69772

D69772

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12402186_c3_12	5188	10410	144	432		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15628378_c1_8	5189	10411	375	1128	356	4.5e-32

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
histidine kinase	gp:AF114442	AF114442

Description

Nostoc punctiforme histidine kinase (hepK) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23633456_c3_10	5190	10412	124	375	302	2.6e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
2,3-bisphosphoglycerate-independent	gp:AF120091	AF120091

Description

Bacillus stearothermophilus
2,3-bisphosphoglycerate-independent phosphoglycerate mutase (pgm) gene,
complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10554662_f3_32	5191	10413	186	561	212	3.0e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YP20_BACLI	P05332

Description

HYPOTHETICAL P20 PROTEIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
11777161_c3_65	5192	10414	65	198		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14648512_f3_34	5193	10415	115	348	280	1.9e-24
Protein name			Locus Name		Acc#	
hypothetical protein MTH1452			pir:D69060		D69060	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16676505_c2_62	5194	10416	404	1215	226	2.7e-16
Protein name			Locus Name		Acc#	
probable hydrolase			pir:T37132		T37132	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16832885_f3_43	5195	10417	310	933	1023	3.5e-103
Protein name			Locus Name		Acc#	
hypothetical protein			pir:JQ1020		JQ1020	
Description						

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19610637_f1_6	5196	10418	229	690		
Protein name			Locus Name		Acc#	
Description						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19728433_c1_49	5197	10419	429	1290	244	4.2e-18
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
DNA damage-inducible protein. PAB1438			pir:C75053		C75053	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f1_8	5198	10420	83	252	64	0.031
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
			sp:SPRC_XENLA		P36378	
<u>Description</u>						

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23601000_f1_3	5199	10421	84	255	75	0.039
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
FAA			gp:AC005565		AC005565	
<u>Description</u>						

Homo sapiens chromosome 16, cosmid clone 444B9 (LANL), complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24410687_g2_63	5200	10422	231	696		
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>	
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415902_f2_18	5201	10423	630	1893		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24625311_f3_42.....	5202	10424	277	834	1272	1.4e-129

Protein name Locus Name Acc#

7-alpha-hydroxysteroid dehydrogenase gp:AF173833 AF173833

Description

Bacteroides fragilis 7-alpha-hydroxysteroid dehydrogenase (hdhA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24726537_f3_39.....	5203	10425	71	216	56	0.021

Protein name Locus Name Acc#

hypothetical protein C0510w pir:T18460 T18460

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25600250_c2_57.....	5204	10426	320	963		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26305349_c1_44	5205	10427	90	273	156	3.5e-10

Protein name

Locus Name

Acc#

sp:FE0B_METJA

Q57986

Description

FERROUS IRON TRANSPORT PROTEIN B HOMOLOG

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26595317_c2_59	5206	10428	156	471	302	8.7e-27

Protein name

Locus Name

Acc#

hypothetical protein SCI30A.19

pir:T36799

T36799

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36150277_f1_5	5207	10429	286	861	199	6.9e-15

Protein name

Locus Name

Acc#

transcription regulator AraC/XylS family
homolog ydeE

pir:G69777

G69777

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4953387_c2_58	5208	10430	134	405	279	2.4e-24

Protein name

Locus Name

Acc#

sp:YUXK_BACSU

Description

HYPOTHETICAL 15.7 KD PROTEIN IN PBPD-COMA INTERGENIC REGION (ORF2)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6048462_f3_35	5209	10431	245	738	573	1.7e-55

Protein name

Locus Name

Acc#

sp:UNG_HUMAN

P13051

Description

URACIL-DNA GLYCOSYLASE PRECURSOR, (UDG)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6053437_c3_71	5210	10432	1062	3189	564	2.2e-87

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6735841_f2_25	5211	10433	105	318	444	7.8e-42

Protein name

Locus Name

Acc#

hypothetical protein

pir:JQ1020

JQ1020

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6837837_c2_60	5212	10434	246	741	285	5.5e-25

Protein name

Locus Name

Acc#

sp:YTFE_HAEIN

P45312

Description

HYPOTHETICAL PROTEIN H11677

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24417250_f3_7	5213	10435	67	204	79	0.029
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
OmpK37 porin			gp:KPN011502			AJ011502
<u>Description</u>						
Klebsiella pneumoniae (strain SD8) ompK37 gene.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6725192_f3_6	5214	10436	815	2448	159	3.1e-12
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
colicin I receptor			gp:ECOCIR			
<u>Description</u>						
E.coli colicin I receptor gene, complete cds.						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2006400_f2_5	5215	10437	74	225		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3218942_f1_1	5216	10438	134	405		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34408328_f2_4	5217	10439	399	1200		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4179002_f3_9	5218	10440	144	435		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15625252_f1_1	5219	10441	253	762		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2712937_f1_2	5220	10442	360	1083	526	1.4e-51

Protein name

Locus Name

Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35351583_c1_3	5221	10443	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36038302_c3_12	5222	10444	752	2256	148	5.9e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein yknZ	pir:E69858	E69858

Description

CLAIMS

1. An isolated nucleic acid encoding an *B. fragilis* polypeptide of SEQ ID NOS:
5223 - 10444.
- 5
2. A recombinant expression vector comprising the nucleic acid of Claim 1 operably
linked to a transcription regulatory element.
3. A cell comprising a recombinant expression vector of Claim 2.
- 10
4. A method for producing an *B. fragilis* polypeptide comprising culturing a cell of
Claim 3 under conditions that permit expression of the polypeptide.
5. An isolated nucleic acid selected from the group consisting of:
- 15
 - (a) SEQ ID NOS: 1 - 5222;
 - (b) a complement of SEQ ID NOS: 1- 5222; or
 - (c) an RNA of (a) or (b), wherein U is substituted for T.
6. A recombinant expression vector comprising the nucleic acid of Claim 5 operably
20 linked to a transcription regulatory element.
7. A cell comprising a recombinant expression vector of Claim 6.
8. A method for producing an *B. fragilis* polypeptide comprising culturing a cell of
25 Claim 7 under conditions that permit expression of the polypeptide.
9. A probe comprising a nucleotide sequence consisting of at least eight contiguous
nucleotides of a nucleotide sequence selected from the group consisting of:
 - (a) SEQ ID NOS: 1-5222;

- (b) a complement of SEQ ID NOS: 1- 5222; or
- (c) an RNA of (a) or (b), wherein U is substituted for T.

10. An isolated nucleic acid comprising a nucleotide sequence of at least eight
5 nucleotides in length, wherein the sequence is hybridizable to a nucleic acid
having a nucleotide sequence selected from the group consisting of:
 - (a) SEQ ID NOS: 1 -5222;
 - (b) a complement of SEQ ID NOS: 1-5222; or
 - (c) an RNA of (a) or (b), wherein U is substituted for T.
- 10
11. A vaccine composition for prevention or treatment of an *B. fragilis* infection
comprising a nucleic acid of Claim 5 and a pharmaceutically acceptable carrier.
12. A vaccine composition of Claim 11, further comprising an adjuvant.
- 15
13. A vaccine composition of Claim 11, further comprising one or more additional
ingredients.
14. A method of treating a subject for *B. fragilis* infection comprising administering
20 to a subject a vaccine composition of Claim 11, such that treatment of *B. fragilis*
infection occurs.
15. A method of Claim 14, wherein the treatment is a prophylactic treatment.
- 25
16. A method of Claim 14, wherein the treatment is a therapeutic treatment.
17. A recombinant or substantially pure preparation of an *B. fragilis* polypeptide or a
fragment thereof, wherein said *B. fragilis* polypeptide is SEQ ID NOS: 5223 -
10444.

18. A vaccine composition for prevention or treatment of an *B. fragilis* infection comprising an *B. fragilis* polypeptide of Claim 17 and a pharmaceutically acceptable carrier.
- 5 19. A vaccine composition of Claim 18, further comprising an adjuvant.
20. A vaccine composition of Claim 18, further comprising one or more additional ingredients.
- 10 21. A method of treating a subject for *B. fragilis* infection comprising administering to a subject a vaccine composition of Claim 18, such that treatment of *B. fragilis* infection occurs.
22. A method of Claim 21, wherein the treatment is a prophylactic treatment.
- 15 23. A method of Claim 21, wherein the treatment is a therapeutic treatment.
24. A method for detecting the presence or absence of a *Bacteroides* nucleic acid in a sample comprising:
20 (a) contacting a sample with the nucleic acid of Claim 5 under conditions in which a hybrid can form between a probe comprising a nucleotide sequence consisting of at least eight contiguous nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-5222 or a complement of SEQ ID NOS: 1-5222 and a *Bacteroides*
25 nucleic acid in the sample; and
(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence or absence of a *Bacteroides* nucleic acid in the sample.

25. A computer readable medium having recorded thereon a nucleotide sequence selected from the group consisting of:
- (a) SEQ ID NOS: 1-5222;
 - (b) a complement of SEQ ID NOS: 1- 5222;
 - 5 (c) an RNA of (a) or (b), wherein U is substituted for T; or
 - (d) a fragment of (a), (b) or (c).
26. A computer based system for identifying fragments of the *Bacteroides* genome of comprising;
- 10 (a) a data storage means comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-5222, a complement of SEQ ID NOS: 1-5222, or a fragment thereof,
 - (b) a search means for comparing a target sequence to the nucleotide sequences of the data storage means of step (a) to identify homologous sequences, and;
 - 15 (c) a retrieval means for obtaining said homologous sequences(s) of step (b).
27. A method of identifying nucleic acid fragments of a *Bacteroides* genome comprising comparing a database comprising a nucleotide sequence selected from
- 20 the group consisting of SEQ ID NOS: 1-5222; a complement of SEQ ID NOS: 1-5222; or a fragment thereof with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
- 25 28. A method for identifying an expression modulating fragment of the *Bacteroides* genome comprising comparing a database comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1- 5222; a complement of SEQ ID NOS: 1-5222; or fragment thereof with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said

target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

2709.1001-001

ABSTRACT OF THE DISCLOSURE

The invention provides isolated polypeptide and nucleic acid sequences derived from *Bacteroides fragilis* that are useful in diagnosis and therapy of pathological conditions; antibodies against the polypeptides; and methods for the production of the
5 polypeptides. The invention also provides methods for the detection, prevention and treatment of pathological conditions resulting from bacterial infection.

SEQUENCE LISTING

<110> Gary L. Breton

<120> NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRAGILIS FOR DIAGNOSTICS AND THERAPEUTICS

<130> 2709.1001-001

<160> 10444

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<211> 420

<212> DNA

<213> B.fragilis

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<211> 1836

<212> DNA

<213> B.fragilis

<400> 2

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<211> 750

<212> DNA

<213> B.fragilis

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<210> 4

<211> 1446

<212> DNA

<213> B.fragilis

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<212> DNA

<213> B.fragilis

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<211> 2514

<212> DNA

<213> B.fragilis

<400> 6

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<211> 1221

<212> DNA

<213> B.fragilis

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<210> 8

<211> 3258

<212> DNA

<213> B.fragilis

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<213> B.fragilis

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<212> DNA

<213> B.fragilis

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<212> DNA

<213> B.fragilis

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<211> 1653

<212> DNA

<213> B.fragilis

<400> 29

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<211> 2943

<212> DNA

<213> B.fragilis

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<211> 2361

<212> DNA

<213> B.fragilis

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<211> 183

<212> DNA

<213> B.fragilis

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<212> DNA

<213> B.fragilis

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<211> 1272

<212> DNA

<213> B.fragilis

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<210> 36

<211> 1464

<212> DNA

<213> B.fragilis

<400> 36

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<210> 37

<211> 1113

<212> DNA

<213> B.fragilis

<400> 37

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<210> 38

<211> 747

<212> DNA

<213> B.fragilis

<400> 38

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<210> 39

<211> 2307

<212> DNA

<213> B.fragilis

<400> 39

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<210> 40

<211> 1218

<212> DNA

<213> B.fragilis

<400> 40

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gaaatggcag	gctctgatag	cgtttggtgc	tgccacttgt	ctatgttgaa	ggatacgggt	180
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atggggcatg	tccctttcaa	actttttact	aaaagcggga	cttatttgag	ggatatcggt	360
tcctttgggtc	aagggtgcggg	tgaatatggc	ttagcttatg	atgcacagat	ggatgaggag	420
aataaccgac	tttatgtgtt	atggtggcag	gccgaccata	tcttggtatt	cgattttacaa	480
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aagctaaccg	aactgcttag	gagtactaaa	gaaaacgata	acaattatat	tttctatggt	1200
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<210> 41

<211> 1203

<212> DNA

<213> B.fragilis

<400> 41

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tgctgctgct	gcatgattaa	tggcttcttt	ggtctggggc	attacatcat	catcggcagc	180
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<210> 42

<211> 525

<212> DNA

<213> B.fragilis

<400> 42

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ggtttctctt	ctttcttctc	tgttttttct	ggagacacca	cgacttttgg	ttcttctttc	180
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aaatcaattt	ttccgacagg	tttaaacttc	ggacgcacat	cttccggaat	gaccgtctta	480
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<210> 43

<211> 1269

<212> DNA

<213> B.fragilis

<400> 43

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<210> 44

<211> 855

<212> DNA

<213> B.fragilis

<400> 44

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ctgcatgccca	gcattaacgg	caaagagata	ttgaaaggca	ttaacctgac	ggtgaagccg	180
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<210> 45

<211> 195

<212> DNA

<213> B.fragilis

<400> 45

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gtggccgcta	atctttacat	tgggtggcttc	agtattaacc	aaggcattgg	aggcggtttc	180
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<210> 46

<211> 348

<212> DNA

<213> B.fragilis

<400> 46

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<210> 47

<211> 1662

<212> DNA

<213> B.fragilis

<400> 47

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aacaccttcc	gagtacatat	taatgaagaa	ctaattaaag	agacagctga	tgccatggtc	240
aaccggggtc	tgaaggatgt	aggctatgga	tatgtgaaca	tagacgacgg	atactttgga	300
ggacgaaatt	cggaaaggacg	tctttttgcc	aataagaaaa	aattcccga	tgggatgaga	360
gtcctgtccg	actatattca	ttcaaaggga	ttgaaagccg	gtatatattc	tgatgcgggc	420
agcaacactt	tggtctccat	ctatgacgca	gatacactcg	gtatcggtgt	agggctttgg	480
aaacacgatg	atatagactg	ccaaacttcc	ctcaaagact	ggggatatga	tttcattaaa	540
atagactggg	gtggcgggtga	agcaaccgga	caaagtgagc	agcaacgtta	tacggatatc	600

tacaaagcga	tcagacggac	aggacggaca	gatgttcgat	ataatatatg	ccgttggcag	660
tttccgggca	cttgggctac	ccagttggca	ggttcctggc	gaatccatac	agacatcaat	720
ccacgattca	caacaatcga	ccgaatcatt	gaaagaaatc	tctacttagc	accttacgca	780
agccccgggc	actataatga	catggatatg	cttgaagtag	gaagagggct	cacggaagac	840
gaagaaaaaa	ctcatttttg	aatatggtct	atcttgtcct	ccccgttaat	gatcgggatgc	900
gatcttcgta	caattcctga	aaaaacttta	tcgatcatta	ccaataagga	agtgatcgca	960
ttaaatcagg	attcattagg	tctgcaggct	gaagccattg	aacggggaaa	agactatctg	1020
attttatcaa	aagccattca	gaaacgtgaa	ggcaaactac	gtgcagtagc	actatataac	1080
agaagcaata	cagatcagca	gatcagagtc	gatttcgata	agctctatct	atcaggggat	1140
gtacgagtga	gagatctatg	gaaccatcaa	gaaatgggaa	cattcaccga	ttactatgaa	1200
acgctagtct	ctgcacatgg	aacagcttta	ataagacttg	aaggtagcaa	acgtcacgac	1260
cggacatggt	atgaagctga	atatgctttc	atgcaagaat	ttctgccaga	caacaaacag	1320
gcagctcatt	ttacaccaa	atcaggagcc	tcaggagaat	atattatgaa	aaatcttgga	1380
aattcacctt	ccaattgggc	agaattcaga	aacgtgtata	ttagcaaagg	aggagattat	1440
caacttaagt	taacttatta	ttcaggtgat	aaacgcgata	tccaaatagc	tgtaaacgga	1500
acagaatata	aacagtctaa	cctttattcc	ggtacatggg	atcaagcagc	tacaacaact	1560
atcaagggtta	aacttcgcaa	aggctataac	acgatacgtc	tgtataattc	gtacgggttg	1620
gcacccgata	ttgataaaat	ggaaatcatc	aaaggtcggt	aa		1662

<210> 48

<211> 1350

<212> DNA

<213> B.fragilis

<400> 48

ataacccgac	aattcatgaa	aaacaccaac	cgttccattc	tccataaaga	tggagtaagt	60
tatatcctac	catttatctt	agtacacct	tgttttgcct	tatggggggt	tgctaacgat	120
attaccaatc	caatggtgaa	ggctttctcg	aaaatattcc	gtatgagcgt	cactgatgga	180
gcactagtac	aagtcgcttt	ttacggggga	tactttgcaa	tggcctttcc	tgtgcaatg	240
tttattcgca	aatactctta	taaagccggt	atcctgttgg	gactggggct	atatgctttg	300
ggtgccttgc	tgtttttccc	agcaaagatg	acaggcgatt	attacccttt	tctgctcgct	360
tattttatct	tgacatgtgg	actctcgctt	ctggaaacaa	gtgctaattc	ttatatatta	420
tcgatgggta	cagaagagac	ggcgacccga	cgattgaatc	tggcgagcgc	gtttaatccg	480
atgggatcat	tgctcggcat	gtatgttgcc	atgaatttca	ttcaggcgcg	tctgaatcct	540
atggatagcg	tagaacgcag	ccaattgtct	ccggcagagt	ttgaagtatt	gaaagagtcg	600
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tttgtgatac	gtgccgttaa	aatgcctaag	aatggcgata	agaaccataa	tattgatttt	720
ataccacat	tgaagcgtat	ctttaaaatt	ccccattata	gagaaggagt	catagcaca	780
ttttttatgt	taggtgcaca	gattatgtgt	tggacttttg	ttatccaata	tggaacgcgc	840
ttgtttatgt	cgcagggaat	ggaggagaag	gctgctgaag	tgctttccca	ggaatataat	900
ataattgcta	tgattatttt	ttgcataagc	ccgtttcgct	tgtacattta	ttcttcgcta	960
cctgaatccg	gggatgcttc	tcaagattct	tgcgattgcg	ggtggtgctt	ttacgttagg	1020
tgtgattttt	ttgcaagaca	tatggggatt	gtattgttta	gtagctgttt	cggcttgat	1080
gtcactaatg	tttcccacga	tttatggcca	ttgctcttcg	tggtttgggt	gatgatgcca	1140
aatttggggg	ctgccggttt	gattatggca	attctgggag	gctctgtgtt	gccaccatta	1200
caggcttgta	ttattgacca	acatacattg	ttgggtatgc	ctgctgtaaa	cttgtctttc	1260
atacttcctt	ttatctgttt	cgtagtgtat	atcatttatg	gacatcgtag	gtgtgcacgt	1320
gtgaagaaga	taaaagcagc	acgaaagtaa				1350

<210> 49

<211> 1722

<212> DNA

<213> B.fragilis

<400> 49

gcaaagcggc	atataccatt	aatacggctt	tcgaactgga	acagaaactt	gacttccttt	60
accaaaggat	tgaattttta	agcactgggt	tcttttaaaa	actggtcgaa	gacgactgtc	120
aatcgctcct	tttcacctta	cttttatgaa	ttacagaatc	ctcaggagca	agaagacgga	180
agctatcttt	atgattataa	ctctatcagt	aaggagcgta	ccgctcttga	gacatcgact	240

tccactactg	gcgaccgtct	gatgaacctg	caggctacac	tgaactatca	gcgcattgttc	300
ggtgataaac	atgatgtcgg	agcaatgttg	gtatatcttc	agcgcgaata	caatctgaac	360
aatcctgaca	ataactatta	caatacattg	cgggaacgta	atcaggggct	ggccggacgt	420
gttacctatg	cttatgacgg	acgctatttg	gctgaattca	atttcggcta	caatggtagt	480
gagaacttcg	aaaaaggaag	cggttacgga	ttcttccctt	cactcgctgt	cggctatctt	540
atctccaacg	agaaattttt	cgaaccattg	acaaaagtta	tctccaactt	aaaaatacgc	600
gcttcgtacg	gattggtagg	taatgcggat	atcggtcca	accgtttccc	ctatcttact	660
aaagtagatt	tgggtggagc	cggatttgta	ttcggtgacc	agtggcaaac	ctcatcctaac	720
ggagctacca	tcactactta	cggagctgaa	aaggtgacat	gggaaatcgg	taaaaagtat	780
aatgtaggat	tcgacctggg	attattcaac	aaattaagcc	tcaacgtaga	tttctttaga	840
gaagaccgta	aagacatctt	ccttagacgt	aatacaatcc	ctgcagaaag	tggtatcacc	900
ggagatctcc	gaccctatgg	taatctgggt	aaggtacgca	atcaaggcgt	tgacatgtca	960
ttggactata	atcacgctgt	cagcaaagac	ttcatgatct	ctgccaaagg	tactttcaca	1020
tacgctaaga	accaatatat	ggaaatagac	gaaccggact	acgaatatgc	atacatgtca	1080
caagtaggac	gccccctgaa	tcagtataaa	ggctatatattg	cattaggact	cttcaaagat	1140
caggaagaga	ttgacaacag	tccaaaacaa	atactaaccg	gagttgtgca	accgggtgat	1200
attaaatatg	cagacctcaa	taatgacgga	aagatcgacg	gaaacgatca	aacttacatt	1260
ggtaatccgg	aattacccca	aatcagctat	ggtctgggag	tcagtatcca	gtacaaaaaa	1320
tgggatgctt	ccatcttctt	tcaaggagta	ggcaaaaagaa	gcacatgtt	gagcgacatc	1380
catcctttcg	gtggagaatc	gtatggtgtc	atgcaatttg	ttgccgataa	tcattggaca	1440
gaggcaaaacc	cgaaccccgga	agcaatgtat	cggagactga	caaacgggaa	aaacaacaat	1500
aataacccca	actctactta	ctggctgaga	gatggttcgt	atatccgact	taaaaacgtg	1560
gaattaggat	actcttataa	atttttacctg	gcctatatca	gcggacaaaa	cctgctgaca	1620
ttctctaaat	ttaaatttatg	ggatccggag	ctctatacct	caaacggatt	aaaatatccg	1680
acacaaatca	tgggttccat	cggtttacag	ttcacttttt	aa		1722

<210> 50

<211> 1668

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (1640)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 50

aatcaatgta	aatgtatgaa	aaagaaagca	attccttgtc	ataaggcagg	gaggattacg	60
tccctttttt	tatttaattag	tattttttta	cttataccga	gtatcactac	tccggtttat	120
gctgtagaaa	cttataccga	gcaaaactgtt	tttacgcttc	acgcaactaa	taaaacagta	180
aaagaagtgt	ttgaatacat	cgaaaaaaac	agtgaatttg	tcgtttttgta	ttcaaaaagat	240
ctttttacctg	tactgcagaa	gaaagtgtct	gttttcgatag	ataaacagaa	tgtagaatcg	300
attctgaata	tcttgtctaa	agaagcggga	ttgaagtaca	acatcaacga	ccgtcagatc	360
acaattacca	aagttacggc	agaagcacct	caacaggaaa	aaaaaatcaa	aatcaccggt	420
caagttcttg	acgaaaacgg	agaagggtatt	cggggagcaa	atatcgtaat	aaaaggcaat	480
agtacattgg	gaacagtaac	caatgtcgaa	gggaacttta	cattaatggc	tccggaaaat	540
agcacattag	tagcctcctt	tatcgatat	acccctgttg	aaattccgct	aaaagggaaa	600
aagatagttg	ttttcaaatt	ggtacctgac	gccagagtc	tggaagaagt	agtggtagta	660
ggattcggaa	cacagaaaaa	agccagtgtt	gtaggtgctg	tacaatccat	caaaccggct	720
gaacttcgag	taccttcocag	taacctgagt	acatcatttg	cgggacgtat	agcaggcgtg	780
attttctatgc	aacgcaccgg	tgagccgggt	gccgatggag	caaacttctg	gatacgcggt	840
gccgcaacct	tcagcgggaac	gactgatcct	ctgatcttca	tcgatgggtg	cgaagtttcg	900
gcaggagata	tgaacgctat	tccctcggaa	gctatcgaaa	acttctcaat	attgaaagat	960
gcctcggcta	cagccctcta	cggagcacgc	ggtgccaatg	gtgtcatcct	gatcactacc	1020
cgaaccggta	aagatcttga	aaaagcacgc	atcaacgat	gcacgataa	tacatttacc	1080
gcaccgacac	gtacactcaa	actggcagat	cgcgaacacg	ccatgaaatt	gagaaatgaa	1140
gccattctga	cccgtaaccc	ggatgggtaca	cgggctttct	cagatgataa	aattcaagga	1200
acgcttgaag	gcagaaatca	gtatgtatat	cccaacgttg	attggttcga	ctatatgttt	1260
aaagactact	ccatgaacca	atcagccaac	ctgaatgtaa	tgggtggtac	aaagaaagta	1320

gactattttca	tcagcgcctc	catcaataat	gataatggta	tgctgaaaaa	agatccgaat	1380
aacacattcg	acaacaatat	acagaatctt	cgctactcgt	tccaaagtaa	cggtgggagca	1440
tggttgacat	caagtaccaa	agtaaagtgt	agaatcaact	cgcaaatagt	caattacaat	1500
gggtccgtcaa	ccagtatgga	cgatttgtat	aaatacgtaa	tggaagctcc	gtcaatgtat	1560
tttgcacctg	tatatccgaa	tatcaaccgt	gaagatcaca	ctatattcgg	aaacaaatca	1620
gggtggtccta	tcggttcogn	aggattcagt	atttatcgca	acccttaa		1668

<210> 51

<211> 411

<212> DNA

<213> B.fragilis

<400> 51

atattaagaa	aagaagttta	tattttatat	ttttgcagcg	cacatatggg	aaccattact	60
ctatatatga	acaacaacat	agaatatatc	agcaagataa	agaaaggaga	agagacttct	120
ttccgtcatt	ttgttaatag	ctattcgaaa	gacttggtct	actatgcaca	gtgttttcgta	180
cgaagcaaa	aaaccgctga	agaagtagtc	agcgacgtct	ttctggatgt	atgggagacac	240
cgcgaaagaa	tagatgaaat	caagaatata	aaagcttggt	tgctcacatt	aactcataac	300
aaagccatct	tctatctgag	aaaagcggaa	aattcaagtgt	aaattgcttc	atgggaagaa	360
atagatgatt	ttcaataaat	cggaaatctg	caactcccca	tgaagagatg	a	411

<210> 52

<211> 1851

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (920)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 52

ataattatga	aactaaaaaa	tataattgta	gctttactaa	tcggagctag	cttacactct	60
tgtgattatc	tggacattgt	acccgatgac	acccctatct	tggtgatgac	gttcaagaac	120
gaacagactg	ccgagaactt	tgtcttcgcc	tgctattctt	tcattcccaa	ttatctgaac	180
ttccgtcaga	acttcagttg	gtgcacaact	ccggaaactg	tcggatctgc	ccactggacc	240
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attgatgtgt	ggcaaagtgc	atacaacggt	atccgccaat	gttatacgtt	cttggataat	360
attgatgatg	taaagccatc	acaaatctca	gaggcagacc	tcgcagccaa	gaaagtactt	420
tggaagggtg	aagtaaaatt	tctgattgcc	tactaccact	acctgctatt	acagaactac	480
ggtcctatag	tcatactgga	cgaagcaatc	cctcttaatg	cacccaaaga	agaacttttc	540
aagccgcgtg	taccctatga	tgaatgcgtt	agccgaattg	ctcaaatgtt	cgataatgcc	600
tctgccgacc	tgcttatgac	agtgaagctt	tccaactacg	gtcgtgctac	aaaagtcatt	660
gcacaagcac	taaaggcaag	aatgtacttg	tacgcagcca	gcccacagtt	caatgggaat	720
gctgatatgt	ataagaatct	caagaacaag	gacggacagt	tgctcatgaa	cctgacttat	780
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caagccggag	cagaattgta	taagtataca	aagaaaggta	atctgccgga	attcaaccaa	900
gccattgcca	atgcacgtan	acctgttgta	gacgcagcca	ataaagaact	gatctgggga	960
tatagtggct	ggaaagaaac	atggggccgat	ggaaactcta	ttcaaacaca	cgtaattccc	1020
aaaggtatca	gtacttcctc	gggagcacct	tatggagctt	taggtgcaac	ggctttcagt	1080
gcgacatgt	atctgaccaa	gaacggactt	ccgatagatg	aagatccaga	gtttgattat	1140
gcacatcggt	tcacagtagc	cgaaggggat	tcggtagcag	tgctccatcg	caaccgtgaa	1200
ccacgtttct	atggttctat	cggttccaac	cgcggggact	acctgatcaa	cggagacacc	1260
attaacctca	aaatgcgctt	caaagagcaa	aatggaacac	gtgatgcggg	aagtgaccaa	1320
ttatatggat	cgtagtctat	cgccaaactg	gctcatccag	aaacttttgt	tagtggtacc	1380
agcaactctc	tggtagcttt	ccctttccct	atcatccgct	taggagaatt	gtatttggac	1440
tatgcagagg	cttactttga	atacaatgga	acactggaag	gagatgcact	tacttacttc	1500
aacctgatcc	gccagagagc	cggtatctct	aatgtagaag	tttcctacaa	aggacttccg	1560
tccggagaca	aacttcgtga	ggtaattcat	cgtgaaagaa	ccatagagct	gatgttcgaa	1620

ggacatatgt	catacgacta	tgcgcgttgg	ctgattgccc	tgaaagaatg	gagcgggtatg	1680
gaaaatggta	tgatcggatt	gaactcttac	ggtacaacca	acgaagagta	ttataaaaaat	1740
gcacgttttg	atgctcaacc	attcatcttc	agggatgaac	agtatttgag	tccaatcaaa	1800
caggattacc	tgaatgtaaa	ttcaaatctg	gtccagaatc	cgggttggtg	a	1851

<210> 53

<211> 339

<212> DNA

<213> B.fragilis

<400> 53

acgataaaga	aagaaaaagg	ttgcaggaat	ccttcattta	ttatctatct	atacggatcg	60
gtcgtttggaa	gtaatactgt	acgggtacttg	ctccgccttc	ccttggttga	cggaggaaaa	120
acagacctcc	tccccaaaaa	agttaaagac	agagccctaa	agtcattcaa	cacatttcag	180
caagccccta	tcaaacataa	aaaaatgtcg	caaaagcaac	aactttcacg	acacttcaat	240
atctgtcaga	atacacatgc	ctcagaacat	cttactgacc	cgttcgatac	cagctacaag	300
agcatcaact	tcctcttttg	tattatacac	ggcaaatga			339

<210> 54

<211> 1134

<212> DNA

<213> B.fragilis

<400> 54

aagcagcacg	aaagtaatat	tgagaatcgg	atgcggtgtt	tgacgattct	tctgggcaac	60
tgttttcttc	tgcttgtgtc	attagcctct	tgcgggaaag	tgctcattagc	ggaagaagca	120
gtgttttcta	taccggtgga	tacgacattt	atgaggcttc	gtcaatggga	gtggtattgt	180
cagaaacggg	ctgacagttg	tctgacagag	aataattatc	agggagcttt	atcttggctg	240
gattccgctc	gtatccaagt	ggaacattac	ggacgtcctt	attatatatt	ggcacgcggg	300
gacgtatatt	attccatcca	tcaatatgat	tctgcccgtc	gttatttttag	tatggcagtc	360
cattccattc	atccacatat	tgctatcgaa	gcttggagga	aacttgcaga	actggaactt	420
atggaaggaa	atgagaagca	agggttctat	tctacgcaga	aggcagatgc	acttttccgg	480
gtggagatag	gccatgtgca	gagtataaac	agtgaagctc	tatatcagga	agagagggtg	540
aaaaacgagt	taaaccaatt	gaagattgcc	aaacagaata	gggaaattgc	catgttaact	600
ttgagccttt	gtctgattat	actgattgct	ttgtttatct	tctaccggca	aaataagata	660
aagcgtgaaa	aagagcgtct	gcttcttgaa	gagaaagcca	agttggagca	agagaaccaa	720
atactgaaac	aaactgaaga	gttaagtgtc	ttgagagaaa	aagaggcggg	tttgcgagag	780
tctttgttcc	gtaaggtcga	tgttttgcgt	aaaataccct	ccctcaatga	agaagaacag	840
gagagtgggtg	aacatcgcat	agctttgtcg	gaaagggagt	gggaggaaat	tcgtcagaca	900
ttggataatg	cttatgatgg	gttttcacaa	cggttgcttg	cacgctttcc	tttgttgacc	960
ttaaaagata	tttatttctg	ttgtctgggtg	aagatcaatg	tcagtataaa	ggacctttcc	1020
gatattttatt	gtatttagtcg	tacctcggtt	agtaaaaaga	aatttcgcat	caagcgagag	1080
aagcttggag	cagaggattc	ggactcttta	gatgactttt	tacgtgggtt	ttag	1134

<210> 55

<211> 471

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (228)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 55

tcaatgatag	aaaaaagaac	tgtttgtcag	attgttgaag	aatggctgga	ggataaagac	60
tattttctgg	tagaagtgac	cgtcagccct	gatgacaaga	ttgtgggtcga	aattgaccat	120
gcagaagggtg	tttggattga	agactgtgtg	gagttgagtc	gcttcattga	gtcgaaactg	180
aaccgtgaag	aggaagatta	tgagctggaa	gtacgtttctg	ccggaatncg	acagccattt	240

aaagtattgc	aacagtacta	taaccacatc	ggcctggagg	tggaagtgct	gactaaaggc	300
ggacgcaaac	tgagcggggg	cttgaaagat	gctgatgaag	aaaagtttgt	tgtgaccgta	360
caaaagaaag	taaaacccga	aggagccaaa	cgctctcaat	tggtagaaga	ggatgaaacc	420
ttcacctatg	atgatataaa	atatactaaa	tacttaatta	gttttaataa	a	471

<210> 56

<211> 1566

<212> DNA

<213> B.fragilis

<400> 56

ccaaacaaaag	aaggagcagt	ccttggtata	ttatcttatg	gaaagctttg	cggggatctt	60
ctttcctgca	gcaaaagagg	ttacacaaca	atatatatc	aaataaaaat	gatgcaacaa	120
gaagaaccca	ataaatatgt	aaaagaactc	acgcaggaga	agtataaata	cggcttcaat	180
acggagggtac	atacagatat	catagagaag	ggactcaatg	aagacgtggg	acgtttgatc	240
tcgtctaaaa	agaacgagcc	ggagtgggtg	ctggagtctc	gtctgaaagc	ttatcgtcat	300
tggttaacgc	tggagatgcc	tacttgggca	catttgcgta	taccggaaat	tgactatcag	360
gcaatctcat	attatgccga	tctacgaaa	aagaaggagg	gcccgaagag	tatggatgaa	420
gttgatccgg	aattgataaa	aacattcaat	aaactcggca	ttccactgga	ggagcagatg	480
gcattgagtg	gtatggctgt	ggatgcagtg	atggactctg	tgtcagtga	aacgaccttt	540
aaggaaacac	tgatggagaa	aggtattatt	ttttgctcat	tcagtgaagc	tgtgcgtgaa	600
catcccgact	tggtgaaaaa	gtatctcgga	tctgtgtgtg	ggtatagaga	caacttcttc	660
gcggcattaa	actcggctgt	attctcagac	ggttcttttg	tctatatccc	caagggggta	720
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gaacgtacat	tgattgtggc	tgatgacgat	agctatgttt	cctatctgga	ggggtgtaca	840
gctccaatga	gagatgagaa	tcaattacac	gctgctattg	tcgaaatcat	ggtacatgat	900
cgtgcggaag	tgaaatatag	caccgtgcag	aattgggtatc	cgggcgatgc	cgaaggcaaa	960
ggtggagtgt	ataattttgt	gacaaaacgt	ggcaattgca	aaggagtaga	cagtaaactt	1020
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acagaagatg	ccattggatt	gacgtgaaac	ggctatgcta	aggaggtact	taataaactt	1500
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<210> 57

<211> 246

<212> DNA

<213> B.fragilis

<400> 57

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ggagctttta	aatatctttt	attggtgagc	ttgggtatat	gtgtcattca	gtttatagac	120
tccgatagtc	agttgattag	ccaaacaaaag	aaggagcagt	ccttggtata	ttatcttatg	180
gaaagctttg	cggggatctt	ctttcctgca	gcaaaagagg	ttacacaaca	atatatatc	240
aaataa						246

<210> 58

<211> 1341

<212> DNA

<213> B.fragilis

<400> 58

ctttttacgt	ggttttttagt	tctcggaaac	ttgtttgtcc	atgctaattt	aagaaatatt	60
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aaatgctctc	atggagctac	tgtagggtcaa	ctggatgaaa	acgctctttt	ctatatgcgt	1200
gctcgtggta	tgcgccgaaa	ggaggcccg	ctgttgctga	tgtttgcatt	tgtcaacgag	1260
gtgattgata	ccattcgtct	gaaggcgttg	aaagatcgtc	tgcatttggt	ggttgaaaaa	1320
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<210> 61

<211> 762

<212> DNA

<213> B.fragilis

<400> 61

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atagagaaga	ccaattctcg	tggaaaccgga	tttgtacgta	gcaatgggat	gcggcagacc	660
gtaagtgtag	gggtaaagg	taacttccct	tttactatta	cgcacgcgga	cggaaattcc	720
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<210> 62

<211> 879

<212> DNA

<213> B.fragilis

<400> 62

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agtgatatgt	tcgaaattaa	agctattgaa	atgatcaatc	gttatcttgt	gactgccgtt	420
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cgtctggcca	cagcagcggt	tgctgatgta	tgtacgccgg	gcaatccacg	ggaagtaaca	840
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<210> 63

<211> 648

<212> DNA

<213> B.fragilis

<400> 63

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gcgcttggtt	ccggaacagg	ttcttgggtg	ccgaatttgc	agaaagagaa	agtatccatt	180
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catctgggga	ttcttcgtga	gcgtccggat	gtaaatgtcg	ttttgcattt	tcagtcggaa	300
tatgctacgg	ctgtttcttg	tatgaaaaat	aaaccatcta	acttcaatgt	aactgcggag	360

atcccttgctc	atgtacgtaa	agagattcct	attatttcctt	actaccgtcc	cggttctccg	420
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catgggcagg	tggtatgtgg	caaggacttt	gatcagggtat	acgaacgtgc	tactttcttt	540
gagatggctt	gccgtatcat	agttcaatcc	ggaggggact	attcgggtctt	gacgccggaa	600
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<210> 64

<211> 1167

<212> DNA

<213> B.fragilis

<400> 64

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gataagctcg	actttctctg	gaaccgatgt	ctccccgaag	aaacgggtga	accggatata	180
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aaaaacaatg	taatctatat	agaataa				1167

<210> 65

<211> 1467

<212> DNA

<213> B.fragilis

<400> 65

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gaaggtaagc	taaaactgga	agaggatata	cgttttgcca	atcggcagat	aaaacttgga	180
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<210> 66

<211> 3051

<212> DNA

<213> B.fragilis

<400> 66

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<210> 67

<211> 1251

<212> DNA

<213> B.fragilis

<400> 67

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<210> 68

<211> 204

<212> DNA

<213> B.fragilis

<400> 68

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ttgtattgtt	tagtagctgt	ttcggcttgt	atgtcactaa	tgtttcccac	gatttatggc	180
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<210> 69

<211> 2088

<212> DNA

<213> B.fragilis

<400> 69

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<210> 70

<211> 2085

<212> DNA

<213> B.fragilis

<400> 70

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<210> 71

<211> 783

<212> DNA

<213> B.fragilis

<400> 71

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<210> 72

<211> 792

<212> DNA

<213> B.fragilis

<400> 72

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<210> 73

<211> 231

<212> DNA

<213> B.fragilis

<400> 73

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<211> 210

<212> DNA

<213> B.fragilis

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<210> 78

<211> 1149

<212> DNA

<213> B.fragilis

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<211> 1257

<212> DNA

<213> B.fragilis

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<210> 80
 <211> 291
 <212> DNA
 <213> B.fragilis

<400> 80
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 attagttata atttatatca aaaccgctca caaccgtag ctttcatttt ctacgaagag 180
 tacaaaagacc agcgtgccat ggatatacat gcggcatccc cccatttcca ggcttttggg 240
 aaggcaatca aggaaatgct ggcacccgat ttgataattg aaacttttta a 291

<210> 81
 <211> 3183
 <212> DNA
 <213> B.fragilis

<220>
 <221> unsure
 <222> (2747)
 <223> Identity of nucleotide sequences at the above locations are unknown.

<400> 81
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 aacacaaaaga gcatttcggg tacggtgaga gagaaaggca gtaatgaaac tgttattggg 180
 gccactgtac aagtgaaaag aacacacaat ggggtgatta ctaatgagaa tggggagtat 240
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 gtatccagtt tgagttccga tcagttcatg caaaccaacc cgtaagtct ggagcaggct 480
 ttgaaaggaa aaatatccgg tgtgcaggta atgaataatg atggtgcgcc ggttggtgga 540
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 atcgatggtt ttcctctccc tatttcggac gatcctctgg aaagtccttt ggctactatc 660
 tctcctgatg caatcgagag tatctctatc ctgaaagacg tatcatcaac tgccatttat 720
 ggggcacagg gggctaattg cggtgtgttg attactacga agaaaggatc ggccggtatg 780
 agtgaaatct ctgtgaaggc tacttacggt atcagtaaac tggcaaattc tattccaatg 840
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 caaaatgctt atttctatca ggaataataa gatcagatat ggaataccaa tccttcccg 960
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 aacggattgg ccacatacgc tacgcaaagt ggattaaata tgcgtggagt agtccaggcc 1560
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tcgggatatg	atcctgaggt	acgtagtggc	agctctgtaa	ataatcgat	tcttccggga	3120
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taa						3183

<210> 82

<211> 1149

<212> DNA

<213> B.fragilis

<400> 82

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acaattgacg	gaaagcaa	cgatctctac	tttctgagaa	acaaaaacgg	cattgaaatt	180
gccatcacca	atttcggagg	acgagtcggt	gaattctgga	ctccggataa	aaaagggcat	240
tttgaagaca	tcgtcctcgg	acacgatcat	gtggacaaat	atctccatta	taaaggtgaa	300
agattttttg	gagccactat	cggacggtat	ggcaaccgga	tcaacaaagg	aaagtttacc	360
ctgaacggac	aaacttacca	gttaccatc	aatgatacac	ccaacagtct	acatgggtggc	420
tttaaaggat	ttgatatggt	agtatggg	gttgaacagc	cggacagcca	gactttacaa	480
ctcacgtatt	tatccaaaga	tggtgaagag	gggtatccgg	gaaatctcca	agtatccatg	540
agttacaagc	ttacggataa	aaacgaattt	attatcactc	accaggctca	aacagacaaa	600
gagacgggtca	tcaacctcac	ccatcattcc	ttcttcaacc	tgacaggtgc	aggcaataag	660
gatatcaatg	accatatact	catgatcaat	gcggataagt	ttactcctgt	cgatcagatc	720
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cgagcttccc	tcgcattgga	aaccagcac	tatccagata	gtcctaacca	accggcattc	1080
ccgtcaacaa	ccctcttacc	cggagatact	tacaaacata	tatgcatcta	taaaatcaat	1140
gtacaatga						1149

<210> 83

<211> 816

<212> DNA

<213> B.fragilis

<400> 83

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gaagccggga	attttttgag	aaaagaacgg	aggagcttta	gtcgggagcg	tgtggtggaa	120
aagcatgcgc	atgactatgt	gtcgtatggt	gataaagaat	ctgaacgctt	gttagtggca	180
caactgtctg	cgttgctccc	cgaagccggg	tttattgctg	aagaaggttc	tgccgtttat	240
aagaatgagc	cttattgtctg	ggttattgat	ccgttgagcg	ggacgactaa	ctacattcat	300
gacaatgctc	cttattgtgt	cagtatcgca	ttgaggagct	gtacagaatt	acttttagga	360
gtggtgtatg	aagtttgcag	ggatgaatgt	ttttacgcct	ggaaaggtgg	gaaggcttgg	420

atgaacggag	atgaactgca	tgtctcgaaa	atagaaaaca	tagaagaggc	gtttgtaatc	480
actgaacttc	cttataacca	tcggcaatac	aaacggactg	cggaaatatt	actgaaacaa	540
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gctgcccac	tgattgtgtt	ggaagccggc	ggaaaagtaa	ctgatttctt	tggaagttag	720
tattttattg	aaggacatca	tatcattgcg	acgaatggcc	ctttacatcc	tgtctttcaa	780
cggctgctga	aagagatgcc	tccactggaa	atgtaa			816

<210> 84

<211> 288

<212> DNA

<213> B.fragilis

<400> 84

ggtactgcc	tgaaaaaat	attattagcc	cttttaacct	cttgccgctt	agtgtcgtgt	60
gaggggtatt	tcgaccagtt	accgaaaaca	gaacttcctg	ctgaaacttt	ctatacttcc	120
tatgatgctg	ctttacgtaa	tgtagctata	ttgtatgcta	atgcagggca	tgtcaatgat	180
ggaattatga	ccactgaccg	gtttatgatg	ccttcattga	tgaatgaagg	tccgttcgac	240
ctgaacttga	catcgggtctt	caccacgggg	ctgcaagggt	gcacatag		288

<210> 85

<211> 1332

<212> DNA

<213> B.fragilis

<400> 85

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tcattgggag	gattactttt	tggtattcgat	accgcagtga	tatccggagc	cgagaaatcc	120
atccaggtgg	tatatgatct	atccgacttc	agccatggct	tcaccattgc	tatcgctttg	180
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aaagcactga	aaattattgc	ttttctctac	tttgcttctg	cagtgggcag	tgctgccatc	300
atcgattggg	attccttttt	attcctccgt	tttgccggag	gtttagctgt	cggagcctca	360
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gtcgcattct	tccagtttaa	tattgtactg	ggattgttac	tggttacttt	ttccaactat	480
tggtattcacg	gcattgcgca	tgattggcaa	tggtatttag	gagttgaagc	cattcctgcc	540
atcgcattcg	ctcttctatt	atacacccga	cctgaaagcc	ctcgttggct	ggtaaagcaa	600
gatcgggaag	ccgaagcccg	acacgtcata	aagaagggtca	gcaatgcaaa	tattgaacag	660
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cagcataaat	accggaaacc	gatcctctat	gctttcctta	tagctacttt	caaccagtta	780
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ttctttgctc	tcaggctacc	cgaaacaaag	aacaagtctc	tgagagcagat	acaaaaggaa	1320
ttgaccaatt	aa					1332

<210> 86

<211> 198

<212> DNA

<213> B.fragilis

<400> 86

gccagtacaa	tacccagtac	aatattaaac	tggaagaatg	cgacaaaacg	gccgcgccaa	60
cgcgaggggg	atatttcggc	aatgtacatg	ggaccgacta	cggatgaggc	tccgacagct	120
aaacctccgg	caaacgggaa	gaataaaaaag	gaataccaat	cgatgatggc	agcactgccc	180

actgcagaaa caaagtag

198

<210> 87

<211> 207

<212> DNA

<213> B.fragilis

<400> 87

tctcaaagat	ctctatcaca	aagatactgc	atatttttcga	atgcaacaaa	tcaatcgatt	60
ttttttattg	aggactggca	ttattttgctg	gttctttttt	attggaaatc	tgaagggtata	120
tcgatacctt	tttttaatcc	gatagcaata	cccaatcctg	ccacacccta	ttcggacaaa	180
caaagaatga	aagataatag	atcttga				207

<210> 88

<211> 240

<212> DNA

<213> B.fragilis

<400> 88

aaaaactttc	catactatgg	gtgggatgct	ttcgctaattg	acaaatcaaa	acaagatgct	60
attgttcttc	tacctatgat	attacccgat	tttgactcgc	aggaaagatg	ctattattat	120
tctgcacaac	cggttatatc	agatgtttgt	gaaatcagta	gagattattt	caataaagac	180
ttttctaaaa	attataaact	tgaattttaa	ttgaagatag	taaattattt	ttttaattaa	240

<210> 89

<211> 489

<212> DNA

<213> B.fragilis

<400> 89

atcaccatgt	tgtcttttga	atcagaaatc	gattctttgt	gogccgtttc	gcacgaactt	60
ctccatttag	gtctggatgg	cgaaccocat	tattccgacc	gtttccgtca	gttgaatacg	120
gatgtgtatc	atcgttgtga	gcatcttttc	ggttcacatg	gacgtaccct	cgaagaggaa	180
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aaggaagata	aatccagtc	ggctcctcaat	cgtagttggg	atctcttggg	tacacttccc	300
gtctctctgc	tgaatgtcg	tttgttggtg	gcttggttac	ccgaggtctt	tgacgaagag	360
ctggcggcgg	aggcacatgc	aataatagac	ggttgggaagg	atcgggaatt	gacgagggaa	420
gagtttgaga	ttgtggagca	tttaaagagt	ttggaggaaa	atccgtatcc	gaatacggat	480
atagaataa						489

<210> 90

<211> 630

<212> DNA

<213> B.fragilis

<400> 90

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ttgctgaagg	cgttctgcga	ctacggtaag	ggttcgacaa	gctatcaaga	aaccctgtga	180
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gaagaagagg	aagcagaatc	tttggattaa				630

<210> 91

<211> 603
 <212> DNA
 <213> B.fragilis

<400> 91
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 attggctgtg atgctaccaa tgaagacgct gtgcgccggg tgtatgagat aaaacgacgt 180
 gctgacagta aggcgatgct ggtattggta gactcgccgg tgaaagtgga attctatgtg 240
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 atttattccg gtgcccgcga cctggccttc aatctgcttg cagaggatgg aagcgtaggc 360
 atccgggtga caaacgaggg gttttcccg cgtttgtgcc agcagtttcg caaagcgatt 420
 gtctcgacat ctgccaatgt cagcggacaa ccgggagcag ccaattttta tgaaatcagc 480
 gaagaaataa aatcgctcgg ggattacatt gtcaattttc gacaagatga tatgagtcgt 540
 cctaaaccat cgagtatcat taaactggat aaagggtggag tgatcaagat tattcgcgaa 600
 tga 603

<210> 92
 <211> 1923
 <212> DNA
 <213> B.fragilis

<400> 92
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 ggactgatgc ccaccggagg cggaaagtca attacgtttc aggttccggc ccttgccaaa 180
 gagggattgt gcattgtcat caccctactg attgctctaa tgaaggatca ggtgcagaac 240
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 actcccgaag tagtgaagga catacaggag cgcctccgct tccgggaaga aaacgtgttc 600
 cgtatgagct tcgaacgaaa gaatctggca tacatcgctt gccccactga taataaaaaa 660
 ggggagttgc tgcacatact gaaccggata caaggcagcg cgattgtata tgtacgaagc 720
 cggcgaaaaa ccaaagaaac aaccgagctg ctggtaaacg aaggaatcac ggccgacttt 780
 tatcatgcgg gactggataa cgcaaccaa gatcttcgcc aaaaacgatg gcaaaacgga 840
 gaaagccggg tgatggtagc taccaacgca ttccggtatgg gcattgacaa accggacgta 900
 cgtatcgtca tccacctgga cctgcccgcac tcaccggaag cctactttca ggaagcggga 960
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<210> 93
 <211> 1740

<212> DNA

<213> B.fragilis

<400> 93

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cttttggtac	aaagggggaat	tacgaaggca	caggatgcc	agaaattctt	ccgtccgcaa	180
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aacatggcga	tgggaaaagaa	agaacgcatt	ctgatttatg	gagattacga	tgtggacggt	300
accacggcgtg	tggcactggt	ctacaagttc	attcaacagt	tctattcgaa	ccttgactat	360
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<210> 94

<211> 1203

<212> DNA

<213> B.fragilis

<400> 94

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<210> 95

<211> 258

<212> DNA

<213> B.fragilis

<400> 95

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<210> 96

<211> 1320

<212> DNA

<213> B.fragilis

<400> 96

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<210> 97

<211> 840

<212> DNA

<213> B.fragilis

<400> 97

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<210> 98

<211> 636

<212> DNA

<213> B.fragilis

<400> 98

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<210> 99

<211> 1923

<212> DNA

<213> B.fragilis

<400> 99

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<210> 100

<211> 306

<212> DNA

<213> B.fragilis

<400> 100

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<210> 101

<211> 2118

<212> DNA

<213> B.fragilis

<400> 101

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2118

<210> 102

<211> 1386

<212> DNA

<213> B.fragilis

<400> 102

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<210> 103

<211> 2571

<212> DNA

<213> B.fragilis

<400> 103

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<212> DNA

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<212> DNA

<213> B.fragilis

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<211> 195

<212> DNA

<213> B.fragilis

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<211> 195

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aatgtggatg	aacagcgatg	gacgacattc	cagatggaga	acttcatgga	gtggagaccg	420
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<210> 114

<211> 1233

<212> DNA

<213> B.fragilis

<400> 114

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acaattaccg	acctgtctaa	agaattggat	cttagtgtcc	ctacagtcac	taagttttatc	180
agtgaatgt	gcgaagaagg	ttatatcaac	gactatggta	aattggaaac	aagtggagga	240
cggcaccccta	acctatatgg	cttaaatcct	gaatccggct	acttttatagg	agtcgatatc	300
aaaagatttg	ccattaatat	cggcttgatc	aacttcaaa	gtgatatgat	ggaacttaaa	360
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gactacatta	ctcaaccaat	aaaaacagct	gtccgcaagt	actcacttaa	tctgggtcaat	1140
aaagactcgg	caatcgtcac	ttcaaaaacta	aaagacagag	ccggtattgt	cggagcttgc	1200
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<210> 115

<211> 285

<212> DNA

<213> B.fragilis

<400> 115

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aaacaaatga	tctacagtca	cttcagagca	caatatttca	atctgcagaa	gctttatttt	180
aacgttacgt	taaagttcgt	ttttcgtctg	caaataagca	attcttttaa	tgcaaaagac	240
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<210> 116

<211> 588

<212> DNA

<213> B.fragilis

<400> 116

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caagatagta	tccgtgaaat	attccagcgg	aaaggcgatg	caatagtcga	attgaattta	540
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<210> 117

<211> 969

<212> DNA

<213> B.fragilis

<400> 117

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969

<210> 118

<211> 270

<212> DNA

<213> B.fragilis

<400> 118

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ataccgatat	gggcgggatg	tccgggcatt	catacgctt	ggaaaagaga	agtgatgcag	180
gaaagcgggt	gttgcaaac	gtatctgccc	aaaaaactgc	ctgactcctc	acgtatcgaa	240
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<210> 119

<211> 1131

<212> DNA

<213> B.fragilis

<400> 119

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tttgagcaat	ctttggccga	atattttgcat	gaagaccgtc	gtgtagtggc	tttgagtgtc	180
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<210> 120

<211> 1569

<212> DNA

<213> B.fragilis

<400> 120

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gatatgacat	tgaaagtatt	ttattcaaac	gaaacgtctg	aaatagttcc	tgtaaaaaaa	240
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aaccttgtcg	aaacatacaa	gcagaacaaa	gcctggaagc	cattcgctga	aaaaatcggt	1560
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<210> 121

<211> 978

<212> DNA

<213> B.fragilis

<400> 121

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ggtaaaaaga	gactgaagac	agatgaactt	ttacgtggat	tccatctgac	tgaagcattt	960
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<210> 122

<211> 546

<212> DNA

<213> B.fragilis

<400> 122

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gttgaaagggt	tgggatgtgc	tttggttaca	gtctcaacgg	atttgttagc	ttcaaaagag	540
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<210> 123

<211> 1026

<212> DNA

<213> B.fragilis

<400> 123

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<210> 124

<211> 1182

<212> DNA

<213> B.fragilis

<400> 124

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<210> 125

<211> 1821

<212> DNA

<213> B.fragilis

<400> 125

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caggtgatgc	agacttttga	cgatacaaaa	gcatggaact	tacctgtggg	caatgaagag	1740
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<210> 126

<211> 252

<212> DNA

<213> B.fragilis

<400> 126

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ttggatgctt	gtctgattaa	agccaatgac	tctgatccgg	tgtatctgag	tacgaacggg	120
gtgaaaagtc	atattaaatc	ggtagaagat	tttaataagg	tcggttttga	ttgggataaa	180
atcaagggtga	tgtctccggc	agaagtggat	gcaatcccta	ctgctccgga	atatgagatc	240
gccaattggt	ga					252

<210> 127

<211> 936

<212> DNA

<213> B.fragilis

<400> 127

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ttttatgaaa	atggagaggt	taattatgaa	ccaattgaag	cgtatgctaa	gatgttagta	120
aagaacggac	tgcaaggagt	atattattaat	ggatcttccg	gtgaaggata	tatgttgacc	180
gatgaagaac	gtatgaagct	tgctgaacgt	tgggtagaag	tttcacctaa	aggatttaag	240
gtgattgtac	atgtaggtag	ttgctgtgta	aaatcaagtc	gcaagcttgc	cgaacacgct	300
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gtcgaagagc	tgggtgaagta	ttgtgaagaa	atcgcttgcg	gtgctcccga	tcttcctttc	420
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gaataacaatc	agtgtcgttt	gtataaaggg	ggtaagtttg	atatgcttca	cggacaagat	600
gaaacgatcc	ttccatgcct	agctatggga	ggtgcccgag	gaggtatttg	cggaaactacc	660
aactacaatg	gtgtaaatct	ggttgggtatt	atagaagcat	ggaaagcagg	tgatcttgag	720
aaagcacgtg	aattacagaa	tttctctcag	gaagttatta	atgtcatttg	tcatttccgc	780

ggaaatatcg	taggtggaaa	acgaatcatg	aagttgatag	gattggattt	gggtaaaaat	840
cgtactcctt	tccagaatat	gacggacgat	gaagaagtac	gtatgaaggc	tgaactggaa	900
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<210> 128

<211> 1113

<212> DNA

<213> B.fragilis

<400> 128

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ggaaaggctc	actttcctaa	tgcggaaggc	gaacagaagt	tgcgtcaa	gattgaaatg	180
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atggaaaaag	atattgagtt	tgttttgaag	aaaatagaga	tgtctcgaga	agagtttgaa	1020
gaacttataa	atagaccagg	gaaacaacat	tcagattata	gaatggacaa	atttctacct	1080
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<210> 129

<211> 1473

<212> DNA

<213> B.fragilis

<400> 129

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ttattgggtc	tatataactt	ttatatagcg	atttgtggac	gaattagggt	ttttactatt	180
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cttgtttggg	tatttacttt	gttaggttta	ctgttcttgt	tattaggctt	tgcgatagca	360
aatatcgtat	ttaaaaaatat	ttgttatccc	agaaaaata	gagatctaca	attaattaaa	420
gtttcaatta	gctgttttga	taattcaaat	aaaaatttct	ttgttatttt	atttcttttt	480
attttaagtt	tctttgtttt	gcttgtttat	agaaatgcaa	ttggaggatt	tccattggaa	540
tctgttttct	ctgctgataa	tggaaactgca	cttgcccttt	tgagaagtga	ggctactaat	600
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tttatagttg	tttcttttat	aaaaagttgt	aagaagaaaa	aatggaaata	tttatatata	720
gctttgtttc	tttataatct	tttttattca	ttatctacta	tacaaaaggc	gcctatcctt	780
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gtagaaatta	tgaattatgc	gaaaggagat	cttttagggg	atttagtagg	ttcaatgcct	1140
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ttaatgtttg	ggtttatatt	acaaacatta	gatattttat	ttgttaggta	tcttttagtg	1260
aataagagtg	tttttagtttc	aagtttatat	atatatatga	tttattattt	ctcacagttt	1320
acagaaacag	gaataagtgg	aataataata	gatacacatc	tttatatagt	cttattttatt	1380

tcattttatatt attgtttgat aaatagatat aatttgagaa gatatgggaa aaaaaagggt 1440
 ttgccatggtt acaagtgtac atcctgcaga tga 1473

<210> 130
 <211> 378
 <212> DNA
 <213> B.fragilis

<400> 130
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 tcgattttatt cctctgtttt tattcatcac ataaccgct atgcagctca caaacggga 180
 aaatatcttc gaaaacaaat ctcaaacag cttcgagtga aatttaaaca gacctcaaag 240
 ggcaacgatt ttttcagcga atggcttcca ggctttgttc tgcttgtatg tttcgacaag 300
 gttttgggga actcttatct tttgaattcc tggcgctacg gggtaatagt cggcagtaac 360
 catcgtaggc gacattaa 378

<210> 131
 <211> 213
 <212> DNA
 <213> B.fragilis

<400> 131
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 aaagcaagag tggcactcgc ccagaaaaag gctatctatg ccgccaatgg agaaatgctt 120
 tctatgtatt gggacatcgg caagttattg tccgaaagcc aaacacaaat tggctgggca 180
 acaatacgtt ggagcagttg cccggtgatt taa 213

<210> 132
 <211> 498
 <212> DNA
 <213> B.fragilis

<400> 132
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 cagcaattag ctgagatgat tgcggaaaaa tcgtcgttga ctccgggtga tgtgcataat 180
 gtggttcgta acttgatgac agcgatgctg agtgcatgac tggacagtaa gacggtacgt 240
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 gcgagtggga tccgtgcttc gggcaataat ggttccggag gtggtgatgg agacatagta 480
 gatgatccga ctgcgtag 498

<210> 133
 <211> 1251
 <212> DNA
 <213> B.fragilis

<400> 133
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 ttcttttggg tttatggcct tatgagcccg atttccggta tgattgccga tagattgaat 240
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 gctactgttg ccgtgcttt ctcatggcat accacattcc attgggtcgg tattgtaggc 540

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<210> 134

<211> 684

<212> DNA

<213> B.fragilis

<400> 134

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ataataaacg	ggcgttgccg	ttgggtgcga	agtgacgaac	tgtatgtgaa	gtacctgat	180
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ggaactacga	tttgctatgc	tcaattgcag	gcctccggat	ttatgaatga	tcatctgggtg	660
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<210> 135

<211> 222

<212> DNA

<213> B.fragilis

<400> 135

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aaagccgtgg	tcattaccga	cttcaccgat	gaaaacggta	tcgaccggat	gaaggagcag	120
atacaggaga	agtacaaccg	tatcaaagcc	gacgtgcgtc	agattgtcgc	cgacgaattg	180
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<210> 136

<211> 630

<212> DNA

<213> B.fragilis

<400> 136

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gcccttcgta	tcacctatag	ccgtgagctt	gcctttaagg	aatacctgga	ctcccgcgga	180
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gaaatgaaat	ccactgtcgg	ggcttctctt	cctattcggt	atatcatgga	ccgtgagacc	360
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ccctctttaa tcgaattaat aaagaattaa

630

<210> 137

<211> 1236

<212> DNA

<213> B.fragilis

<400> 137

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<210> 138

<211> 2316

<212> DNA

<213> B.fragilis

<400> 138

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<210> 139

<211> 279

<212> DNA

<213> B.fragilis

<400> 139

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tcttccaatg	tagaacaatg	tacacatata	acggcttttt	ccgtaggagg	aagaggaact	180
aatttttagtt	ttaactctgt	gattaaggct	aatgtacctt	ccgaacccgc	taacaatttg	240
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<210> 140

<211> 597

<212> DNA

<213> B.fragilis

<400> 140

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gatgacgggt	gccgaatcgg	tgcaggcaca	aagatatggc	attacagcca	tataatgacg	120
ggatgtgtgc	ttggtgaacg	atgcaatata	ggtcagaatg	tggttaatttc	tccagatgtg	180
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gaagatgatg	tttttctcgg	tccttcttgt	gtctttacca	atgtgataaa	tcctcgtagt	300
gctgtcaatc	gtaaatcaga	atatgctaag	actcgtgttg	gtaaaggagc	tacaatagggt	360
gctaatagcta	ctattgtatg	cggacatgat	atttggatga	ttgcctttat	tggtgccgggt	420
gcagttgtta	ctaaaactgt	tcctccttat	gctctcttgg	tgggtaatcc	tgcccgtcag	480
ataggttgga	tgagttagca	tggatatcgt	ttagaatttg	atgagagagg	gatagctgag	540
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<210> 141

<211> 225

<212> DNA

<213> B.fragilis

<400> 141

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attactctca	tatatccatc	aatattgaac	gataagctcc	ctctaaaatc	tccttttcat	180
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<210> 142

<211> 534

<212> DNA
<213> B.fragilis

<400> 142

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cggtgggccc	cagagtataa	agacggtgtc	ttttatcatt	atgaaaatgg	tgatacgact	120
aaatgtcata	cagattccat	cttgaattac	atatcggatg	cgggtgagaa	ctggcagatg	180
aagatagagg	gtgatcattt	tgtccatgct	cccaatgggtg	actattcacg	tgcgcatact	240
gatacggtaa	tgcattatat	cggatgggac	ggtcgtaaat	ggcgtgccga	acttttgact	300
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ccggatgttt	attttgcctt	atttctgccc	tgggataaaa	tcacggtgaa	aagtcaggag	480
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<210> 143

<211> 183

<212> DNA

<213> B.fragilis

<400> 143

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gagaccatca	caaacttttc	cacaccatat	ttgacagcta	agtcagccat	aatacgagta	120
cccagcacat	tcacctgtat	ggcttcagat	acattatctt	ccatcatggg	cacatgttta	180
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<210> 144

<211> 1341

<212> DNA

<213> B.fragilis

<400> 144

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attggtgccg	tagcacatga	tgaatataaa	aatttagagg	agaagtattt	taaaaatatg	1260
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<210> 145

<211> 1113

<212> DNA

<213> B.fragilis

<400> 145

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gctcctgagg	tgtcgaatca	gttaaaaaat	ggaattcaaa	ttataggggt	actcaataag	180
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gatgtaaata	gtataactgg	tgctatacaa	tatttaatat	ataatcctgt	tattgctcgt	1020
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<210> 146

<211> 543

<212> DNA

<213> B.fragilis

<400> 146

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aaacctattc	gcaagtgggt	ctcagtagtg	gtaataccca	tcattccttt	ttctaattta	180
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cgttggttatt	tggatgatat	gtgttatgat	ttgattgaaa	taggtgagaa	tgtgaccata	300
tcttatggcg	ttttttttgc	atgccatggt	cgtaaacagg	ggcataatag	aattattata	360
aaagatgggg	catatattgg	catgaatagt	tctattatat	ctcggagaga	agaagggttg	420
attattggaa	aagaggcaat	agtgggtgca	tgtagtttag	taaatagatc	tgtaccagat	480
aataagactg	tagttgggtg	acctgctaaa	gaattaaatg	ctgttctaca	cgggaataaa	540
tga						543

<210> 147

<211> 1200

<212> DNA

<213> B.fragilis

<400> 147

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<210> 148

<211> 1122

<212> DNA

<213> B.fragilis

<400> 148

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gtttgtgggtg	ttgccgtgtt	agtaggactt	gtagtggctt	ttagtattcc	taaagagtat	180
tctacaagtg	taacactggc	accggaaaca	ggtagcaagt	cttctactgg	aggcatgggg	240
gcattagccg	ctatggacgg	tattaatctt	ggcagttcaa	ccggagaaga	tgcactttct	300
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<210> 149

<211> 681

<212> DNA

<213> B.fragilis

<400> 149

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tgggtacaca	ttgatattat	ggacggagta	tttgtgccga	acatatcttt	cggctttccg	180
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gtatatatgg	tgctgggttat	gagtgtgaac	cccggatttg	gcggacaaaa	atttattgaa	480
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gcagatgcat	tggtggcagg	aaatgctatc	tttgtctgctg	agaatccgga	aggaatgatt	660
cacgccatga	aagggtgtga	g				681

<210> 150

<211> 1047

<212> DNA

<213> B.fragilis

<400> 150

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ccaagtaaga	caacttatat	ctatatagac	cgcgatgata	ctacagactc	catcttcaat	180
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<210> 151

<211> 891

<212> DNA

<213> B.fragilis

<400> 151

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<210> 152

<211> 1233

<212> DNA

<213> B.fragilis

<400> 152

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gaaatagcgg	caggtattat	agaaatattt	tcgttttcag	atgtagagtt	aatcaataaa	1140
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<210> 153

<211> 1002

<212> DNA

<213> B.fragilis

<400> 153

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gccatactta	cacagaatcc	ggacgaagaa	gctgccctcc	tgctacgtgg	caaaataaaa	660
gaagccaccg	gaaaggaaga	agaagcagag	acggactatc	tccatgtgac	agagataaac	720
cctttcaacg	aacaagctta	cctatatctg	ggacaactat	ttatcacaca	gaagaaattg	780
acagctgcta	ttgagttgtt	tgacgaagct	atcgagttga	atccaaactt	tggagccgcc	840
tatcatgaac	ggggacgtgc	caaactatta	aacggggaca	aagacggttc	gattgaagat	900
atgaagaaat	cgctggagct	gaacccgaaa	gagggagaga	acctgaacgg	acagttcaat	960
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<210> 154

<211> 810

<212> DNA

<213> B.fragilis

<400> 154

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gcggagcaga	tcgctaaggc	acaaaacgaa	gtgcttgttt	ttatgccgaa	tgccatcaga	120
gacggaatag	aagagtttgt	gttggcggat	gatgaaaaag	taggttttgt	tttccctggt	180
tattcatggg	gacctccgtt	gagcgtattg	cggttcttgg	attggattac	tttatctaata	240
tatcattctc	aatacgtctt	ttttgtctgt	tcctgcggag	atgatacagg	gctgacggaa	300
gaactctttc	gccgggcatt	gtctcgtaaa	ggaatggagt	gtaatgccgg	tttttcagt	360
gctatgccta	ataattatgt	tttgcttccc	ggatttgatg	tggataagaa	ggaactggag	420
aaaaagaagt	tggatgaagc	agttggcagg	gtagaagaga	ttaatgattc	gataaccgga	480
aagaaaatag	gttttcattg	taatgaggga	agttttccat	ggtttaaaac	caaagtactc	540
aatccgctct	ttaatcgttt	tatgacctcg	gcaaaaccat	tttacgccac	tgatgattgt	600
atcgggtgta	aacgttgtga	aaggatatgt	cgggttgga	acgtggtgat	gataggggtg	660
aggcctgtgt	ggggaatgga	ttgtacatcc	tgccctggctt	gctatcatgt	ttgtccgaag	720
catgctgtgc	agtacggaag	aaggactaaa	cgtaaaggac	agtattttaa	tcccaatgtg	780
agtatttcac	atgaggcggc	cgcccaatag				810

<210> 155

<211> 2175

<212> DNA

<213> B.fragilis

<400> 155

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ttcttttgagg	cgttggagtg	gttgcttgac	acagctcatg	agacgaaaga	cccttcgctc	180
ataticggaaa	tgcgcaagtc	ggaattggag	gaagatgaag	cgcacaccat	gtctgtttca	240
atgtttttttg	agcataatgg	agaaaaagag	gtgtcgaaga	gtctgacctt	cgaaaagaga	300
aacggagtat	gtcaagtgc	aaatttttgc	ttcaaagggt	acgagactaa	tggcgctgag	360
cgtatgcaac	gaaagggcag	ctcgctaatt	gacgtgtgct	ttgatgcgtt	catttcgtaag	420
tattgcctgt	tcaaagggtga	gagccaattg	aatgttttta	atgagaaaga	ggcgttgaga	480
acgctttag	ataaattctc	cgacatccgc	aagtttgaag	attatgtcgc	tgttgctact	540
gaacttgaag	caaaatccga	tcgagcatac	gcaaaggagt	gccagtcgga	taagaagatt	600
tcgcagaggg	tttcggaact	ccaatgtaag	aaagagcatc	ttggacaaca	gatagacgag	660
ataaaatgcg	acatcaggaa	acaggaagat	gtggtgagca	cctattctgt	gaaacttgaa	720
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aaggatcgg	cgttgagcaa	agagaagcga	cgtctcagcg	accttgacat	acaggaaaaa	960
gcggcggcaa	aggctaagaa	ggaagtgcgt	gatgaactga	catcaagtct	gcaaagcgac	1020
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gaagtatgca	aggtatgcgg	ccgaccagca	aagaagggca	cgccggagta	tcgtttcatg	1140
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gaattaccag	acactccgct	ttttggtact	caatataatc	aggagcttca	ttcgctttct	1260
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atattcgatg	cgccaacttc	atcgtttgag	aacttcaaag	agaacgtctt	ctacaacatc	1980
atcgacaaaa	tccagaaaca	gtgcattatc	gtgacgaaag	acttgcttga	agtggacaaa	2040
ctgacgggca	agaagactct	gaacgaagcg	caaatagaag	ctttgacctg	ttctgtatat	2100
cgcacgcgaga	aacagacggg	ctataacgag	accgaccttt	caacaatacg	aaccatcata	2160
actccaataa	aataa					2175

<210> 156

<211> 471

<212> DNA

<213> B.fragilis

<400> 156

ttttgccc	taataacaaa	ggttaagaga	aaacaaatgg	aagaaatcga	atttcatcac	60
agttttac	tacaactacg	attcaacgac	gtagacaaat	tcggacacgt	caacaacacc	120
gtctat	catttttacg	tctcggcaaa	acagaatatt	tcgcttctgt	atgcccgga	180
gtcgactgg	aaaaagacgg	cattgtagtc	gtacacattg	aagccgactt	tctggcacag	240
attttttcat	cggaccacat	cgccgtacaa	accgcagttt	gcgaaatcgg	aacccaaaagc	300
tttcatctgc	tgcaacgggt	catcgacacc	gaaacaatgg	aagtgaatg	catctgtcgt	360
tcggtcatgg	tgacattcga	tctggagaga	cacgaatcca	agccactgac	cgaagaatgg	420
atagaggcaa	tctgtcggtt	cgaagggaga	gacttaagaa	agaaaaata	a	471

<210> 157

<211> 216

<212> DNA

<213> B.fragilis

<400> 157

cgaaaaccaa	ttaacaatca	aatagttatt	aattttctatt	tttgggttggt	ggtagagaaa	60
gcgagcatta	tggggcatgt	tttgctgcga	cttccgttac	ttatccgtta	ccttgcaagt	120
acggatattt	caaggagtat	aaacgattat	ttttcaatgc	tttgcgtcac	ttttcataac	180
ttcaaaaagc	tcaatattta	tttagtttgt	aactaa			216

<210> 158

<211> 525

<212> DNA

<213> B.fragilis

<400> 158

agggtttgga	tgtgcttttg	ttacagtctc	aacggattgt	gtagcttcaa	aagaggaata	60
atgaaactga	ttaccgaagg	gcttcttgat	aaagtgactg	atcaggcaaa	agagaattca	120
cgcctgcgga	tgaattacaa	tttccatgac	tccatggatg	ctcctattca	caggatgttg	180
aatgcttttg	agccgggaac	ttacttgccg	ccacatcgtc	ataagaatcc	ggataaggaa	240
gaagtttatc	ttgtattgag	aggtagcttg	ttggctatcc	tgtttgatga	tgagggtaat	300
gtaacggaaa	aggttcattt	gaatccagct	gagggaacatt	atggaattga	gattcctccc	360
tgtgtatggc	atactatcgt	tgtcttagaa	tctggaaccg	ttatttatga	aataaagcaa	420
gggccttttg	ctcctcttat	tcctgaaaat	ttagcatctt	gggcacctcc	tgcaactgat	480
gaggaggcgg	cccagagtatt	tatgcagcga	atgcttgagc	tttaa		525

<210> 159

<211> 975

<212> DNA

<213> B.fragilis

<400> 159

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ctgatagcag	gctttcttgt	tggcaatggg	ttgtttttta	ggggagtctg	tgtttcgaag	120
ggcgtgctgg	caggagggct	ggcaggatta	tttcttctgc	tcctagtcgt	ttatttttct	180
caccgttact	ctttacgttg	gatgttcggc	tgtattttgt	acctgttcgt	gttttttggc	240
ggagcagggtg	gaataaatca	ggctttgcaa	cagacgcttt	attctttttc	ggaacaaaaa	300
tgtgtttacc	gggctgtagt	gttggaaaca	ccggagccga	aggaacatag	cttcctttgt	360
cgggcatttt	tggaggaaag	gcaggattca	gtgtgcacca	tgccggtaaa	tcgaaaagtt	420
ttgctttata	tatcgaagga	ttcattgtcc	gaagggttac	gtagtgggga	tgagttaata	480
ttttttgccc	atgtatctcc	accttcaaat	aatggtaatc	ccgatgaatt	tgattatgoc	540
cgttatctgc	gctacaaagg	gattagcggg	attgcttttg	ttgcaagtgg	gaattggaaa	600
attaccggat	atcggttttc	ccgatcatgc	aggcagattg	cattggaata	ccgggatcgg	660
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ggagccagtc	atgtactggc	actttccgga	cttcatatcg	ggtttctgta	tatgatgctt	840
ctgttttttc	tgaagtggct	gccagggaat	gcttttggtg	tgagactttt	tcgtgcggta	900
gtgataatca	ccgcattgtg	gggattcgct	ttttttaccg	gtctctctcc	ttcgggtcgtc	960
cgttccggtg	tcttc					975

<210> 160

<211> 252

<212> DNA

<213> B.fragilis

<400> 160

cttatcattg	ttttaacgat	ggcacattac	aacaataaca	gcaacagaat	cttgcaggct	60
gtttttggccg	atgagaaact	gatagagttt	ggcgagtaca	atcccgtga	ctatcaaagc	120
ttggacgagg	ctcttggtgc	tgataacctt	gtggtgaata	ctgtggcaag	gattatcaac	180
gaggtaaatg	aggagagcag	ctcacgggaa	atatataata	tggttaacaac	ctatctaaag	240
aataatatat	ga					252

<210> 161

<211> 615
 <212> DNA
 <213> B.fragilis

<400> 161
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 tttctcggtc tcctttttct ttctccaatt ttattagtaa cagctattct tttcgtggt 120
 aagatgcctg gaggtcctgt tatattcaaa cagaaaagag ttgggcggta tggtagatta 180
 tttaccatgt ataaaatttcg ttctatgacg gttgggcatt ccggtggttc tgtttctgta 240
 aaaggagaaa gccggatcac gccattgggg gccaaattga gaaaatataa gattgatgaa 300
 cttccggaac tgtggaatgt gctgatagga gatatgagtt tggtcgggtcc tcgtcctgat 360
 gttccgggat atgctgacaa tttgctggga gacgatagga gaatgttgct tttaaaacca 420
 ggtattactg gacctgccag tttgaaatat cgtaatgaag aagaattgct ggcagggcag 480
 gataatcctc aaaaatataa tgatgagggt ttgttcctcg ataaagtgcg aataaatata 540
 gagtatttgg ataactggtc attttggaat gatattaaaa tcatcgttta taccgttttt 600
 gggaaagata tgtag 615

<210> 162
 <211> 927
 <212> DNA
 <213> B.fragilis

<400> 162
 gaaccaatcg ttgaaagatg gcaagggtgcc cattatggga cgtataacga tcaacaagac 60
 caccgcctgc ttcagttgca agcggaaagt tccactggcat tatgggatgc caaggccaag 120
 agggcgaaag ggaaatccga cgaggccaga cggctgaatc aggagcttga caatgtcaag 180
 gccagatca caaggcatta ccagtatgtc tgcgaccatg acagcctggt gacagctaaa 240
 agtgtctaca accgctatct tggtttcggg gacgattatc acacccttat gggactgttc 300
 agggagcagc ttgcctccta caaggaaaag ataggcaagg aaaaggcggc aagcacctat 360
 cgcgggctgg tggccgacta caagaatctg cagcttttcc tcaaagagaa gaggcgcac 420
 gaggatatag ccatcgccga gcttgacaag aagttcatcg aggactatta caactggatg 480
 ctccggacat gcgccttggc gagttcaacg gctttcggcc ggggcaacac cctgaaatgg 540
 ctgatgtata ccgcccagga aagaggctgg ataaggcttc atccgttcat cggtttcgac 600
 tgcctgtccg aatacaagtg gcgttcttcc ctcaccgagg aggacttgca aagcgtcatc 660
 catgtcaagt tgaattacaa gcgccagcgg gctatccgtg acatgttcct gttcatgtgc 720
 tttacaggtc tggcgtacgc ggatctgaag gagatcacgt acaagaatat ccatacggat 780
 tccgaggggt gtacatggct gataggcaac cgtataaaaa ccgacgtggc ctatgtgggtg 840
 aagctgcttc ctatcaccat cgaactggtc gagaggtaca gggggacaat gaaaagaaaa 900
 gttcgcctga caagggtgtt tccgtag 927

<210> 163
 <211> 249
 <212> DNA
 <213> B.fragilis

<400> 163
 aatattttat taataaaaag agattccaaa gatctactta ataaaattca ttcactatta 60
 ttattaatta aaaacaatag agaaacatct tttcacctta taaaccctaa attaataaac 120
 aaattaacta tctttgtaga tattacccaa attattaatc tatatgaaac aacatctttt 180
 aaaagaaata gaactaggta ccaaaagcgc tcttctcaaa aagaaaatta ttacacatta 240
 tatatataa 249

<210> 164
 <211> 573
 <212> DNA
 <213> B.fragilis

<400> 164
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ctcaaagtag	acagtttcat	caaccaccag	atggaccaccag	tgctaatagaa	gtcaattggc	120
gtagaattcg	tacgtctctt	tgacagggaca	aacgtcaata	agatcatgac	cattgaagcc	180
agcggaatag	ctccggccat	aatgacggga	tatttaattgg	acttgccggg	cgtttttgcc	240
aaaaaaaaat	cgcccagaac	aattcagaat	gcgctaagta	ccacagtaca	ctctttcacc	300
aaagaccgtg	attatgaagt	agtcattcagt	tccgacttcc	tcactccgaa	agataacgta	360
ttattcgctg	atgatttttt	agcttatgga	aacgccgctt	taggtgtcat	tgatttgatc	420
aaacagtcog	gtgcaaactc	ggttggaatg	ggattcatca	ttgaaaaagc	atttcaaaat	480
gggcgtaaaa	cacttgaaga	aagaggagta	agagtagagt	ctcttgccat	catcgaagat	540
ttatccaatt	gccgggattac	aataaaagat	taa			573

<210> 165

<211> 204

<212> DNA

<213> B.fragilis

<400> 165

gacatttttt	ccaacagtct	ttccacacag	gcagttttcc	aaggcgagga	tgaagctgga	60
tttgccagtg	ccgtacgagc	cgatgaggca	aaacgaatga	atgccactgg	caaagtgatt	120
gataattttg	ccgatgggtc	ggcgagcatt	ggcagtgacg	atatagtggg	gtatcttgcc	180
aaagtcacgc	tctatgttga	ttga				204

<210> 166

<211> 372

<212> DNA

<213> B.fragilis

<400> 166

tattttgcat	cgttttat	ttttagggat	aagatatatt	ttattttctt	tcttagaact	60
tatgaaggaa	taccaagag	ggcgattgaa	ccggaattca	gttcatttcg	gaatagttat	120
aaatcggagg	agcataataa	gtttcaagaa	ctgggttaaga	aatatgggtt	ctatcctgag	180
ttgtgcgata	cctgtagaaa	agggaaatcta	ctgaagataa	aatcaaaaag	gcgggtttat	240
aagtcactct	gtgggggcat	gacccgcgat	ttgcttataa	aaccgttttt	cgttttataa	300
ggcttaagtt	tcaactcgat	ttgtgttaact	gaacccgggc	gtacggtacg	tcctgcagac	360
catatttcat	aa					372

<210> 167

<211> 1008

<212> DNA

<213> B.fragilis

<400> 167

ataaataaat	caatcatggg	aaaaataatc	ttaggtgttc	tgtcactgct	tgatcatgtt	60
tcgtgcagca	ctgccgtgaa	agagaacact	acacaaccgc	atataatgga	gacaaacaag	120
aaaaatctcg	gaaatctgtt	ggcactctat	cccaaaccac	tgacggttgt	cggggcggag	180
gtcgaaggga	aagtaaactg	gcttgtggta	ggacacacgg	gagtcacg	ccatgaccgg	240
atactggtca	gcatgagtaa	aagtcattat	accaatcaag	gtgttaaaaa	atcaaaacga	300
ctttccgtca	atcttgtgag	tcgtgagatg	ttaccgaaag	ctgactatgt	aggaagtgtg	360
agtgtgcca	cggtcgataa	gtcggagggtg	tttgcttacc	atatcggaga	gaacgatacg	420
cccgttatag	acgcatcacc	actcacgatg	gagtggtgaag	tggtggacat	ttatgaaacc	480
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cgtaccgaac	cgggcgta	gacgatgtat	gtgtcggcg	aaaaggagaa	tcctgtgaaa	840
gtaacgatc	tcgaaacctc	tgcgagccgt	agagcatacg	agcagcatat	cgcttcggaa	900
cactttcaga	agtacaagca	gggaacggtg	catatgggtc	aatcggttgt	attgtccgac	960
cagacaccgc	tcaatccggc	caacaaaactc	aataacttca	tgcaatag		1008

<210> 168
 <211> 1248
 <212> DNA
 <213> B.fragilis

<400> 168
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 gaacgccatg tcatacctcga tgctctaaga ggattttgcat tgctggtaat ctgctttgcc 120
 aactttccgg aattctcgtt ttacactttt caaaaaccgg aaattacgga ggctatgcct 180
 acggcggaaa tagataaggt aattcgcttt cctcaatacc ttttcgtgga tggtaagtct 240
 tacaccatat tctcgtcgtt gttcgggtatc ggattttcaa tcattatcag caacgcggcc 300
 aaaaagggaa cggacggatt ccgtatcttt taccggcgga tgattgttct ggccgccatt 360
 ggttttctgc atctgatgtt tatctggagt ggggacatct tgttggttga tgccttattg 420
 ggcattgttg tccctctttt ccggcatgtt tcggacagag tgttgctggg gacttccgct 480
 gtcttattgc tacttcctat tctgattgat tggttggcgg gtacattcgg agtgtcccgg 540
 tcgtctcccc cagtgcgaat gcaacagcac tattgcaatt tatatgggat aacggaatat 600
 aacttcggaa tctggctacg cgacgcggaa aactacggag gggctcttca attcctggta 660
 caaggtgcat ggtgctgctt gcaggaattt atcgacggca atcgctattt taaggtattg 720
 ggattgttct tattgggctt ctacatcgga cgaaagcaaa tatacgccga tcttgaggcc 780
 aatcgggtac tactgaaaaa aacgggtgaca tacgggtttt tgctgggact tcccctatcc 840
 gttctctatg cctggagtgc ggtaaacggg catcctttcg gaacggctgc acacaccgcc 900
 atctatacgg caagtgtcta tcccttaggt tttgcatacg tttccgctat ctgtcttctg 960
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 ctgactaatt acgtgggaca gtcgggatgg ggcatggctt tcttctacgg tatcggttc 1080
 ggactggggg ccggcattgg attgacagga acagaatcca tagctttcta cgtctttctt 1140
 gtccagatgg cattcagtgc cttatggctc tctatattcc gctttggggc tctggaatgg 1200
 ggctggcgga tgctgactta tgggaagtgg ttaaaaataa ggaaataa 1248

<210> 169
 <211> 228
 <212> DNA
 <213> B.fragilis

<400> 169
 gccgtttgtc cgttgttgga agttctgccc cacaacctgt cagtatgggt cctgtcagga 60
 aacacttttg taggatatgc cgaccagcat cctttggtea gcgtgataga ttacgatacc 120
 gtcacgcccc tcttgcatat gcacagccaa ttttcagtct atgcacttta taaagggatg 180
 ggcgttactc ttctctccgg acttggttga tggaaactcc ttgggtaa 228

<210> 170
 <211> 237
 <212> DNA
 <213> B.fragilis

<400> 170
 attacgatac cgtcacgccc atcttgcata cgcacagcca attttcagtc tatgcacttt 60
 ataaagggat gggcgttact cttctctccg gacttggtgc atggaactcc gttgggtaat 120
 cacatcaaag acttctcttt cttttcttat cagtccaatg aagccggaga gcacatccgt 180
 tgtcatatca tcgatatggc caaaagttaa cttatcaacg gagaacaaat catgtag 237

<210> 171
 <211> 627
 <212> DNA
 <213> B.fragilis

<400> 171
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 gacgtgaaaa aatgtccggc aggcactttc cccgaatatg cctttatcgg ccgatccaat 120
 gtaggaaaaat ccagcctcat caatatgctg accggacgaa aggggctggc catgacttcc 180

gctactcccg	gtaagaccat	gcttatcaat	cattttctga	tcaacaacag	ctggtacctg	240
gttgacttac	cgggatacgg	atatgccaga	cgaggtcaga	aaggacagga	acagatacgc	300
accatcatcg	aagattacat	cctcgaacgc	gaacagatga	ccaatctatt	cgtattgata	360
gacagccgctc	tggaaaccca	gaaaatagat	cttgaattca	tggaaatggct	gggtgagaac	420
ggcatttcctt	ttgccattat	cttcaccaaa	gcagacaaac	tgaaaggggg	acgactcaaa	480
ataaatatca	gcgcttactt	gagagaatta	cggaaacaat	gggaagaact	ccctccctat	540
ttcatcactt	catcagaaga	gcgccttggc	aggacagagg	tattaaacta	catcaagtca	600
atcaataaag	aacttaattc	aaaataa				627

<210> 172

<211> 528

<212> DNA

<213> B.fragilis

<400> 172

aaaaataaaa	cgatgcaaaa	tatcattatt	acattttattg	ccttttttgt	actcagatta	60
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tatggtaaag	ttaattecgt	attactgaca	ttagcacata	tcgtctacta	tttttcggcc	180
ctctatgaag	catacacttc	gggaactacc	ttcaactact	tctctgtttg	tggtgttttt	240
ataatgggct	ttgcttatgc	tatgctattc	tatgtgatct	ataaactcca	tgatgtatgg	300
acagtaaaac	tttatatcat	tcccgatcat	cgcattgaaa	aaagcttcct	tttcagaaca	360
gtaagacacc	ccaattacta	tctgaatata	atacctgaac	taattggaat	tgctttactc	420
tgcaatgcct	ggtatacatt	actcattgga	ctccctatct	acgcttgttt	gctcgctata	480
cgtatccgac	aagaggaaaag	ggccatgaaa	gaactattgg	agaattaa		528

<210> 173

<211> 1488

<212> DNA

<213> B.fragilis

<400> 173

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ctggggcagc	agttgcgcct	gactgcatac	ctcagtgtcc	ctgccattat	ggcacagata	180
tcttccatcg	ccatgcagta	tattgatgcc	tcgatgggtg	gcagcctggg	gcggaatgcc	240
gctgcttcca	tcggattggg	ctcgaccacg	acatggctgt	tttgggagct	gtgtgcagcc	300
gccgcaacgg	gcttctccgt	tcaagtagcg	cataaaatcg	gagccgggga	tttcgtggga	360
gcacgaaaaga	tactccgcca	gtcgattgct	gccacattgg	ttttcagctc	attgttggcg	420
gctgtcggca	tttccatcag	tggtatgctt	cccggctggg	tgggcggtga	tgaagtaata	480
cggagcgatt	catccctcta	cttttggata	ttcgactttt	tccttcctgc	cctgcagttg	540
aattttccttg	cgggtggcat	gttgcgatgc	agtggaaata	tgcgtgtgcc	cagtatgctg	600
aacgtgctga	tgtgtcttct	ggatatcggt	ttcaacttct	tcctgatttt	cccttcgagg	660
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gtagcctacg	gtatattcgt	gggtgtgggt	aatacatteg	taccagctct	gatgaacttc	1320
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cgcggcgtgt	ggtttgccat	gtgcatcgag	ctttgtttcc	ggggggtaat	cttcctcgcg	1440
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<210> 174

<211> 1083

<212> DNA
<213> B.fragilis

<400> 174

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gtcatggcac	aagaaacgac	aacaacaaaa	tatataaatt	caaccgatat	ggaagcattg	120
aaattgacgc	aggaatggga	taagaccttt	ccgcagagcg	ataaggtgga	acatacgaaa	180
atcacgtttc	acaaccgtta	cgggtattacg	cttgccgcag	acctttacaa	gccgaaaaat	240
acacaaggac	gtctggcagc	cattgccgtc	agtggccctt	acggtgcggt	gaaagaacaa	300
gtgtcaggcc	gttatgccc	gacacttgcc	gaacgaggct	ttctgaccat	tgctttcgat	360
ccctcctatt	acggcgaaa	tggtggtaca	cctcgctatc	ttacgtcacc	cgaaatcagc	420
acggaggatt	tcagcgcggc	agtcgattat	ctgacatccc	gtgcggacgt	cgatccggaa	480
cgtatcggaa	tcttaggc	ctgcggttgg	ggcgggtttg	cacttaatgc	tgccggccaat	540
gaccctcgta	tcaaagcgac	ggtaacatcc	actatgtatg	atatgagccg	ggtaaagtcc	600
aacgggtatt	tcgacgccat	gagctccgat	gaccgttaca	aattgcgcga	acaactcaac	660
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cccgtaacgg	acgatactcc	gcaattcgtc	aaggagtatc	acgactacta	caagacggaa	780
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gcattcatca	atatgccgct	gctcacctat	atcagcgaaa	tccgcagtgc	cgtgttgatg	900
attcatggag	aaaaagctca	ttcccgtctat	ttcagtgagg	atgcctacaa	acggctgacg	960
ggtagtaaca	aggaactgtt	gattataccc	ggagccaacc	atgtcgattt	gtacgataat	1020
ctcaacgtga	ttccgttcga	caagatagat	gctttcttta	agaatgcctt	aaaggagaaa	1080
tag						1083

<210> 175

<211> 642

<212> DNA

<213> B.fragilis

<400> 175

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gccgtcggag	agttttctaa	attgccgggt	atcggacgga	aaacagctat	gagactgggtg	120
cttcacctgt	tgcgtcagga	tacctctgtg	gtggaagctt	tcggaagttc	tattataact	180
ttaaagcatg	aggtgaaata	ttgcaagggtg	tgtcataata	tatctgatac	ggaaacttgt	240
cagattttgtg	caaatccgca	gcgggacgcg	tctatggtct	gcgtagtgga	gaatatacgg	300
gatgtgatgg	ccgtagaggc	cactcaacaa	tatcgtgggt	tgtaccatgt	tttgggggga	360
gtgatttcac	cgatggatgg	ggtaggaccg	ggcgatctgc	agatagaaa	tctggtgcgc	420
cgggtagccg	aagggggaat	aatgaagtg	attcttgctc	taagcacaac	catggaagg	480
gataccacga	atTTTTatat	ttaccgtaaa	cttgagaaaa	tgggtgtcaa	attgagcgta	540
cttgcccgtg	gggtatccat	tggtgacgag	ctggaataca	cagacgagat	aacgttgggt	600
agaagtattg	tgaaccgtac	gacttttacc	ggtaccgttt	aa		642

<210> 176

<211> 1167

<212> DNA

<213> B.fragilis

<400> 176

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gacactccc	aagagaaaaa	tgtgctacct	atgtgggtag	cggatatgga	tttccgtacg	120
gcacctgcc	ttgtagaagc	cttgcaaagg	cgggttgac	acggtatttt	cggttatacc	180
aaagtaccc	aaacctatta	cgatgcggtc	gtccggtggt	tcgagagccg	tcacgcgtgg	240
cagatagatc	cccgggtgat	tatctataca	agcgtgtcg	taccggctct	gtcggccatt	300
atcaaagccc	tgaccgcacc	ggcgataaaa	gtaattgtcc	aaactccggc	atacaactgc	360
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ctgcggcata	tcggcgacat	ctgtttgcgc	aacggagtgt	ttgttgtggc	agatgaaatt	600
cattgcgaac	tgacctacga	gggacacgac	tatacgccct	ttgcctccct	ctccgaacgc	660

ttccaacaaa	attccgtgac	ttgcatttcg	ccaagcaagg	cgttcaacct	tgccggactg	720
caaatcgcca	atatcatcgc	cttggacgaa	gaggtgcgtc	gccgcacga	ccgtgcttat	780
aacatcaacg	aggtgtgcga	cgtcaatcca	ttcggcgtga	tcgctacaat	tgccgcttat	840
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ggattcatcc	gtctgaacat	tgctgtccc	cgcacattac	ttgccgatgg	tctggagcgg	1140
atggcccgtg	tattggaatg	ctgttaa				1167

<210> 177

<211> 615

<212> DNA

<213> B.fragilis

<400> 177

aaacaaggat	atcaaataaa	aagaaaacta	ttatcatttg	cagttcttat	cacactactg	60
cttgtaccga	ccgtaaaccg	tgcacaatct	atcaaggact	tattcaataa	agacaatatc	120
tccaaagtgtg	tcaacgctgt	cacaggacat	accgaaacag	tggtatgac	cgggacctgg	180
cgttataccg	gctcagccat	tgagttcgag	tctgaaaacc	tgctgaagaa	agccggagga	240
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aaagagggggc	aactgagttt	tacattcaat	gcgagacagta	ctttcgtaag	cacttttaggc	360
aaacgcgaagc	tgaacgggaa	atactcttac	gatgccggca	cccagatgct	ccacctgagg	420
tatatgaaat	taatccccat	gaatgcaaaa	gtcaattata	ccactcagca	gatggatctt	480
ctgttcgaag	cagacaaatt	gctgaagcta	atcactttct	tatccagtaa	gagcagcagt	540
gccaccctca	aagccatcag	ttcattggca	gatagctatg	acggcatgat	gctgggatat	600
gaattgaaac	gatga					615

<210> 178

<211> 330

<212> DNA

<213> B.fragilis

<400> 178

aaacaatatc	aaaaatttgt	cacaattctt	gtactattag	ccggcattgt	ccctgtctat	60
gccatcatga	acatcgtatt	cgatccta	gacgatggaa	atctgtta	aacactcggc	120
actctgacac	ctatactggg	tgaccttttg	atggtatatg	ccttcaaaga	caaatatcaa	180
atttttaatta	gcaatcatcg	tttgcaaaa	aagtgttacc	tttgcgctcg	ttatgatgat	240
acttgccact	attgtatgct	actttgcca	tctcttgctg	atagcccgtg	tcaccggacg	300
gaaaggaggt	tcgaatgcag	cgttttttaa				330

<210> 179

<211> 540

<212> DNA

<213> B.fragilis

<400> 179

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gatttggatc	ttatgtacga	aatggaaaat	gatccttcta	tgtgggatat	cagtagtttc	120
acagttccct	attcgcgttt	tgtactcaaa	cagtatat	aaggatcgca	aagtgcacatg	180
tttgccgata	aacagttgcg	gctgatgatt	atgcgtcgga	aagataattg	tactttgggt	240
acggtcgata	taactgattt	tgtaccttta	cattcaagag	gggcagtcgg	aattgccgtt	300
cacagcaatt	atagacagga	ggggtatgct	tccgatgcat	tgaaactgct	ttgtgaatat	360
gctttcaact	ttttatttat	aaaacaattg	tatgcccata	tagctgtgga	taatgaacct	420
agtttgcgat	tgttcaattc	ttgtggattt	atccaattg	gagtattgaa	agaatggctg	480
ttaacacacg	aaggttataa	agatgccgtg	cttgtgcaat	gtatgaatcc	caaacgatga	540

<210> 180

<211> 450

<212> DNA
<213> B.fragilis

<400> 180
atggaagagc aaataaaacg cattgtgaaa agccagaagg tacagtatat ttcttttttgg 60
attattccgt tattgttggg gctattggga gaagccggcg tgttgccctgt aggaataaaaa 120
gcagacaatg tacgggctgt ttatgttttc gaaacagtag gtattttgat gactgccgtc 180
tgtataacct tttctcttaa actatttagt tttgttctga caaagaaaat agatcagctg 240
acgtttccgg tggccctgag ccgttatatg ctttgggggg ctgttcggct ggctttactg 300
gaattttagt tgggtgttta tctggccggg tactacttta cacttagtag tacagggtgcg 360
ttatgtgcac ttataggact gacagcctct tttttctgtc ttccgggaga aaaaagattg 420
cgtgccgaac tgcattattga taaagaataa 450

<210> 181
<211> 213
<212> DNA
<213> B.fragilis

<400> 181
cacagagtta aagcttggtc tttggatgtg aataagaagt tctttaaatg caaaagactt 60
gttatttgcg cacaagaacc tgacaacctg caaaaggcgt taacaatgtt aattgaaaaa 120
aggtacaagg atgaagatac cgggtcagac ggcgtaaact cacttccgaa acttaagtta 180
tcttattcag cctgtgtcta ttttttctta taa 213

<210> 182
<211> 693
<212> DNA
<213> B.fragilis

<400> 182
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aagctggggc cttgctcgaa actgtcagga cggataacta ccgcactcga atgttctgcc 180
gtcaaagagg aaagtactcc gatggaggga actccgatag gtcataaatc cgtatatgtc 240
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gagggatgaag ctgacgggtca tctctactt tgtattgtca gtgaacagggt gtccgaggaa 360
tatctggaaa cgctgcccac attgggtatt tcatggattg cggccgggtgc ggaacgcatt 420
gacttgccgc aagctatgga gctgcttcac gaacatttcg gcgttgaacg cttggcgatt 480
gtcggggggc gacataatct cggcgggttc ctggaggccg gactgattga cgaagtgaat 540
attatggtag ctccgggtat tgacgggctg aaggggacaga cggcgggttt cgatggaatc 600
tcccgatatg aatgtaaccc gtacaaactg aaattagaga gtgtggaaca atgggaaaca 660
ggtattgtct ggctccgcta taaagtaaaa taa 693

<210> 183
<211> 1221
<212> DNA
<213> B.fragilis

<400> 183
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ctgatatctt gcgattcgaa acagagtgcg acccgctcgg cctcttcctc agaggttcac 120
cggaatgacg acggtcatga tcatcgggaa agtgatggag acaaccatag tgaaatagag 180
aactccggca agggacatga ggacgaaatc attttcactc ggcaacaggc ggaagctatc 240
gggttgagga tatataatgt ggtaccggga tcttttgcac aggtaatcag aaccagcgga 300
cagatacagg cagcccaagg agatgaagaa actattgtcg ccacgaccaa tgggtgtcgta 360
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gaaactgcct tgaaagagta tcagcgtgca gaaggtctgg taaaggataa gattatttcc 540
gctaaagagt tcgaacagac tcgtatgaaa tatgaaaatg ccagaactgc ttatgaagcc 600

caagctgcc	atgtaactgt	ttccggggta	aaagttactt	ctcccatcag	tggatatgtc	660
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tccaagaacc	ggagattgca	actgcgagcc	gatgtttcag	aaaactatit	caatgaactt	780
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gagagagtgg	tcgttaaagg	tgcttatcag	gtaaagctgg	cttctagttc	atcgggtgtg	1200
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<210> 184

<211> 372

<212> DNA

<213> B.fragilis

<400> 184

ataacgaaaa	aagaaattgg	atatggaaaa	attaccatca	atagcattag	caacgacaac	60
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gcgctgcaag	ctttcggggc	tacacggagc	atgacctcgg	cacagggtgg	tcttggtgg	180
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gaggaaaaac	tgccgacact	cgacttcaac	atcagctccg	gggagtggaa	agagttagag	300
gatgccgtgg	ctgctattcc	cgttgtggga	gaccgggtaca	atgcggaaca	gcaacgtcag	360
gtaggccgat	aa					372

<210> 185

<211> 1140

<212> DNA

<213> B.fragilis

<400> 185

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ggtgcgggaa	cggctccgtct	ctcagcttgg	gagatggagg	agtttgataa	ggagtatgcc	1080
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<210> 186

<211> 678

<212> DNA

<213> B.fragilis

<400> 186

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tggagaatca	tggaaaagta	tgtcgatgtg	gggaagatcc	gtgccatcgg	ggtgagcaac	540
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cagatcaaga	ttcatcccta	catggaacat	caggaggctg	tgggcaacac	ttttgccaaa	660
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<210> 187

<211> 1029

<212> DNA

<213> B.fragilis

<400> 187

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gccatccgcg	gggcatacga	ctacggctgc	acgcatttcg	atacggcgga	agcctatggc	180
aaagaacaat	tctacgccgg	acataacgag	gaattggtgg	gtaaggcgat	tgaaccgttc	240
cgtaaagaat	tggtgctcgc	caccaaattt	catattggtg	aactctcgaa	accggacgag	300
acgaatctct	accgggaggt	acgccggcat	cttgaagatt	ccatgagcag	acttcgtacg	360
gattatatcg	acctgtatta	cctgcaccgt	atcagtgagg	cagtcgggct	tgaggatgtg	420
gcaaccgtca	tgggacggct	tattcaggaa	ggactgatac	gtgggtgggg	attgtcgcaa	480
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ctttccgatg	atgaattccg	gcagctacaa	tcagcgttgg	atgaatgtaa	ggtacacgga	960
catcgtgggt	gtgtggaaac	ggaacagacg	agtttcggta	aacaatggag	tgaagaaaca	1020
gataagtga						1029

<210> 188

<211> 879

<212> DNA

<213> B.fragilis

<400> 188

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gaatgcagca	acatcgaagc	cgttgattgc	cggttcgagg	gaaattatcc	cttctggcac	180
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tactccgata	atctgaaaat	gacgaacaca	cgtatcgacg	cccccaagat	gttccgcgag	300
atgcacgaca	tcgaaatcga	gaacgtagag	ataaacgatg	ccgacgaagt	gttctggcgt	360
tgcaagaatt	tggacatcaa	aaatctgaaa	ctgcatggcg	gcacttatcc	gttcatgttc	420
agcagcaata	tccgcataga	cggattggag	agtgacagta	aatacgtatt	ccagtacgtg	480
aagaatgtgg	aactgcgcaa	tgccaaaatc	accacgaaag	atgccttttg	ggaagtggag	540
aatgtgacaa	tctacgattc	agaactcaac	ggtgaatatt	tgggttggca	ttcgcacaaac	600
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gtattggaaa	attgtacgtt	cggccccgac	tgcgacggg	ctttcgagta	cagttcggtg	720
caggcgacca	tcaaaggcgc	aataggtggg	gtgaagaatc	cgcgaacggg	ctgtatcacc	780
gccgagagct	acgggggagat	tatcctcgac	gagaatatca	aggctcccgc	cgattgcaag	840
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<210> 189
 <211> 864
 <212> DNA
 <213> B.fragilis

<400> 189
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 gccgtcggct atcggctcat cgacaccgct tcggtctatg gaaatgaacg ggccggtcgg 180
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 ggattggatt acctcgacct ctatctgac ccatgcctt tcggcgacta ttacggagca 360
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 ttcgagccgg acagattgct ggatttatgc cataatgcta atgttattcc ggccgtcaat 480
 cagatagagg tgcattccta tactccgcaa accgatgcga tacggaccat gcaggaactc 540
 ggcatacaag cagaggcatg ggggcctttg gccgaaggac ggaatggatt gttcacggac 600
 gatattctga ccggtatcgc tcgcaaatat gataaatcgg cagcacaggc cgtactgcgc 660
 tggcacttac agcgcggagt tgtcgccatt cccaaatcgg tacatcggca gcggatgcaa 720
 gagaatttca acatcgggga tttcatgctg acaccggagg atatggccgc aattgcttcc 780
 atgaatatgg gatacgatat gattctcgac ctacacgctc cggaagaagt acagcgactc 840
 tatggtattg agtgcctcgc atga 864

<210> 190
 <211> 684
 <212> DNA
 <213> B.fragilis

<400> 190
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 ggaccctcag gatgtggcaa atcgacctg ctgaatatac tgggactatt ggacaatccg 180
 acttccgggtg agttgtggtt catcggtaaa gaagtttccc gctactcggg aaatgatcgt 240
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 ctgactgtat ttgagaatgt agaattaccg ttgctatatg ccggtgtgcc ggttcgtgag 360
 cgtgtagatc gagtgaacaa agcgttagaa aggatgcaga taagccatcg tacggagcat 420
 tatectcaac aactttccgg aggtcaacaa cagcgtgtgg ctattgcccg ggctattgtg 480
 acgaaccgga aaatttatatt ggctgacgaa ccgacgggta acctcgattc taccaatggc 540
 aacgaggtga tgcttttatt gaaggagtta aataaagatg gagctacagt cgtgatggta 600
 actcactctg aagaaaatgc ccaggaggca ggccgtattg tgcggatgat ggatggttgt 660
 atcctgacgg agaacagacg atga 684

<210> 191
 <211> 1368
 <212> DNA
 <213> B.fragilis

<400> 191
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 tcaaaagcaa ccattcgtga agtaaaagcc atagcagcta aagcagaaac agcatccgga 180
 gtogaattta taaaaatgga aatgggcgta ccgggtctcc ccccttctac ttaggagta 240
 aaagccgaga tagaagcatt gcaaaatgga atagccagtt tgtatcccga tattaatgga 300
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 gctgttatat actcaaatcc gaataacccc agctggatct gtttaaaaga tgaagaactg 660
 aaaatcatcg gtgaactagc cacccaatat gatgtaatcg tccttgaaga tttagcttat 720

tttgccatgg	acttccgcca	agatctgagt	actccgtatc	atgcacctta	tcagccttcg	780
gtggcacact	atacagataa	ttatatatttg	cttatatccg	gttccaaagc	cttcagttat	840
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ggattcgata	aacgctacgg	aggcgggtact	tttggcactg	tatttatcca	tcgtgtgctt	960
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gagctggcaa	aagagttgat	gtattatggg	gtcagtgcaa	tttccttggg	tactacaggt	1260
agccaacaac	agggactacg	tgcattgcact	tcctttatca	aagagcacca	atatgctcaa	1320
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<210> 192

<211> 1497

<212> DNA

<213> B.fragilis

<400> 192

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ggttcgaatg	cagcgttttt	taaaggagaa	aaccagcttc	catggtagct	cgttgctttc	180
ggaatgattg	gcgcattctat	ttcgggagta	acctttgtat	ccgtaccggg	catggtaaaag	240
gcgatggata	tgacgtatat	gcaaaccgta	ttcggctttt	tcttcgggta	tctggctgtc	300
gcccatatac	tcctccact	ctactataaa	ctcaacctga	ccagtatata	cacttatctg	360
gatacccgta	tcggaaagcg	tgccatccgt	acaggagcct	cttttttccct	tctttcgcgt	420
atgctgggca	cagctgcaaa	actatacctt	gtctgtctga	ttctatatac	ctacgtatatt	480
cgtgatatgg	gtatcccat	ctggagtatt	gctgccggat	cggtagcttt	agtatggata	540
tacactcaca	aaagtggcat	taaaacaatt	gtctggacgg	atactttaca	gactttctgc	600
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<210> 193

<211> 426

<212> DNA

<213> B.fragilis

<400> 193

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cgatactcca	tcgtatcgcc	cgcatttggc	gtatttttat	cagataaatt	tcctgataaa	120
gaagagatag	gggttcgggt	aaacacacgg	gaaacaccgg	ttgtagctcc	ggccgcgagt	180
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attgttcatt	ttatgattgc	aaatttaaccg	cgattgaata	agtcggcttg	tatacgattt	300
acggatattt	ataccggaat	cctcgaaata	gtgcattagc	tcagatttcc	ttcgatacaa	360
tatttcagtt	ttctttttta	gaagataatg	gggcttgctc	ctaataaata	tcggttaata	420
aattaa						426

<210> 194
 <211> 495
 <212> DNA
 <213> B.fragilis

<400> 194
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 aaaaccaaac agatgaagcg tatcttttttc gtatatccac ttgccatagc gacactattc 120
 ttaatagtgc tttccgctat tccgcatcac catcataaag agatgatgtg tacgggtgatg 180
 gaattatgtg aacaagacga tatctacaat gatgggcata cggatcatga ggcgggggcaa 240
 gatgcacata atgaaaacac ctgtgtatca caagctgggtt atattttttcc ttccagcggt 300
 gataaaagta atctgcatga tgggaagcctg atgaatatcc acttgccgggt tctatatctg 360
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 tatttttttct cttaa 495

<210> 195
 <211> 600
 <212> DNA
 <213> B.fragilis

<400> 195
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 gtagtattgc ttgttgatca tactgaagaa ggaagtatgg gattgattat aaataaacca 180
 ctcccattga tgctcaatga tatcattaaa gaattttaat atatagaaga tattccgtta 240
 cacaaaggag gtcctatcgg aactgacact ttgtttttatc tgcatacttt acacgaaata 300
 cccggaaccc ttccgatcaa caatggatta tatctcaacg gagattttcga tgctatcaag 360
 aaatacattt tacaaggaaa ccctataaaa ggaaagatac gcttttttccct cggatatttc 420
 ggctgggaat gcgaacaact gattcaggaa ataaaggaga atacctggat tatttcaaaa 480
 gaagaaaata cctatttaaat gaatgaagat ataaaaggta tgtggaagga agccttaggg 540
 aaattgggca gcaagtatga aacctgggtcc cgcttccccc aagtttccttc tttaaactaa 600

<210> 196
 <211> 228
 <212> DNA
 <213> B.fragilis

<220>
 <221> unsure
 <222> (10), (11), (13), (14), (15)
 <223> Identity of nucleotide sequences at the above locations are unknown.

<400> 196
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 tttttggggg gcggactgat tattgcgggg attacgttat taactgttat cggacaaacc 180
 tggcggacgg cttcacagaa tccggtgaga tcattgagat atgaataa 228

<210> 197
 <211> 249
 <212> DNA
 <213> B.fragilis

<400> 197
 aatccatgct ttggctcgtga tgaacagttc ctacgcgga ataccacttt tccgaatagc 60
 cataaccgacc gcccgttcat ttccatagac cgaagcgggtg tcgatgagcc gatagccgac 120
 ggcaagcgca tcggtaacaa ctctttcgca ctcggtggca tcgggtatct gaaagacacc 180
 aaagccttgt atcggcatct ttactccggt attcaattct ttgaaatcca taccataata 240

tcgttataa

249

<210> 198

<211> 423

<212> DNA

<213> B.fragilis

<400> 198

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atgttaattt	cctgtagcaa	cgatgatgaa	aacaaaaatg	atgcgaggt	aacagttact	120
gtagtcagtg	ctgatggcaa	acctctgccc	aacgaaattg	tgcaaatgtt	cgatgaaaag	180
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gcaggacgta	cgtacgccc	gggttcagtt	acacaaatcg	agttgaaact	taagccttta	420
taa						423

<210> 199

<211> 186

<212> DNA

<213> B.fragilis

<400> 199

acttcatcat	cagatatattt	atttttaaat	tttataagaa	gtacatgtgt	gtttttcata	60
tcatttgtaa	ttgttatggg	tgtaatgata	gcaatatcgc	gtaataaaaa	gcagaaaagc	120
aagaaaatcg	atgtttattt	tcttgctttt	ttacatgggg	acgattcctg	tcacggtata	180
ccgtga						186

<210> 200

<211> 384

<212> DNA

<213> B.fragilis

<400> 200

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aacgagtatc	tggcacaatt	cctggggctg	tttatctacg	gaacagttaa	cttcatcggt	360
aataagaagc	ttacattcag	ataa				384

<210> 201

<211> 3177

<212> DNA

<213> B.fragilis

<400> 201

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gccggattgg	taacattaaa	tatattgcct	gtgcacagat	ttccggagat	aactccgcct	180
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ttaagcggta	ttaattcgtt	gacactgacc	ccggcattat	gcgcactggt	tctggagcat	1560
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gtgtgtgttt	tcggtatggc	cctgaacacg	ttactggcaa	cgatatatat	cccgaatttc	3120
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<210> 202

<211> 450

<212> DNA

<213> B.fragilis

<400> 202

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cagcactttg	tacactttct	tattgttcat	aaggggtatc	cgtcgtcttt	gatggcaaat	180
gaagtgtgc	tgaacctgaa	cgggactaaa	aaacgatgtg	acacagtgtc	atataaacgc	240
gatcttagtg	ccagaatgat	tgttgaatat	aaagctcccc	acattgagat	tacgcaggct	300
gtttttgatc	agatcaccgc	ctataatatg	gttttgaaag	ttgattatct	ggttgtcagt	360
aatgggatgc	aacactattg	ttgccggatg	gattatgata	ctcaaagtta	ttcgtttctg	420
tcggatatctc	cggattatga	cgttttataa				450

<210> 203

<211> 426
 <212> DNA
 <213> B.fragilis

<400> 203
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 gaggccgata gccttccccg tgcgacagcc attttttggc ttgataaata tcatatgaaa 180
 gagctgaaaa aggacgatgt gcttactttc cgtacggcta aggcataaagt catcattcgg 240
 aatgatggga caatcgagct tctgtcgttt gtggaacaac agcctgggaa tgcacaacga 300
 tatatccgtt accgactgaa agatttcaag gttaagaaaa tcttgatgga taacggctat 360
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 aaatag 426

<210> 204
 <211> 1062
 <212> DNA
 <213> B.fragilis

<400> 204
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 gaaatgtata cttgggaaat tgtgtatacc gaaagggccg gacatgcaat cgaaatagca 180
 gcagatgcgg cagataaaaa tacagatata gtagttgctg taggaggaga cggaacaatt 240
 aatgaaattg cccgttcatt ggtacacacc aatacagcat tgggaattat ccttgcggc 300
 tctggaaacg gattagcacg acatcttcaa atttcaatgg atccgcgtaa agcacttgaa 360
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 ggtgataaaa aaaaagataa tcccaacgta ttacaaaaag cacaagaata cgtaaacggt 960
 attaaattga taaacgaagc tatagtagaa gatatagcac ataaaaataa agttattctg 1020
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<210> 205
 <211> 951
 <212> DNA
 <213> B.fragilis

<400> 205
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 gatacaactg ctgatttttt cagaaaaacc aatcagagaa tcaactgctta tcaattaaat 180
 tccgaatcac cattagttgc agcattcaac aaccattttg gtacaccggt gcaactaaaa 240
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 gaattttaat taggatttca atttgattat actaccggac ttccctatat tcccgatca 360
 tctatcaaag gaactttgcg cagtatgttt cctttttcat tgaaagataa aggccttact 420
 aaacgtattc taccggaata tagaaaagaa cgtatggaat atatccgaga cttataata 480
 gaagtaacca atataaatga aatttcagac acagaaattc aggcattaga atatgccata 540
 ttcactaaca gtactccatc tggcaaaacg atagaattct ctcttgaaga aaaagatgtc 600
 ttctatgatg cttttgttgc agattcaaag gctgaagtaa tgttaagcga tgactatatt 660
 actcctcatg gcgagaatcc attaaaagat cccaaacctt ttttgttctt aaagatcaga 720
 cctgatgtaa caataaaactt ttatttcaaa ttgtgtacta ctacttata caaagaaaag 780
 gtatgtagtt caaaacaaat agaagagatt aaaaaacaaa atgatttctc ttcttcggac 840

tacaaaatga	ttacggcaca	ccagaagcga	aacctatttg	agaaaattct	cctttgtatc	900
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<210> 206

<211> 282

<212> DNA

<213> B.fragilis

<400> 206

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gtaactattt	taataagctg	tggatagct	tacaaaaaat	acacaaaggc	gataatacta	180
cggggctgtc	caaaaagcaa	agtgcctccc	aaaagtcgga	tagccctttt	taccattggt	240
tatttcggtg	aaaagcctca	tattaccgtt	gtgaaaaatt	aa		282

<210> 207

<211> 405

<212> DNA

<213> B.fragilis

<400> 207

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aatcctaata	aaggatttga	atcttatttc	atcagttttg	atcagggatt	tgcttctctg	180
gaaattatgc	aaagagaaga	tatcacaaca	cctgcattaa	aagactgcct	cgggttagct	240
catttttccct	tttctgtcgg	tagcaaaaga	gctgtattgg	aactcacaga	acaactccgt	300
aaggatgggt	ttgttatcga	gagtgcagca	cgaaccaccg	gagacggcta	ttttgaaagt	360
gctattcttg	atcctgaagg	aaacatagta	gaaatcacta	tttaa		405

<210> 208

<211> 711

<212> DNA

<213> B.fragilis

<400> 208

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ttccttgtat	tgttgccaaa	acatctgata	gattacgtcc	ttttgcatga	actttgccat	600
acttgcgaga	tgaatcatgg	agatcgcttt	tgggacttgc	taaatgggct	taccgatggg	660
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<210> 209

<211> 249

<212> DNA

<213> B.fragilis

<400> 209

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ttagtgaatg	ttgaagcgct	tgctacaggt	gaaggagatg	ttcctacaag	ttgttatggc	180
agtggtaatg	tagattgccc	tataagcgat	agcaaagttt	cctatgttat	gaatgggcgc	240
agtttttga						249

<210> 210
 <211> 1506
 <212> DNA
 <213> B.fragilis

<400> 210
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 ccattttaaatt gggaaattat gggattagaa aatcaagcat tttctgacca agttaatttg 120
 gacaacattc aatataaaccg gaattccttat tgggaacgct cacaaaagcc agatcctgga 180
 gaagaggagt cattatataa cgaaaagaac tattattata cattttgtaca caatatatta 240
 tatgatgaag agcacagtcc attaaatcta attcaccatt tcgaacgcaa agaacctaaag 300
 ctaagtaatc acattttacta ttatataaag aaaaaagggc gtaataatcc atataaaactc 360
 attgtagacg cgatgaatat taatctatat gctacagggtg tcggattcctt gtcattttat 420
 ctaaaaaaatg aagattgcac tcaaaacagc ccggaagaca tattggctat caatcaatat 480
 gggcgccgta tcatgcccc ctttttcaat gatacaagac tacgaaatga gatttcagaa 540
 tacattcgga tagaagggtt aaatcaaaca gtttattttg aagatttcaa atcatatact 600
 ccctatgaca gctggcagcc ttccctcgcc ataaaaaagc taatttgtga attagttacc 660
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 aatcagctat ctcaacaatt tacaataat gcgaaagctt actttgatag ccaggatcca 780
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 aatgatattg ctactttatt tttaccatt acagtaatta ccggtttttg gggaatgaat 1380
 caaatcagtg aagtgatgga agaaaatgga gaactctcga ccggttttat cattcaatct 1440
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 ctatga 1506

<210> 211
 <211> 798
 <212> DNA
 <213> B.fragilis

<400> 211
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 acagcacgca tgatcgtgca actcttctctg ataggtatgt acctgaaata ccttttctctg 180
 tgggaataacc catggattaa ctctctgtgg gttatcatca tgatttttgt agccggacaa 240
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 aatgtattca gcgccagta ttttattccc attttcggaa tcttaatggg aaatatgtta 420
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 gcacttccag gcacgatgat cgggcaaat ttgggaggca gcagtcgaa cgttgccata 660
 aaatatcaaa tgatgattat ggtcattact ttcacagcct ctatgttattc attaatgatc 720
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 aaagaatctc aaaagtag 798

<210> 212
 <211> 2004
 <212> DNA
 <213> B.fragilis

<400> 212

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gccgcacogg	gaacattgaa	attacaaaat	tccgccatcg	tggcttcccg	taagctggat	660
gcctatctct	attatctgct	tggcgataat	ctgccgactg	acggacatta	tgaaaatctg	720
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<210> 213

<211> 609

<212> DNA

<213> B.fragilis

<400> 213

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<210> 214

<211> 1815

<212> DNA

<213> B.fragilis

<400> 214

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attatccagc	aaaacacgat	tctgacatca	gatgaaaaag	aaatattaat	agtttctcct	1740
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<210> 215

<211> 918

<212> DNA

<213> B.fragilis

<400> 215

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ataggcggta	tcattgtaaa	gggtactact	cttcacaaac	gtgaaggtaa	cccgtatccc	180
cgcatggcag	agaccccttc	cggtatgtta	aacgctgtag	gactgcaaaa	taagggtgta	240
gaatatttct	caaatacacat	ttatccccgt	atcaaagaca	ttcagacca	catgattgtg	300
aatgtttccg	gatcagccat	tgaagactat	gtaaagactg	cagagatcat	taatgaactt	360
gacaaaattc	ctgctatcga	attaaacatc	tcttgtccta	atgtaaaaca	aggaggtatg	420
gcatttgggg	tgacaactaa	aggagtatca	gaagttgtac	aagcagtgcg	ttctgcttac	480
aaaaagacac	ttatcgtaa	gctatctccc	aacgttacag	atatagcaga	aatggcacgg	540
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gcagtaaaac	ccatcgcaat	aagaatgggtg	tggcaagttg	ctaaagcagt	aaatattccg	720
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gcttcagcca	tacagattgg	tacggcaaat	ttcatagatc	cggctatcac	catcaaagtt	840
atagatggta	taaacgatta	cctggaaaga	cacggatgca	agtctgttcc	tgaaattata	900
gggtgcacttg	aggtatag					918

<210> 216

<211> 1296

<212> DNA

<213> B.fragilis

<400> 216

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agatgcagca	gtatcttcgg	atatcagttc	agcagatag	tccgttcgct	gatgagcgtt	180
tattttctgtg	gcggtcatg	cgtggaagat	gtaacgtcac	aactgatgcg	ccatctctcg	240
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gaggaatacg	atgttgactt	tgaccatcag	ttccttgaaa	cggagaagta	tgatgcaaaa	480
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ctgcttactg	catgatatac	caatttctac	aagaccatca	tgagcaggct	tgacaccaag	1140
gctttttggcg	tcaagaaaac	gagtcgcata	aagtcttttg	tcttcagatt	catctccgta	1200
cctgccaaagt	ggatcatgac	tgcaaggcaa	tacgtgctga	atatctacac	agagaaccga	1260
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<210> 217

<211> 2286

<212> DNA

<213> B.fragilis

<400> 217

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tctcattttg	agaagcggtt	gaacgataat	ttgattgaat	tacaacatga	acttattttcc	180
caaacatgga	atcccgaacc	ttacctaaga	atagaaatta	ctaagaatga	aacagaaaaa	240
cgtaaatttg	gattattgtg	catcaaggac	aaaatagtac	aacaagccat	taaaacagcc	300
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ggtccggaac	gagctatcaa	acgggtcgtg	cacgatttaa	agaagttaaa	gagtgggttat	420
gtagccaaat	tggatataga	caactatttc	gatacgatca	atcatgaacg	gcttttctact	480
cgtcttgcca	attgggttaa	agatgatgaa	acactcaggc	tgatccgcct	atgtatccaa	540
acaggaatag	ttactccgca	actgcaatgg	caagaaataa	ataaaggagt	acctcaagga	600
gctatactat	ctccttttatt	ggcaaaacttt	tatcttcacc	cttttgatca	gtttgctgcc	660
aataaagtcc	ctatgtatat	acgctacgca	gacgattttc	taatcgctac	atccacagaa	720
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gcaaagcaag	atggcaaacc	tacttttagta	tttgatgttg	tgagactatt	tcgtgctcaa	2040
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ggtctattaa	atgaatcatc	caaacgagtt	ttgatccgat	atatattaga	gcgactcaat	2160
cggtatgaaa	aatatagagg	agaagaaata	accttctctc	aaataatttt	aagacaagcc	2220
caagaaatag	cactttttat	ttctggagac	aatttaatat	ttaaacctta	tgttgcgaaa	2280
tggtaa						2286

<210> 218

<211> 219

<212> DNA

<213> B.fragilis

<400> 218

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gttccgataa	atccattaat	accgcctccc	caaaagatat	tacttattgg	ggtgtatcgc	180
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<210> 219

<211> 1038

<212> DNA

<213> B.fragilis

<400> 219

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gacttaatag	ccgattacat	taccgacaac	gtactgacgg	atactgagaa	agagtttaac	180
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taccgatga	tgtcagaaca	tcaggtagtg	atagtaaaaag	aggcacaagc	catccgcaat	300
atagaagaac	tatctttatta	cctgcaaaaa	ccgttaaact	caacaatatt	agtggtttgt	360
cataaacatg	gcgctctgga	ccgcagaaaag	aagtttagctg	cagaaattga	aaaaacaggt	420
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aaatcgaaag	gtgtaggcaa	tacctcgata	agcgatggag	atattcttcg	tgaattagta	1020
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<210> 220

<211> 2334

<212> DNA

<213> B.fragilis

<400> 220

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ggcggcgggtg	ctaaaggact	gacgcatatt	ggaattattc	gtgctctaga	agagaataat	180

atccccgatag	attatataaac	cgggtacttct	atggggagcca	ttgtgggctc	cctttatgcc	240
atgggggtatt	cgcttgacga	catggaaacc	ttactgaaat	cagaagattt	caagcgatgg	300
tattccgggtg	aggtggaaga	aaaatacatg	tactatttta	agaagaatct	tcccacgccg	360
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cgcaccagtg	ttgttaatcc	tatccagatg	aaccttgtct	ttatcgatct	gtatgcgcgc	480
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attcaccgta	gggttaaatgt	ggataaatatc	cgtttaaggc	ggttgggtga	taaaagcaat	1020
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tacataaaga	aagagtttca	tacctcgac	gataaagaat	ttacgtatga	ggatctgaaa	1140
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agtgagtttg	ccccactgc	acatagcaaa	ttgacgtata	acgaagcttt	ccgtgccaat	2040
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tattatggaa	aagcattttc	ccgattcgaa	tatttaggag	aaatttcagt	ggtttgtcaa	2220
ttaccatttg	gagctatctc	tgcataatga	aatcattata	gctcaccaag	aagggtggtg	2280
aatgtagggc	tgacactcgg	ctggcaactg	tttaattacc	ggttcacga	ataa	2334

<210> 221

<211> 225

<212> DNA

<213> B.fragilis

<400> 221

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aatctgtcca	tcccggatgg	ccatttaatg	gtacatctgc	ctttttccgc	cgggtcttgc	120
gaggtggttag	ttgggggtgt	actgcaaaaag	gctgcagagt	gtcatatatt	gactatgacg	180
tgccaaacta	tcgtgatgaa	tatggaggtt	ttaggcttgt	tttag		225

<210> 222

<211> 300

<212> DNA

<213> B.fragilis

<400> 222

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attcctcaag	gaataagcgg	cttttttaaa	gaaaagtag	ataaaatata	tcatggtgcc	180
agcgggaagaa	aattttattta	tcaaaaatca	ggttggcgca	tggcattttac	attctatcct	240
accgaccggg	tagtcgatga	gaaatatgca	atgaagaaca	aaatgataaa	gaagcgataa	300

<210> 223
 <211> 186
 <212> DNA
 <213> B.fragilis

<400> 223
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 gaaaaggccg tatctttgca cccgttaaac aaaaacaatg gtcgcgtagc tcaactgaat 120
 agagtagctg actacggatc agccggttac aggtttgaat cctgtcgcga tcactttaag 180
 gtttaa 186

<210> 224
 <211> 852
 <212> DNA
 <213> B.fragilis

<400> 224
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 ggcagtgggtg aggtcaatta tggagtgata gacaatctaa ttcagcgtga ctctgtcact 120
 aatctaccca atatcaactc ttccggtttg aaaggagcta tacgcgaata tttcaaggag 180
 aatgaaaatt tagtaagaga attattcggc agtgctccca aagacgaaaa aacactcccc 240
 ggaaaagtgc gtttctttga agccaacctc ctatcgatgc cagtaagaag tgacaagggtg 300
 ccctttctga tggctacctc agacgaagta cttcaagaat tgataaccaa aatgaagttc 360
 tcaatttgcg aagaagccac tcaatacata tcccatctgt ccacattgct tgataatata 420
 aaaacacaag cgcaagggtac tgattttgcg tacgtgtttg acccttctact gcaagggtgca 480
 atcattgaag aagtttctat acggggtact tgcccaagcc acattcctct tcaactgtct 540
 ctaaagaaac ttttaggcga tagactgggtg attttatcac ataaatattt ctctatacta 600
 tccgatgaca atcatcttcc agtcctgtca cgcaataatc ttgaaaacgg gcagagcgcc 660
 aatttgtggt atgaacaggt tttaccgcgc tatagccgac tttattttat gtaaatggac 720
 ggaaatgcac aaagtgaagta tctgaaaaaa ttcagagata ccctatgtac cccttctacc 780
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 tcaccttttt aa 852

<210> 225
 <211> 540
 <212> DNA
 <213> B.fragilis

<400> 225
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 aacttaccga tagcaaaatc aatctgttct ttagagtgtg tagccatcaa cgagaaacga 360
 atcaacgtat cgttcggaga acatgcggga ggcacaactg gatttacaaa cacaccttcg 420
 tcaaataaca tcttagttac cataaatgtc ttctccatat cacgtacata tagaggaatg 480
 ataggagtgg aggtatgtcc gatctcaaaa ccaagttcac ggaaacactt taaagagtaa 540

<210> 226
 <211> 798
 <212> DNA
 <213> B.fragilis

<400> 226
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 atattcaagg accgttattt acaatgggat aatgcgttat taagtcaata cgaagaagag 180

atacaacaat	atggtaataa	agagccggtt	attatctatg	gtgtagaatt	gaaagaggac	240
atcacgcccc	ccactaacta	tattcgaatt	gatacaccata	atgaatatgc	tacctatcct	300
tccggcattgg	aacaagtagc	ttctattctt	gatcaccttc	tcaatcgata	tcagacatta	360
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gaaataaatc	taatcagaca	agaggatcga	aaagcacagg	gagtaataga	ggatgacgaa	480
aagttggctc	aagaagcaat	tacaaacgga	acagaaaaaa	ttggtagttt	atatgttggtg	540
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atattaaagc	gatacacccc	aataagtaat	atcttttggg	gaggcgggtat	taatggattt	720
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aaactatttag	aattatga					798

<210> 227

<211> 747

<212> DNA

<213> B.fragilis

<400> 227

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agagactata	aagtgaagga	gttcaataag	attgatgcgg	ggactgtggg	caacatctat	180
tatacacaat	ccacagacgg	aaaaacggat	ctgcaaactc	acggaccgga	taacatcgta	240
gcactgatac	aagtgcgct	aaaggacaat	acactatttt	tgagtatcga	taaatcaaaa	300
aaggtacgca	acttcaaaaa	gatgaaaata	accattacat	ctcccacctt	aaatgggtatc	360
tccttttaaag	gagtgggcga	tgtacatatc	gaaaatggat	taactacgga	taatcttgat	420
atagagagta	aaggggtagg	taatgtggac	attcaatcgc	tgacttgcca	aaaattgaac	480
gttcagtcga	tgggtgtagg	tgatgtaaag	cttgaaggca	cagctcagat	agctgctctt	540
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agctcacaag	gcgtaggaga	tataacctgt	aatgcaacag	agtcatttga	tgcagccgta	660
cgaggagtgg	gaagtattaa	atataaagg	agccctacta	taaaatcact	cagtaaaaaa	720
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<210> 228

<211> 2355

<212> DNA

<213> B.fragilis

<400> 228

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gaaggttttg	accgtattca	tttggtgtat	cagaaatcgg	cattaagtga	cacaggcggt	240
acaacaacaa	ttccatatcc	ggtatccact	tcttttagaaa	agcagtttcc	ggaagtggaa	300
gatgcctgcg	gttttctttt	ttatgaacag	gaagtgcag	tagacgatgg	cgctatccgg	360
caactgtatg	aaatcaatgc	agactcttgc	ttcatgcata	tgttcgggat	acaagtactc	420
tccggcagcc	ttgatttcct	ggaatcggaa	gagcggatag	cactgcagaga	gcatgcggcc	480
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<210> 229

<211> 396

<212> DNA

<213> B.fragilis

<400> 229

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ggcaaaaccg	actccacgcc	caaactcttt	caactggcgg	gttccgatat	tcgatgtcat	180
gataataaca	gtattcttga	agtcaaccat	tctgccataa	ctgtcagtca	gccgaccttc	240
gtccatcacc	tggagaagca	gattgaacac	atcgggatgc	gccttttcta	tttcgtcaag	300
caatacgata	gaatagggtt	tacggcgta	tttctctgtc	aattgtccgc	cttcctcgta	360
tcctacgtat	cccggaggcg	ctccaaccaa	gcgtga			396

<210> 230

<211> 1152

<212> DNA

<213> B.fragilis

<400> 230

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aagttccctc	aacaatccgc	tcttttaggc	atgatccgtt	accaattgct	gaaacagcac	180
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gcacttattg	gagaacagag	tttcaggatg	accgaaagaa	aggctaaatc	acttggctta	300
ggcgtcatca	aacagatttc	cccactcatg	cttatagagt	gcaaggatga	tacctcgtca	360
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agcagtagta	aataccactt	cttaaagccg	gggtcagtac	tttattttaa	gcaagggaaa	1080
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atatatatat aa

1152

<210> 231

<211> 183

<212> DNA

<213> B.fragilis

<400> 231

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acgagaggaa	cagcttcccc	atcgcccacg	gctcgaattt	atctgcacgc	tctcgtaggg	180
taa						183

<210> 232

<211> 297

<212> DNA

<213> B.fragilis

<400> 232

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caactgaata	gagtagctga	ctacggatca	gccgggttaca	ggtttgaatc	ctgtcgcgat	180
cacaagaacc	tccataatca	aattatggag	gttttttggt	ttccttgcat	tatctctttt	240
attggatcat	acctaaattc	tgaggggattc	ctcttttttaa	ttggcagtc	gtactga	297

<210> 233

<211> 285

<212> DNA

<213> B.fragilis

<400> 233

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acaattgttg	ttgtaaatgt	gcttaatggt	gttgtgaaat	cggatgatgc	tgagacatta	120
actctatctg	gaatagaagc	tgtagcagct	acttatgaaa	acagtcgggg	aaactatact	180
ggagcccata	atcaatattg	tacaagtcgc	aaaaatgcta	caggatgtgt	ttcggatcct	240
gatccaaccc	gcacttggtc	atattcaatt	tttgttaaaa	aataa		285

<210> 234

<211> 1431

<212> DNA

<213> B.fragilis

<400> 234

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ttattagata	aattcattct	tacaaaactc	ggaaatggag	atattagaga	aggacggctt	180
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caagaaaagt	gcgttgggtat	aaatacaaac	tctaccatta	tcttaaaaaa	aagcaatagt	420
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gaaataacag	agcgggacaat	gcatataaat	gagattgaaa	tgaactataa	taatagaatt	1320
aattatcatt	atacgccaac	ctccttttca	ttaatcgatt	ttatgcaata	tgcaatgtct	1380
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<210> 235

<211> 888

<212> DNA

<213> B.fragilis

<400> 235

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gttctgcaag	aacttcataa	ttctttgtat	ttctgtcaga	cagagaatac	ggatttatatt	180
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aatcggatag	tgcttggttac	ttctttgttt	gagaaacgtg	ctccgggact	atatcataat	300
acagctgttg	tctttgaccg	ggatggaagt	attgccggaa	aatatcgtaa	gatgcatatt	360
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tctcagcgtg	cgcatgcggt	agccaatggg	cttccgggtga	tttcagtcaa	tcgtgtcggg	660
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gccggaccgc	agggtgaata	cctggctcag	gcgggaaatg	accgctctga	aaatatgatt	780
gttgagggtgg	atcttgaacg	ttcggagaat	gtgcgtcgtt	ggtggccatt	tcttcgtgat	840
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<210> 236

<211> 1839

<212> DNA

<213> B.fragilis

<400> 236

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gatgttaata	aacaagtcaa	gctgtcggga	tgggtacagc	gcagccgtaa	aatgggaggt	180
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aaaaataact	ccggtcgtga	cgttatgttg	gatgctcccg	cagcactcga	tccgtcacia	1800
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<210> 237

<211> 1245

<212> DNA

<213> B.fragilis

<400> 237

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ggcgttcgcg	aaagccttga	agaaaaaaca	atgaatctgg	caaaagctgt	tgccgagttg	120
atcacttcta	atltgaagaa	tggagacgga	acccctgtgg	agtgtgtgat	tgcatatgga	180
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cgcatgtac	aagacttgaa	tgacaattct	attccggcag	atgtagctga	aaaaattctg	480
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<210> 238

<211> 411

<212> DNA

<213> B.fragilis

<400> 238

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ggtatgactt	gtttcagcat	catccacttt	tttatcaatg	aaatagatgg	agcatcacgt	180
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ccgggtatta	agcaaatctg	cttccactct	ttocaaagag	aagacgaagt	tgtattcatc	360
aatagggagc	aggggaagaaa	agccttacat	catctcatat	atggatactg	a	411

<210> 239

<211> 495

<212> DNA

<213> B.fragilis

<400> 239

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ttgacagtaa	ttgagtgtgt	gaatatggga	cagaattccc	ctaaagacat	tacatgtctt	120
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gatgaaaaga	tgaaaacatg	gctactcgcc	cgtgaagcaa	ttatcaagga	taaagaaaaa	300
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<210> 240

<211> 186

<212> DNA

<213> B.fragilis

<400> 240

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cacattataa	tgcatacttc	ttatatggcc	aatgcttttc	ccacaactcc	gaaagaagtt	120
gtgttgctcc	aaagttgtgc	ccgtaaagta	tacgggaaaag	agcaaccg	tagggcacat	180
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<210> 241

<211> 318

<212> DNA

<213> B.fragilis

<400> 241

agagttaacc	tccagccaaa	atgttctttt	ccggttcgtt	tatcggaaaa	aatatctccc	60
aaccatcttg	ttcgtgttgt	aagttacatt	gtagatgctt	tggatattag	ttacctgctc	120
tcggcttata	atggaggagg	caccaacagc	tatcatcccc	gtatgatact	caaggctctg	180
ttttatgctt	atctgaacaa	tatctattcc	tgccgcaaaa	cccaaaaggc	cttgcagaag	240
aatattcaca	tcatgtgggt	gtccggtaat	agtacatcca	atttccgcac	tatcaatgat	300
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<210> 242

<211> 186

<212> DNA

<213> B.fragilis

<400> 242

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cccaaagaat	gggtcgtcaa	aagcagaaaa	gaatttaaaa	tgttcttttc	tattccaatt	180
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<210> 243

<211> 768

<212> DNA

<213> B.fragilis

<400> 243

tgcaatgaag	attcgcaaaa	atatcgtgtc	ttcccctgga	gagcaaggac	tgcatactgt	60
tggtgtttta	cacatccttt	gagtgtagat	acgttgaata	tactatggag	gactatgttg	120
aatgaaagac	agaaatttcc	tattcgtaca	ggattaaaaa	taactgtttc	tgataataat	180
ggagtgggtc	gctcttcttt	tagtcgggat	agcctttctt	gtttatctta	ttcttcgata	240
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ctttgtgtga	ttcttacaat	ctatatatat	aagttgtctg	ttcaccctcc	taaaataaaa	420
gaggttacta	cttatgttca	gacagttgct	gttaaaaagg	ggactctgcc	tatatacgat	480
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actctgtcta	tgtctcaa	tatggcagat	gtttggccgg	gaaaatctat	ttctcccgat	660
tgtttccata	aagcaataga	acgtttgcgt	gatttgttaa	ggcagcttcc	tatgaccata	720
caaattgaat	atttggggga	ggaaatttat	cagatgcaaa	ttttataa		768

<210> 244

<211> 204

<212> DNA

<213> B.fragilis

<400> 244

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gcaattat	atagtaatca	tttactctac	aaccaacaga	gctactctta	cttaaata	120
gaaaagcatc	ccttgtgtta	caagaaatct	aaatctattg	actttactaa	tttaaagtac	180
aagtccaagt	ctatat	atga				204

<210> 245

<211> 1827

<212> DNA

<213> B.fragilis

<400> 245

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ttctctcatt	tgagagaaga	gaacagacaa	caaggataca	tcacagaagg	tacactggaa	180
acagcagacg	gattgaataa	agccaatgaa	agcctaaagg	ggataacaac	tcttcataat	240
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caagttaaac	tttatatagg	gctgttactg	atctgcaccc	ttgtaatgct	atatcccatc	660
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aaggatagcc	cgatcagcag	tattaccgga	tttgcattggg	ggatttacct	cttcattctg	1740
ataggtttac	ttatctttgt	aacaacagcc	tataaaatct	acagaatcat	gcactc	1800
ccggcagaaa	taataaaaaa	cgaataa				1827

<210> 246

<211> 894

<212> DNA

<213> B.fragilis

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 cgactgcctg ctctttcttt tactgtaaat ggagagagct ttgaaatgat tccggtagaa 180
 ggtggaacct ttattatggg aggcacaagt gagcaaggta atgattgoga aaacaatgaa 240
 aaaccaacgc atgaggaaac tctaccgttc ttttatatcg gaaagtatga agttaccag 300
 aaactgtgga aagcagttat ggggactgat ttcgatcaat catacaattc aggatgtgaa 360
 gattgtccgg cagagtatat cagttggaat gacacgcaaa agttttataag caaattgaac 420
 acccttacaa acaaaacatt tcgcctgcct accgatattg aatgggaata tgccgcacgc 480
 ggtggcaagt atagtgaaaa atacaaatac agcgggaagta atgatatcga tgaagttgcc 540
 tggatatattg aaaattatca aaaaagtaaa tatggagaca aagggactac acatccggta 600
 ggtatgaaaa agcctaataa attaggattg tacgacatga gtggcaatgt atgggaatgg 660
 tgtgacaatt ggtacactca agaatactct caaaacggtg aatctgtcca tcccggtatg 720
 ccatttaattg gtacatctgc ctttttccgc cgggtcttgc gaggtggtag ttgggggtgg 780
 actgcaaaag gctgccaggt gtcatatatt gactatgacg tgccaaacta tcgtgatgaa 840
 tatggaggtt ttaggcttgt tttagtaccg gactcagtac agactgccaa ttaa 894

<210> 247
 <211> 840
 <212> DNA
 <213> B.fragilis

<400> 247
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 tatgtgctgc tgaaattgac ctctcagacc gtctctccgg atatgctacc gggacagttt 180
 gcggaaattc ggatagatgg ttcaaccacc actttctctg gtcgccccat ttctattaat 240
 tatgtagaca gacaacgcaa cgaagtatgg tttctgatcc aacttgtagg tgatggaaca 300
 aaacgtcttg cgcaagtaaa tcgaggagag attatcaatg tagtactccc actcggaaat 360
 agcttcacaa tgcccgaaaa gccttctgat aagctattat tagtgggcgg aggtgtaggg 420
 actgccccta tgctctactt ggggtgaacaa cttgctaaaa acggcagtaa accaactatt 480
 cttttggggg cagcgacgaa caaagatctg ctccaattag aagatttttg cgcttacgga 540
 gaggtctata ctacaaccga agacggcagc catggagaaa agggatatgt gacccaacat 600
 tccatactga ataaaaataa attcgagcag atttatacat gtggcccgaa acccatgatg 660
 atggcagtag ccaaatatgc caaaggtaac gatatcaatt gcgaagtatc attggaaaat 720
 acaatggcat gtggcatagg agcctgcctc tgttgcggtt aaaacaccac agaggggcat 780
 ttgtgcgttt gtaaagaagg tcctgttttc aatataaata aactattatg gcagatttaa 840

<210> 248
 <211> 306
 <212> DNA
 <213> B.fragilis

<400> 248
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 caagatgacc gaagtcgtat acaaatatca aaaatattag aaaagtatgg aacacgtatc 120
 aactatagtg tttttgaatg tatgtttaca gacagacaat ttcagaagat ccaaattaat 180
 ttagaaaagat ggattaacag gcgttatgat actgtgggat attatccgat gtgcatcaat 240
 tgctatacaa gaattatata tcaacctata cgaaaaaaga taattaaaac cgtcgaaata 300
 gtctaa 306

<210> 249
 <211> 744
 <212> DNA
 <213> B.fragilis

<400> 249
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 aagattatgc gtatcgatat tataacggtt ttgcccgaat tgattgaggg ctttttcaat 120

tgttctatta	tgaaacgggc	ccaggacaaa	ggactcgctg	aaattcatat	tcacaattta	180
cgtgattata	ccgaagacaa	gtatcgccgg	gtggatgact	atccatttgg	aggttttgcc	240
ggtatggtga	tgaagataga	acctattgaa	cgggtgatta	atgccctgaa	agcagagcgt	300
gattatgatg	aagtgatatt	taccacacct	gatggagagc	agtttgatca	gaaaatggct	360
aatagtttgt	ctttatccgg	taatcttatc	attttatgcg	ggcattttta	aggatcgcg	420
tatcgcatcc	gggagcattt	gatcacaaaa	gaaatcagta	ttggagatta	tgttttgacc	480
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gtttatactc	gtccggcaga	atataagggg	tggaaagtac	ccgagattct	gctttcaggg	660
cacgaagcga	agattaagga	atgggaactc	caacagtcgt	tggaacgtac	taggagactg	720
cgtccggatc	tgttggaaga	ttaa				744

<210> 250

<211> 840

<212> DNA

<213> B.fragilis

<400> 250

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cagaagttga	aagctttgta	ccagctgcaa	acaacattat	ctaagattga	cgagattaaa	120
acgttgagag	gtgaacttcc	attggaagta	caagaccttg	aagacgaaat	tgccggctcg	180
agtacacgta	tcgacaaaat	caagtcggaa	gtagacgaac	tcaaatcagc	tatcgccggg	240
aagagagtgg	aaattgaagc	agccaaagct	tccgttgaga	aataataaat	acagcaggac	300
aatgttctga	ataaccgcga	atatgacttc	ctgacaaaag	agatcgaatt	ccagtctttg	360
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gaagaaatag	agaaaaatac	caaagcgctg	gaagaacgcc	agaaagacct	cgaccagaag	480
aagaatgaac	tggatgaaat	catcgaagag	accaaacagg	aagaagagaa	gttgagagac	540
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cgtaaaaatt	cacgtaacgg	tttaggtatt	gtatacgtac	agcgtgatgc	atgtggtggt	660
tgtttcaata	aaattccgcc	tcagagacaa	ctggatatcc	gttcacgtaa	aaaaattatc	720
gtttgcgaat	actgtggacg	tatcatgatt	gaccgcgaac	tggcaggtgt	agaaatagaa	780
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<210> 251

<211> 1359

<212> DNA

<213> B.fragilis

<400> 251

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aagaaaaaag	agagaagtaa	cggtaaaaa	gccttcattg	gtttgagtct	ttataaatat	180
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tatacaaaag	aaatttttta	ttctataata	cggtatttat	ttcctaattt	tgcaactcaa	1320
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<210> 252

<211> 192

<212> DNA

<213> B.fragilis

<400> 252

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agtaaaatga	atcaagaatt	actcagattt	atcggttaca	tctcttttaa	ttgcgtatcc	180
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<210> 253

<211> 1191

<212> DNA

<213> B.fragilis

<400> 253

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<210> 254

<211> 2448

<212> DNA

<213> B.fragilis

<400> 254

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ggcttgtcta	tcggttttac	agctttcttg	ttaggcgggt	attggcatta	ctgggaatat	180
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ttatztatca	aaagggtggt	ggaaacctat	gcgtaccata	ctgatattca	cggatggctg	2340
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<210> 255

<211> 1191

<212> DNA

<213> B.fragilis

<400> 255

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tttggttggt	aagaagatgc	tatcattttat	tctaccggat	ttcaggtaaa	tctgggtgtg	360
gtttcgtgtg	tgacagggtcg	tgaagattat	gtgatctgtg	atgaacttga	ccacgcttct	420
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cacggacgcg	gtacttgtga	tcatttcggga	ttgactaaag	aggtggatct	tatcatgggc	720
acattcagta	agtcattggc	cgctatcggt	ggctttattg	cagcagacga	gtccatcatt	780
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ccgaacgata	cgttgattcg	tttctcgttg	atggctacac	actctaaaga	acagattgat	1140
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<210> 256

<211> 570
 <212> DNA
 <213> B.fragilis

<400> 256
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 gggcaagagt tggaacatca gaaaaaacia aattatgaat taatagttaa tcaaatagaa 180
 tcagggatta ttccacatgt aattttctgat aaaaaagaat ttgcaggata ttttgtcctt 240
 gtgtttccta atggtatttg tgatgtttgt aataaatggg tgtttaaaca aatctctgaa 300
 ttatccagta cttcggattt agtgggtgggt gtccttgata aattgaagaa gaatatggaa 360
 atctataata ccgtttataa acttaagttg tcgtctattt tttgttcgga aaagtatgcc 420
 atgcctcagg aggaatttaa agatatgaca tatatattct attgctcaaa aactggaacg 480
 gttttatata ctttggcact tcatcataaa aatatagact tggacttgta ctttaaatta 540
 gtaaagtcaa tagatttaga tttcttgtaa 570

<210> 257
 <211> 786
 <212> DNA
 <213> B.fragilis

<400> 257
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 atattttgag agaaatttaa tgttcccatt ttgggtaaag acgccaatat gatctctgcc 180
 agtgcagaag gaatcacaaat catcaacttt ggcatgggaa gtcccaatgc cgccataatt 240
 atggatctgc tgagtgccat ctctccaaaa gcctgcctgt ttctgggaaa atgtggcgga 300
 atcgataaaa aaaataaaaat aggtgacctg attctgccaa ttgccgctat ccgtgggtgaa 360
 ggtacctcaa acgactattt cccgcgggag gttccgtccc tgccggcatt tatgctgcag 420
 cgtgccgtat catcggctat ccgtgactat gctcgcgatt attggacagg aacagtctat 480
 acaaccaacc gccgtatttg ggagcatgat gacaccttta aagagtatct gaaaagaact 540
 cgtgcaatgg cagttgatat ggaaacggca actctgttca gttgcggttt tgccaatcat 600
 atcccgaccg gagctttact actcgtatcc gaccaaccta tgattccgga aggagtgaaa 660
 actgataaaa gcgacaacat cgttacccaaa aactatgtag aggagcatgt agagataggc 720
 atcgctcgc tacgaatgat cattgatgaa aagaaaactg taaaacacct gaaattcgac 780
 tggtaa 786

<210> 258
 <211> 1395
 <212> DNA
 <213> B.fragilis

<400> 258
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 caattttttg taaaaataaa tagttacttg ttcaaagtgt accggaagag gtgttttcct 180
 cttccggttt attctaataa tatgttagtt atgaagtact tgaatttggt tatattcgtg 240
 ttgttgttgg caggatgtaa tcgacctgtt aaacactcog atattatcca agccgatact 300
 atggtaagta tcatacccca agaggatact atcacattat ctgctctctt ttctagatgt 360
 gaaattgtaa aattgaatga tattgtttta gcgtcaataa ataaagtatt taaatacgat 420
 tctttgtgga ttgtgcaagg aaagtctgat cagggtgggg tccatttggt taataatgaa 480
 ggccgatatt taaaaaccgt tttgaaatgg gggcaggggac ctgaagaagc atatgatatt 540
 tggagtatta aactattaga tggatctatc tatttattga ttaattctgg aacagaagtt 600
 gtggaatatt ctttgcagaa acaaaaaatg gtagagcgct ttcggctacc gtctgagata 660
 ctttcagcta cagattttgt tgttgataat ggtggaaatt atatattctt aaaatcgatc 720
 tcccagagaa aaaaaaagga agagtataaa ctttatgtgt ataataagaa agaggggaca 780
 atcgtaataa gaatatgaa tatggataaa aagtctagtg agtatatttc ttttgatcaa 840
 agtgattgtt tatatcgtgt tcaggatgaa atctattatt acgaggtttt tagaaatggg 900
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agttctactt	atatgtataa	aaaagaactg	ttttggaata	ttatagataa	atctgattat	1140
agcgtacatt	catataaatg	ggtatatgat	gacttgatat	taaatgaggt	tgtccctggt	1200
gaagattatt	tatatcgtgc	taatgttcag	gagaatatcc	attattatac	attgtctttt	1260
tacgattttg	atagaattat	gcagttgaaa	aagaagtgtg	aaaaaagcgt	aggagaaaag	1320
tggatggtaa	aactagatga	tatgttagat	gaaaattcaa	atgatataat	agtttggttt	1380
tatgagaaaa	agtaa					1395

<210> 259

<211> 1416

<212> DNA

<213> B.fragilis

<400> 259

cctaagctta	tgaaactacg	aataggaagt	atcacgttct	tgctgtttct	ttcatccggt	60
gcctttccac	aggccacgag	ccgctatctg	gacaaaccat	taccacaagg	atgggaagaa	120
gatacacaaa	tatttcagca	agtattgcca	gtggacgacc	aatggtggaa	agcatttcag	180
gaccccggtc	tgcactcact	catctccggt	gcagtcaagc	agaattattc	ggtactgact	240
gcgattgac	gtatcaatat	ggcaaaagcc	aacttaagaa	tggaacgtgg	aaattttttc	300
ccaacaatcg	ggttgaatgc	cggatggacc	cgccagcaaa	gcagtggcaa	caccagtgc	360
ttgccacaat	cgactcaaca	ttattatgat	gcctcgctca	atatgagctg	ggagttagac	420
ctctttggaa	gcatacgcaa	tcgctgtaaa	gcccagaaaag	agaactttgc	ggccagtaaa	480
gaagaatata	ccggcacaa	gatactcact	tgtgcccagg	tagcctcagc	atacatcaac	540
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gtattaaaaa	ttacagaagt	aagatacaac	accggactcg	tatctaaact	ggatgtggca	660
caggctaagt	cgggtgttct	cagtaccaa	gcacgcattc	ctcaaactga	atcgggcatt	720
aatcaataca	ttacgaccct	tgccatacta	ttgggtactt	atccccagga	agtgcggcca	780
gctctaaccg	ctcccggaac	attaccggac	tatatggaac	ctatcggagt	ggggcttccg	840
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gccgctttag	taggagcgtc	taagtcggac	tgggtgcctc	aggtctttct	aaaaggatcg	960
gttggttatg	cagcaaagga	cctgaaagac	ctgaccatc	ataaaaagt	gacctatgaa	1020
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ttggccaaag	cacaattgga	cgaagctatc	aaccagttca	atcagacagt	attgaccgcc	1140
gtacaagaga	cagacaacgc	tatgaacgct	taccggaatt	ctatcaagca	aatagtagct	1200
ttgcgcgaag	tgcgcaatca	gggacaagag	accctgactc	tctcgctgga	actttacaaa	1260
caaggattga	ccccattcca	gaacgtactg	gatgcccaac	gctcactgct	cagttatgaa	1320
aaccagctgg	ttcaagccag	aggatattct	ctgctgcaac	tgatagctat	gtaccaggca	1380
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<210> 260

<211> 408

<212> DNA

<213> B.fragilis

<400> 260

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ttggcatttg	cogtcatatt	tgctgtggtc	atctttgtat	atatgagttt	aagattacaa	120
cgagaaaaag	aagctaactg	tcattttagt	gaaacatact	ccattcagtt	gacaaaaggc	180
ttcgtgggtg	attctatttc	actgtttgtt	aacgacagtc	tgatcatgaa	taaacagatc	240
aaagaggaac	ctactgccat	cgaagtgcga	cgcttcgcag	agcaaagtgc	actgatgatt	300
gtaaacaaat	aaactgaaac	agtagccgca	tttgacctaa	gtgaaaaagg	aggtacttac	360
cgttttgaaa	aggatattga	cggtatcaaa	cagctgccac	aaaaatga		408

<210> 261

<211> 192

<212> DNA

<213> B.fragilis

<400> 261
 aagtttgatta tctggttgtc agtaatggga tgcaacacta ttgttgccgg atggattatg 60
 atactcaaag ttattcgttt ctgtcggata ttccggatta tgacgcttta taaaattaac 120
 aatgttaatg actctttccg gcactctatta tctcttttcc aggaagttaa tatcgtaa 180
 gcaagaagtt aa 192

<210> 262
 <211> 459
 <212> DNA
 <213> B.fragilis

<400> 262
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 aagaataacg atacctttgc tgaaattaac tgtgaaaaac gaatggtaat gtcttggggg 120
 aaaacaattc tcggttgttt gattggaggg tatgcccttc ttggtttgtt agggggggaac 180
 tatgcatatg aacaagaagt aaaggcattg catgtatatg cggatagtgt ttttcattgaa 240
 gcttttcatg tagaattgca aaaacgaggt atggatcaag tggaaagtgt gagatatgga 300
 tgtgaagact ctttcgtctc ttcagtggat acagccttca aaaaagttac tatacaggac 360
 gagtacggta cgtatagttt tccgggttgat gcaatgaaga ttcgcaaaaa tatcgtgtct 420
 tcccctggag agcaaggact gcatactgtt gttgttttaa 459

<210> 263
 <211> 378
 <212> DNA
 <213> B.fragilis

<400> 263
 gctatgaata tagaagaatt tagagaatat tgcctttcat ttaaagggtg gcattgaccgg 60
 atgcccttta aaaaagcaac atctgaatat gatagagatt tactcgtctt ttatgtaatg 120
 gataaatggt tctgttttgt gaatatagac gcattcgtatt tctgtaatat aaaatgtaat 180
 gccggacaga tagaggattt gctagacaaa tatgaaggag tacaaccggg ctatcacatg 240
 aataaaaagc attggattag tgtctatttt gataaagacg ttccggataa aatgattaag 300
 gacctggtta agcaatcgta tgaaattgtt gtatcttctt tggcgagacg agagagggaa 360
 atattacaag ctatgtaa 378

<210> 264
 <211> 744
 <212> DNA
 <213> B.fragilis

<400> 264
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 acaattacaa atgatatgaa aaacacacat gtacttctta taaaatttaa aaataaaata 120
 tctgatgatg aagttcaatt ctttagaagt tcaattatac aaaaactggg tgaccagcca 180
 gatataattat accacaatca tgtagagaaa aataaatatc gctactctta tcccttaata 240
 caatacaaga atatcgaaca acaagcaaca atcgtatgta ttgatcaagg aacaaaagca 300
 attgagaaat tcttttcaca atgtgatttc aactttcaac tgggaaatag aaaagtcaat 360
 atgaagtttg cctctgtaac tcttacaaa ctattgattg aacgacaatc aaaaatgata 420
 aattatcata ttcataactg gttgccttta aattcggata actacaaaa gtatcaaaat 480
 attagcattc tttcagaaag aattaatttt ctggaaaaga ttttgatagg taatatatta 540
 tcatttacaa aaggagtcaa ttattttatt gactttccac tacaatgtaa actccttcaa 600
 cttagttttg ccaaactaat atctaataaa aatattaaat taatgtcgtt tgatgcagat 660
 ttccaatgta atctaataat tccggattat attggaatag gcaaacatac aagcattgga 720
 tatggtacga taactcgaaa ctaa 744

<210> 265
 <211> 1152
 <212> DNA
 <213> B.fragilis

<400> 265

agacttgtca	taatgaaaaa	actaatgtat	attttcctca	tcctcccttt	gataatgagc	60
ggatgtaaag	ggaaaaaaga	aaccgaaaaga	ggaggggatgc	ctactccgga	aatcagtgtg	120
gcataccac	tcgtacaaaa	cattacccta	acaaaagatt	atccgggata	tctgactacc	180
gaacaaacag	taaactctgg	agccagagtc	aacggtgcct	tgcagtccgc	ctctttcaca	240
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gataatgtaa	ctcaagccga	agcccaactg	aaaaccgcac	ttgcacagtt	ggaatatgcc	360
cgtaacaact	atagccgcat	gaaagaggct	ctaaaaagtg	atgcggtcag	ccgtatacaa	420
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actttggcta	cgatctataa	agacgaccgc	atgtacacct	attttaatgt	tgccgacaac	660
caatggcttt	caatgctact	ctctcaaaac	ggtaaagaaa	aggaactccc	caaaaatgtc	720
atcgtgcgcc	tgggtgagaa	cggcacacaa	aactatccgg	ccacattgga	ttattttatcg	780
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gtaaacgatt	cgaatatagt	acgctacagg	catatcgaac	cgggacaact	ggtcaatgac	1020
acattgcgcc	agataaagag	cggactttca	cccaaagaac	aatatgtcac	cacagcactg	1080
atgaaagtac	gtgatggcat	gaaagtcaag	cccgtatcag	tcaatcacga	gtcaccaacc	1140
tctaactcgtt	aa					1152

<210> 266

<211> 1239

<212> DNA

<213> B.fragilis

<400> 266

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tttgcattga	atatgaaaac	acaattcttc	acattgttct	tcaccattat	atgtttatca	120
ctccaagcac	aacaaccctg	tattattgaa	ggaaacatca	atgggattcc	tgatgggacc	180
gttatcagta	tgatgcgtca	acaggggaaca	ggtatgaaac	gaattgccaa	cgatacaatc	240
gataatggaa	agtttaagtt	cattatacat	actcttaata	atcagactga	agctttgaga	300
atagtaaagta	aaggagaagg	ctttcccaat	acatggctgg	acgtatatgc	ctctccggga	360
gaaacggtat	ccatcatcgg	cagtgataaa	ctactccgta	catggaatat	agtaagtaac	420
atcaaagagc	agcaagaaga	aaatcaatac	acaaatgagg	gtttccgcaa	tttgacagac	480
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gactccctcg	agctgttact	gtccaaagaa	gaaatcaatt	taatgaagaa	tcttcctgtt	660
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<210> 267

<211> 636

<212> DNA

<213> B.fragilis

<400> 267

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ttcttttctg	cttttgacga	cccattcttt	gggatcacta	cttttggtcga	ttttacgaat	120

acctaccatc	aaagcaagga	tgagaaaaag	tctttctttt	tgtactctgt	acattttctg	180
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aaatatgatt	ttatccattt	atcacctacc	ataggacgtg	aagatggaac	attcggtttc	300
ggttttttcg	aatacgatgc	agaccttgaa	gtattttatac	aaaatgctga	aaaagaaata	360
gaaagagtga	aaaacagtac	tggcctgtct	ttttccgaaa	atataggccg	gttagatcct	420
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tacctgcttc	caatttcaat	ttccggtcac	cacgctctta	tggatgggcg	taatgtggca	600
gaacttatcg	agaagttaga	aacaacaaag	aaataa			636

<210> 268

<211> 432

<212> DNA

<213> B.fragilis

<400> 268

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aacggatatt	acatcaaaaag	tgttacacgt	cttaatcctt	attatactgg	aatacatcta	180
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tatactggaa	tacatctaca	ttgtttgtgt	tccatccgtg	aagaaggcta	tcggcgtcct	360
aatccttatt	atactggaat	acatctacat	attacttgtt	tgggcagtta	tctgtcttgt	420
atcgtgtcct	aa					432

<210> 269

<211> 285

<212> DNA

<213> B.fragilis

<400> 269

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aaggctatcg	gcgtcttaat	ccttattata	ctggaataca	tctacatatt	acttggttgg	120
gcagttatct	gtcttgtatc	gtgtcttaat	ccttattata	ctggaataca	tctacatggt	180
acaatcaaca	atcaggatat	gggccttggg	gtcttaatcc	ttattatact	ggaatacatc	240
tacatgaaca	gtgacatcct	ttaccggacg	ccacacgtgt	cttaa		285

<210> 270

<211> 420

<212> DNA

<213> B.fragilis

<400> 270

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aacaatatta	tcaccaacga	caatcaatat	ccaaggtct	ttaagggata	tatctcttcg	120
tttggagcag	ctgtcatcca	atccggcctg	attccggcta	ttataattctt	tgaaaacgaa	180
gataatgatg	ccaacgctga	cagacataaa	atcattggag	ttttaaaaga	tatcatcaat	240
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gcaaattatt	ctatggcaca	gtatatcata	gaacatggaa	acactgatca	actgctaaaa	360
gagataacag	aagcagctgt	tgccatgaaa	ttagcattaa	gaatgtacaa	aagtgaatga	420

<210> 271

<211> 2250

<212> DNA

<213> B.fragilis

<400> 271

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ttcagtgat	gcaactatta	taatcgtatt	ttcagtacag	gtaacaagga	tttggcaact	180
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cagcatcgag	tcatattgtt	tgattatgcc	gatccatggc	tttggatggg	tccctcatg	2160
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<210> 272

<211> 426

<212> DNA

<213> B.fragilis

<400> 272

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tcgtgcgaac	aaagacgcaa	agagatcgct	atccgcaaag	tgaatggagc	caccatagga	180
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gcattcccgg	caagctatgg	aatgatgaga	gtgtggatag	aaagttacgt	cagacaaact	300
tccaccccat	tttggatata	tatcgctcctg	tttgcaggta	tcgggtatcat	catcgtcate	360
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<210> 273

<211> 996

<212> DNA

<213> B.fragilis

<400> 273

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tctattaatc	agctcagtc	ggcgtatgaa	gtttcccgtg	atactgtgtt	taaagctttt	180
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attgtgatga	acttcgataa	cgaaaaactg	tctcctaate	tttataaaat	aaatccatct	480
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aatgatacac	ctgcttatga	agtgatagat	caggggaata	ctgcactaag	tgtggattgg	900
gaaaagatgg	gagataaagc	tgctgagttt	gttttgcagg	ggaaaacccat	acaagattac	960
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<210> 274

<211> 687

<212> DNA

<213> B.fragilis

<400> 274

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atgggacctt	cgggttgttg	aaaatctact	cttctcaata	ttctcgggtt	actggataat	180
cctacaggag	gagagtatta	tctgaacgga	aaagaagtat	ccaaatatac	agaatcgcag	240
cgcaccaatc	tccgcaaagg	agttattggc	tttgtattcc	aaagtttcaa	tctgattgat	300
gaactgaatg	tatatgaaaa	tattgaattg	cccttactct	acatgggtat	tccggcctct	360
gaacgtaaac	aacgagtggg	aaaagcaatg	gagcgcatgg	ccattaccca	tagaagcaag	420
cattttccac	aacagctttc	cggaggtcag	caacaacgtg	ttgccattgc	acgcgccgta	480
gtagccaacc	ctaaaactgat	tcttgccgat	gaacctaccg	gtaatcttga	ctctaaaaat	540
ggtaaagagg	ttatgggact	attgagcgaa	ttgaataagg	aaggcactac	catcgttatg	600
gtaactcact	ctcagcatga	tgcaggtttc	gcagaccggg	taattaattt	attcgatggg	660
caagttgtaa	cagaagttac	tatttaa				687

<210> 275

<211> 630

<212> DNA

<213> B.fragilis

<400> 275

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gtagatgaac	cgacatctgc	actcgatgcc	ggttccacag	acaaagtttt	agctttcttc	540
cgtaatcagg	cagaaaaggg	aacggctata	ctcgccgttt	ctcatgaccg	gacattcgct	600
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<210> 276

<211> 513

<212> DNA

<213> B.fragilis

<400> 276

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gccgaaaagca	taggtattca	gcaatccact	ctctctcata	ttttgaatgg	gcggaacaac	180
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ccttccttat	ttgctgagaa	tgccataatt	ccgcccacg	ggacagttac	tccggaaaat	360
cgcagggaaa	tgccgttaga	aagttcccaa	aacaccccg	aagagattgt	aaaacaagaa	420
attagatata	tagaaaagcc	ttccagaaaa	ataactgaaa	taagaatttt	cttcgatgat	480
aatacgtatg	agacattcag	aggagaaaaa	taa			513

<210> 277

<211> 189

<212> DNA

<213> B.fragilis

<400> 277

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atTTTTTggtc	TTTTTTgtat	tagtttcgag	ttatcgtacc	atatccaatg	cttgtatggt	120
tgccatttcc	aatataatcc	ggaagattta	gattacattg	gaaatctgca	tcaaacgaca	180
ttaatttaa						189

<210> 278

<211> 2061

<212> DNA

<213> B.fragilis

<400> 278

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gccgttgatg	ccactcagaa	gttgaatata	ttggcttcta	tcagtgaatt	taagggcgaa	180
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cagaaagatt	ctattttttgc	cggatatgca	ggcaaaaaaca	aagtgggtacg	tcagttgatc	1980
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<210> 279

<211> 402

<212> DNA

<213> B.fragilis

<400> 279

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gcctgttcgc	aaggaaagca	aatcagtgga	agttccaact	acatcactaa	aaatataaaa	180
gtcggttcat	tcgaccaaata	aaaatcgatg	agtagttcag	atattgttta	tacacaaaaa	240
cagggcgccc	ccaccgttca	gatttatggg	cccgcacaata	tagttgaatt	gatggaaacc	300
tctgtcagcg	gtcgaacatt	aacgattaaa	ttcaaaaaaga	atacctccat	ccgtaatagt	360
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<210> 280

<211> 912

<212> DNA

<213> B.fragilis

<400> 280

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<210> 281

<211> 2236

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (16)

<223> Identity of nucleotide sequences at the above locations are unknown.

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<210> 282

<211> 717

<212> DNA

<213> B.fragilis

<400> 282

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aatatcgaca taaccttttt ctttaaatat ataaaagaga aaatagccta tgaatataat 240
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aaaaaattaa aagctctcaa aatccatata attcttttaa catgggattt atctccagaa 600
tctgcaactg cacggctgtt gcgggaagaa gcatgtaaac atatagaatt aagtgaatc 660
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<210> 283

<211> 771

<212> DNA

<213> B.fragilis

<400> 283

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accttacgcc	aatatggggc	gatggattat	actattgtgg	tggcggctac	agctggagac	720
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<210> 284

<211> 798

<212> DNA

<213> B.fragilis

<400> 284

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aagtttcggg	gagcgggaca	tggaaaccaag	gcattaattg	cagaactgat	tggcggtgag	180
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acagtgaaga	ataccaatat	gcttatgtgg	cataaagagt	tgtggttgat	agatcatggg	480
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agctggatag	agtggcgtga	taaagatgaa	actcctcaag	atattcgtga	tatctattat	720
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<210> 285

<211> 441

<212> DNA

<213> B.fragilis

<400> 285

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cccgaattccg	ctattgaatt	tctattgaca	ttcctggcgt	tctatctggg	ctatcttata	360
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<210> 286

<211> 1386

<212> DNA

<213> B.fragilis

<400> 286

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<210> 287

<211> 993

<212> DNA

<213> B.fragilis

<400> 287

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<210> 288

<211> 2307

<212> DNA

<213> B.fragilis

<400> 288

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tctcgggtag	ctttcgaact	gagctatgat	aactgttttc	aggatgtgga	caacctttac	180
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<210> 289

<211> 1215

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (295), (339), (357)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 289

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acgggagtc	tatttatatt	ttttacgctt	gcaatgtttt	ttatcgcccc	gttccatgcc	240
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aagaaggtaa	gataa					1215

<210> 290

<211> 1401

<212> DNA

<213> B.fragilis

<400> 290

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cgttactctt	gggacctgaa	tgtatctact	gacggaatga	atgaatttac	cggaggagat	180
gtagtgaag	gagaagatgt	gccatcggct	acgccgactg	tgagtcgttt	tgttacagta	240
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<210> 291

<211> 1395

<212> DNA

<213> B.fragilis

<400> 291

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<210> 292

<211> 1230

<212> DNA

<213> B.fragilis

<400> 292

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gtacttgtcc	ccttattggg	cgggctcgat	ccttctacag	ctttgtttac	tgccggatct	180
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cctcctgtaa	ctacctattc	ggaagttaca	ggagccatgt	cgcttactaa	agtgcagaa	900
cctcaagtaa	taagaatagc	ggcgattacg	gccattctgt	tttccgtaat	cggtaaagtc	960
agcgctttat	tgaagtctat	tccttcgggt	gtattaggag	gaatcatgtt	actcttattc	1020
ggtagcatcg	cttgcgcggg	aattgctaac	cttgtcaata	attgtattga	cttgagccgg	1080
acacgtaata	tcattattgt	ctcactgact	ctgactattg	gcacgggtgg	tgccgtattg	1140
gcatggggcg	aattctcact	gtcgggaatc	ggctcttgccg	cattggtagg	agtaggcttg	1200
aatctggtac	tgccaaaaga	agagagatga				1230

<210> 293

<211> 933

<212> DNA

<213> B.fragilis

<400> 293

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cgtgataccg	gccgacatgc	actggttgtt	tatgatgatt	tgtcgaaaca	agcagtatct	180
taccgtgaag	tgtctttgat	tctccgtcgc	ccctcgggac	gtgaagccta	tccgggcat	240
atTTTctatt	tacactcccg	tttgcctggg	cgtgcagcca	agattattaa	tcaggaagaa	300
gtggcccggt	agatgaacga	tttgcccga	agcctgaaag	gtaaagtga	aggtggaggt	360
tcgctgacag	cattgcctat	tattgaaact	caggccggag	acgtttctgc	ctatattccg	420
actaatgtga	tctctattac	agacggtcag	atattccttg	atacggattt	attcaatcaa	480
ggtaatcgtc	cggctattaa	tgtaggatata	tcggtttccc	gtgtgggagg	taatgcgcag	540
attaaggcta	tgaagaaagt	ggccgttaca	ttgaaaatcg	atcaggcaca	atatcgcgaa	600
ttggaagcat	cttccaaatt	tagtggagat	atggatccgg	ttaccgcact	gaccattgac	660
aaggggcaga	aaaacgcccc	tttgcctggt	cagccccaat	actctccaat	gcccgttagag	720
aagcagattg	ccattctcta	ttgcggtatc	cacggattat	tgcgaaatgt	tccgttggtg	780
aaggtagaag	atTTTtgaagc	agcgttcttc	aatacactcg	ctctcgatca	tcaggcggat	840
gtgctgggat	tattgaaaac	cggagtgatc	aatgacgagg	taacgaaggc	cattgaagaa	900
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<210> 294
 <211> 879
 <212> DNA
 <213> B.fragilis

<400> 294
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 aaaatcactt cagcaatgaa gatggtggct tctgccaaagt tacacaaggc gcagggagcc 120
 attgagaata tgttgcctta tcagaggaag ttgaataaga ttctgactaa ctttctgagt 180
 gctgatcttc cggtagagtc tccgttctgt gtggaacgtc ccgttaagcg ggtcgctatt 240
 gtggcttttt cttccaacag ttctttatgc ggtgctttca atgcgaatgt actgaaaatg 300
 tttttgcaga cgggtgggaga atatcgcgag ttgggacaag ataatacct gatctatccg 360
 gtggggcaaaa aaatagagga ggctgtcaag aagttaggat tctttcctca aggagttat 420
 cagaagttgg cagataaacc gtcgtatgat gaagccgctg cattggctaa attgttgatg 480
 gaactttttc tggaaaaaaa tatcgaccgt gtggagttga tttatcacca tttcaagtca 540
 atgggggtac aagaactgtt gcgtgaaaga tatttgccga ttgacttgtc tgcggttcaa 600
 aatgacgaag agagaggcgg agtagtgaat gactatatca tagaaccttc tgcagctcaa 660
 ttgatagcag acttgatttc gcagggtgtg agtcagaaga tatttacagc tgcctctgat 720
 tctaattgcat ccgaacatgc tgcacgtact ttggctatgc agatagcgac ggacaatgcc 780
 aacgaactga ttcaggagtt gacaaagcag tataataaaa cccgccagca ggccattaca 840
 aatgaattgc tcgatattgt aggtggcagt atggcatag 879

<210> 295
 <211> 858
 <212> DNA
 <213> B.fragilis

<400> 295
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 tatcatccat atgacgtcga cataaaagga gaaagagaca ttaatgcgaa aaatattcaa 180
 aagatcgagg ccaaatgcct gggaaagtct actatacgct ttatcgccat gggtgactcg 240
 caacgctggt atgacgaaac cgttgacttt gtaaacgctg tcaacaaaag agacgacatc 300
 gactttgtag ttcatggagg cgacttcagt gacttcggac ttaccgatga atttctttgg 360
 caaagggata taatgaataa actaaagggt ccttatgtag gacttatcgg aaaccatgat 420
 tgtttgggaa ccggagaaga tgcattccgg caaatattcg gcgatacaaa cttttcgttc 480
 atagccggag gtgtgaaatt tgtatgcctc aataccaacg caatggaata tgattattcg 540
 gaaccgatcc ctgattttga ctatatgaa agacaactca cagaacgtgc cgacgaattt 600
 aataaaaccg tattctgtat gcatgcccg cccctttgtg atcagttcaa taacaatgtg 660
 gccaaagtgt ttcaaatgta tgttcgccaa tttcccgtt tgcaattttg cactgtagct 720
 cacgaacatc ggatcagtg gtcagatgtg tttgacgat gcgtgatgta ttatggaagc 780
 aattgtatga aaaatcgcag ttatttagta ttcacgataa aacctgatgg ttatgattat 840
 gaagtgggtg aattttaa 858

<210> 296
 <211> 981
 <212> DNA
 <213> B.fragilis

<400> 296
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 ggaaaagagg ctgtataccg aagattacga ggcgaagtgg ctttcacctt tgacgaaatt 180
 gccatgattt catgcaaact gggaatatca attgatcaga ttattggaaa tcaccagtcg 240
 aaccgtgtga ctttcgattt aaacctgctt cactcaccgg atcctctgga aagttattat 300
 gagattatag aacgctatct gcgcatattc aactacgtaa aagatgatat cagcacgaag 360
 atatataccg cttcgaacgt aattcctttc accctctatt cttcgtagca atacttatca 420
 aagtttcgcc tgtgcagatg gatttatcaa aatggaaaaa tacgtacccc aaacagctta 480

tcgggaatgc	acataccgga	caaagcggtc	catgcccata	aactgttgag	tgaggctgtc	540
aaagcgtgca	gaaagacctg	ttttatatgg	gacagcaatg	tcttctactc	gtttgtaaaa	600
gagatgaagt	atthttgccc	cctcaatctg	atthtcggaaa	cagacctgat	acatttaaaa	660
aacgaaactg	agctgttgct	gcatgaactg	gaacagatat	ccgcaaaaag	tgaattcagt	720
aacgaaaaca	aagtagccat	ttactttatcc	aatatcgatt	ttgaagcaac	ctacagctat	780
atagaaaaga	aagattttcca	aatcagttctc	ctccgggtat	attctattaa	ctcaatggac	840
tctcaaagcc	cacgaatttg	cggcatacaa	aaagactgga	tacaatcatt	gaaaagacac	900
tccacactga	tttcagaaaag	cggagagtcc	caaagaatta	ctttcctgga	acagcagaag	960
agtttcatcg	acaccttgta	a				981

<210> 297

<211> 987

<212> DNA

<213> B.fragilis

<400> 297

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ttatatatag	gtaaggaggc	catctatcgc	cgactgcggg	gagaagtacc	gtttactttg	180
gcagaagctg	ccgtcatctc	gagaaaattg	ggaatatcgc	tcgacaaaat	gatcgggtgtg	240
agtttcagca	acaatgcggg	attcgacctg	aacgtcgtac	accataccaa	tacattcgaa	300
acctatccag	atatctcac	gaaatatgtc	aatgcattcg	ataacatccg	ggaagatccc	360
actacagaaa	tggcaacctc	ttcaaacata	ttgctccaag	cattatatct	caaacatgat	420
gtactttcaa	agtttcgtct	gtttaaatgg	atgtaccaga	atgaaaatat	caaatgcaag	480
cattttgatg	aactggagat	tccccacaaa	atatataaca	tccagaaaga	ctttgtcaat	540
atgacacagc	agatgaagac	gactgattat	atctgggaca	ataccgtatt	cgaacatgta	600
gtgagagaca	tacagttctt	ttcggaaatc	cacctggttt	cggagaaga	caaagagttg	660
ataaaagacg	atthttatgct	tctgacggat	gaattggaag	agttggccgg	aaaaggtaag	720
tatgaaaccg	gtaacgatgt	acgtatctat	atctcaaata	tcaagttcga	tgccacctat	780
agctatgtgg	caaccagcaa	cagccatctc	agtatgatac	gcataactc	catcaatgcc	840
attacaacgc	aggatgacgg	catgttccgc	agcctgaaag	agtgggtaca	atcactcaaa	900
aaattctcaa	ctcaaatatc	cgaagcgga	gagatgcaac	gtatacgttt	ctttaatgaa	960
cagcgtgaaa	taataaatac	cttataa				987

<210> 298

<211> 1392

<212> DNA

<213> B.fragilis

<400> 298

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cttataattg	ctttcaaacg	gtttgcttca	tgggggagtt	gtactttttgc	ttccaaaata	120
acaaggacta	tgatcagaaa	gttttttatt	ctcttttttc	ttggcttttt	cggatttgcc	180
gaagcccaac	agccgtccgt	cggcttgact	ctgaaggagg	cagagcaacg	tttccctgaaa	240
tgtaattttat	ccctattggc	cgagcgctac	aatgtagaca	tcgcacaagc	caggtttgctt	300
caggccggac	tgttcgataa	tccggttaatt	tcattcgaac	aaaatgtgta	taaccgattg	360
aatggaaagt	actttgactt	cggcaaaaaa	ggcgagtcgg	tagtcgaaat	agagcagggtg	420
atacgccctg	ccggacaacg	gaataagcag	atacggtctg	aaaagataaa	caaggaaatt	480
gccggttatc	agttcgaaga	agtgatgagg	actttacgcc	aggaacttgg	cgaaggcattt	540
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gagcattttgc	tgacagggtat	aaaagagcag	catgcaaagg	gaaatatctc	tttaattggaa	660
atggcgagac	tcgagtctat	gctgctttct	ctgaagaaag	acaagaacga	atgcgaaagc	720
aactattttgt	cccggagagg	agaactgaat	ctgttactga	atctgcctgc	cgaactttcgg	780
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aaaggtagtt	atgatcgcca	aggtaatttt	attaataact	actttgcaat	cggatttcagt	1020
atgtcgggtgc	ctatctttta	ccgtaaccag	gggaatatta	aaatggcccg	tttcaatctt	1080
ctgaaggcgg	atcggggagca	agagtattcc	cgaaataaag	ccgaggccga	actatacgca	1140

gcttatactg	cttttagagaa	agcatgtcag	ttgtatcagt	cgactgatat	gggactggaa	1200
cagaattttg	agaaactgat	agccggagcc	aacgagaact	ttatcaaacg	taacatcagt	1260
cttttagaata	tcctcgactt	ttatgatagc	tacaaagaga	cttgcacccg	gctttacgaa	1320
atcaagaaaa	acgtactgct	cggtatagag	aacctgaatg	cggtggcccg	acaacctatt	1380
tttaactact	aa					1392

<210> 299

<211> 678

<212> DNA

<213> B.fragilis

<400> 299

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gatggtgtaa	ttgtcgatac	agaagggcag	tataccgttt	tctggaatga	aatgggcca	120
aagtatgtaa	atgatgcaaa	ctttgggttc	aagggttaagg	gccagacact	ggtacagatt	180
tatgataaat	actttgcagg	agaaccggaa	aaacagcggg	atataaccga	ggcattgaac	240
cgctttgaaa	taaaaatgaa	ttatgactat	gttcccggaa	tagttgagtt	tatagcagat	300
ctgcgtcggc	atggtgtgaa	aatagctttg	gttaccagtt	ccaatacggc	aaaaatggag	360
aatgtttatc	atgcccatcc	cgagttttaa	tccctttttg	atgaaatatt	gactgcagag	420
cgttttaagc	gttctaagcc	tgatcctgaa	tgtttcttgt	tgggaatgac	aattttcggg	480
tccgattcaa	aagattcgta	tgtgttcgaa	gattcatttc	atggtttgca	ggccggtaga	540
tcattccggag	ccattgttgt	cggattggca	actacgaatt	cacgcgaagc	cattgccgac	600
aaggcagact	atgtaataga	cgatttcaga	gggatgactt	acgaaaaact	gctgactata	660
acttcacggt	atatctga					678

<210> 300

<211> 687

<212> DNA

<213> B.fragilis

<400> 300

tatcattttca	atcttaaaat	tatgacctac	ctcgctacca	accccctatt	ccatggaatc	60
tctccagaaa	cgctttcccg	tgattttgac	ggaatcgtat	ctcacctccg	catgttccgt	120
aaaggagaca	ttcttgccag	gcaagggtgat	gtatgcaatc	ggctgatgat	attactgaaa	180
ggcagtgctc	ggggagaaat	gatcgattac	tccggcagat	tgattaaagt	ggaagatatt	240
attgctcttc	gtgcaattgc	cctctttttc	ttatttgggtg	cagacaatcg	ctatccggta	300
gaagttacag	caaacgaagc	taccgaagtt	ttcgaaattc	cgaaagaaag	cgtactgaaa	360
ttattttcgac	ggaatgagaa	attcttagag	aactacatga	atctttctgc	caattatgcc	420
cgaacacttg	ctgacaaact	gttttttatg	tcctttaaga	cgattcggca	gaaacttgct	480
tcctatctgc	tacggatggt	gaaacaacaa	ggagacagtc	cgatacaact	tgaccgctcg	540
caacaggaac	tggctgatta	tttcggagta	tctcgtccct	ctctggcacg	cgagctggct	600
catatgcagg	atgacggcct	gatcaaaacg	gacaggaaat	tagtgcatat	cttgagaaaa	660
gaagatatga	tgcaactgat	acaataa				687

<210> 301

<211> 213

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (16), (34), (78)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 301

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ctggttgctg	caaccaanac	ccccaaacga	aagcatatcat	atatatttcc	gcttgtaaac	120
atcgacaaaa	taggcatgga	acgggccgat	aaaaaacatt	gcaagcgtaa	aaaatataaa	180
tatgactccc	gtctgactga	caggcacgcc	taa			213

<210> 302
 <211> 396
 <212> DNA
 <213> B.fragilis

<400> 302
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 aaagtggagc gtgaggaatt tatcaacgtt ggggttatct tgttttctaa acaggctgcc 120
 tttatccgga tgcgttatga aattaataag aagagggttg aggccttatc accggaacct 180
 gatatcgatt ctttccggaa atatttggag gctttcagta aagtgtgtgc aggctgtccg 240
 acgggaggag gcattgctaa actggaagtt ccggaacgtt ttcgttggtt gacagcccat 300
 cgtagtctct gcattcagac ctcaagacct catgttggtt attctgacaa tttagaggaa 360
 acattggagc ggttggtcga ggaattgggt ctttga 396

<210> 303
 <211> 207
 <212> DNA
 <213> B.fragilis

<400> 303
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 tatgccgata ctttcttttc gattagaatt ttgcataaaa atgtgagatt cattcgtgaa 120
 atagagaaaa aagataaaaa tagatcattc ttattaggta atatgagcta ttttggttacc 180
 tttgcgcccc cttattccat agcgtag 207

<210> 304
 <211> 279
 <212> DNA
 <213> B.fragilis

<400> 304
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 atcggatttg gtaagatcgg tggctcggcc atggaaggta ttgcgcgtca accggaggca 180
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<210> 305
 <211> 1140
 <212> DNA
 <213> B.fragilis

<400> 305
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 gtgacagcta gcaatgggaa tcaggcattg gaccaagtaa agaaagagaa tcccgacctg 180
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 gcggatcccc aagcggccca tattccgata atctttttga ccgcattgaa tagtactgcc 300
 gatatagtca aaggatttca ggtaggcggc aacgatttta tctctaaacc ttttaataaa 360
 gaagaactga ttattcgggt cagtcacatg atttctttag tagcggccaa acgtattatt 420
 gaagccaaaa cggaggaact taaaaagacg attatcgggc gtgataagct ttattctgtg 480
 attgcccattg acctccgttc gcctatggga tctattaaga tgggtgctta tatgctgatt 540
 cttagttttg ccaaagaaaa aatcggcgaa gatatgtatg aactgctgac tatggccaat 600
 cagactaccg aagatgtggt ttcgttggtg gataacttac tgaaatggac aaaaagccag 660
 ataggtaagc ttaaagtcgt atatcaggat atcgacatgg tggaaagttg agagggagta 720
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aaaaaactgt	tgcataccga	tacacatttc	agtacattcg	gtactaataa	tgaagaaggt	1020
tcgggactcg	ggttactttt	gtgccaggat	tttgttgtga	aaaatggagg	aaagttgttg	1080
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<210> 306

<211> 1599

<212> DNA

<213> B.fragilis

<400> 306

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gcaatttcag	gagaaagtat	tttcttcctc	gggcctcccg	gagttgccaa	gagccttatt	180
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cggcaaatg	aaaaatataa	catacagaaa	gaagagggtc	cacactcaac	gctctatatt	780
tccgaccgtc	gatggaagaa	aatcgatcgc	ctgctcagaa	cttctgcttt	tctgaatgaa	840
acagatacca	tccgcttttc	agattgtact	ttattacttc	attgcttatg	gaatgaaata	900
gaacaaatac	caattatcga	acaaatgggtg	tcacgcggcac	ttgacgaatg	tatcagccat	960
tatctttgtg	gccaacggac	tttagaacia	aagctgagca	gtattcggga	agacatgaag	1020
tcagaacaca	gtttgcgtga	aacaaaagat	ccggccctgc	aaattgtaga	cacttttctat	1080
catcaaattg	aaagatatcc	tgtagcaggc	aatctgttga	tttttgcttc	cgactaccaa	1140
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aactggatat	taaaagtata	tgaccatgtc	cgcaaccgga	acatatccca	atcagccata	1260
gtttcactca	agaaaggcac	acgttctgta	ttcatcaaca	atcaagagta	tccactagct	1320
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<210> 307

<211> 2991

<212> DNA

<213> B.fragilis

<400> 307

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<210> 308

<211> 183

<212> DNA

<213> B.fragilis

<400> 308

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cattactcag	acttgatgct	gttcaccgga	ttttcattag	cgatatgcca	ggatctccct	120
ataatgaaaa	caaagataaa	gaccaataaa	caaataagctg	tcactacata	ccaacctgca	180
taa						183

<210> 309

<211> 369

<212> DNA

<213> B.fragilis

<400> 309

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tttcatgctc	cctgggtgtgt	atattgcaaa	gccctgtcac	ctatactcga	ccaactggct	180
gtagaatatg	atgggaaaaat	agatatTTTat	aaagtggatg	tagatcagga	accggaactg	240
gaggctgctt	ttgccattcg	tacaatccct	aacctgttgc	tttgtccgat	gggaggaaaa	300

ccaagtatga aattaggaac tatgaataaa acccagttaa aagcattgat agaagaagtt 360
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<210> 310

<211> 1347

<212> DNA

<213> B.fragilis

<400> 310

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<210> 311

<211> 1683

<212> DNA

<213> B.fragilis

<400> 311

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aaggatgtag	cccgcaaaat	agccaaattt	cacattatat	tagaaatggc	cggatttcaa	180
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gaactcaatc	aacaacttcc	ggcctactgt	cagattacta	aaatcaaaat	ccacttcgag	1620
gagtttgaga	aaacagcgaa	gaagagcatt	aaacgattca	tgtatcagga	agcaaaagga	1680
taa						1683

<210> 312

<211> 252

<212> DNA

<213> B.fragilis

<400> 312

ggaatcatga	aagaactgca	tttgaatatt	gtatcgccgg	aaaaagaggt	ctttaatggg	60
gaagtgaaga	gtgttaccct	tccgggcacc	agtggagtct	tttctattct	gccgcagcat	120
gcaccgattg	tttcttccct	gcaagaaggg	acagtcagtt	acacgacaac	ggatggcgaa	180
gagcatacgc	tgatatttca	cagcggtttt	gtggagctaa	gcaatgggtga	agcttccggt	240
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<210> 313

<211> 567

<212> DNA

<213> B.fragilis

<400> 313

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catacaccga	tagatgcatt	tcccgatgtg	acgaatacga	aagtgaccat	cattacccaa	180
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aaaacaattc	aggattgggt	gatcgaccgt	aacttgcgtg	ccgtatcgga	agtgacggat	540
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<210> 314

<211> 231

<212> DNA

<213> B.fragilis

<400> 314

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gtgagagtta	aaccaataaa	aacctcttat	tgtttgatgt	tgcaaagtaa	ggcattaatt	120
ccggataata	caccatatcc	gcttcttttt	atccttttaa	atattcttta	ttgtgtaatt	180
agaccaaaaa	ttaacatttc	tctttggcta	tatgtgtctt	atttgttata	a	231

<210> 315

<211> 747

<212> DNA

<213> B.fragilis

<400> 315

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tgtcccggtg	gcgggttcaa	tcagatagct	tcagatcatg	aaggacgtga	ttttgctgct	180

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<210> 316

<211> 204

<212> DNA

<213> B.fragilis

<400> 316

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tcaaaagata	tacttgagca	aaccgcactt	tccacctcct	tcggaaactc	ctcagcaact	120
gtcgatgcta	tcggtattaa	tgtatatgat	cctgcatttc	ctttgatcac	tccatcctta	180
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<210> 317

<211> 765

<212> DNA

<213> B.fragilis

<400> 317

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gataaagaag	ggaaaaaagt	aactttgaaa	gaactgtatc	gctggcagga	tctttttgga	180
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<210> 318

<211> 1050

<212> DNA

<213> B.fragilis

<400> 318

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gtttcctgcc	tcaaagtta	ccggcatttg	ccatgggtgca	gatgctggat	acgtcacctt	180
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<210> 319

<211> 3174

<212> DNA

<213> B.fragilis

<400> 319

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<210> 320

<211> 1095

<212> DNA

<213> B.fragilis

<400> 320

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<210> 321

<211> 627

<212> DNA

<213> B.fragilis

<400> 321

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cctcttcac	agaaaacgta	taaagaaaat	gcctatgtct	ctttcttctc	tacagcttcc	180
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ccaaacaaga	aacttcgttg	ggagaaaact	caatcagtaa	atgttggact	tgatttttctg	540
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<210> 322

<211> 2574

<212> DNA

<213> B.fragilis

<400> 322

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ctttttctac	agatgcgcca	gcatctaact	tcaaataagg	aaagcctttt	tggaagcaag	180
ccaactgctc	agcgatttgt	acttccgaaa	tgcccttttt	ggcaagcaat	tctttgtctt	240
caggtgttat	catactatct	aatttttatta	attcatgccc	aaaaatacaa	aaaaaggaag	300
aggacaccct	acaaaacccg	gaaaaaaaact	atctttaccg	acgataaatt	tgagctgctt	360
atggaaagag	atgaattctt	tacgaaagaa	gagagagaat	tattgttctc	actatacaaa	420
aaactactgc	gtctcaccgg	agaaacctta	caaaaaggag	attgcagaaa	gctgaaaaag	480
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<210> 323

<211> 1479

<212> DNA

<213> B.fragilis

<400> 323

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<210> 324

<211> 312

<212> DNA

<213> B.fragilis

<400> 324

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atcgaccggg	ttgaagtgcg	tacccttttc	aaacatttcc	tttgcttccg	gattattcat	300
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<210> 325

<211> 1248

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (473)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 325

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gccggaatgc	ttgtcttgat	aggaggaaatg	ttgcctgcta	caacctttgc	acaggagcct	180
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<210> 326

<211> 2658

<212> DNA

<213> B.fragilis

<400> 326

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<210> 327

<211> 933

<212> DNA

<213> B.fragilis

<400> 327

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<210> 328

<211> 399

<212> DNA

<213> B.fragilis

<400> 328

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attattatag	taacagtggc	cggattctgt	ttcggcatca	cccggaacga	atggatggct	180
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gcgggttccg	ttctgatatg	tgctatagtt	gctgccattg	taggaattat	catcttcattg	360
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<210> 329

<211> 1536

<212> DNA

<213> B.fragilis

<400> 329

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gcattagaga	taaaaaggca	caacggcaaa	aagctgattg	tagaagttca	acaacacatt	180
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<210> 330

<211> 1809

<212> DNA

<213> B.fragilis

<400> 330

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<210> 331

<211> 1593

<212> DNA

<213> B.fragilis

<400> 331

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<210> 332
<211> 2595
<212> DNA
<213> B.fragilis
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<400> 332						
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<210> 333

<211> 1587

<212> DNA

<213> B.fragilis

<400> 333

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<210> 334

<211> 948

<212> DNA

<213> B.fragilis

<400> 334

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<210> 335

<211> 375

<212> DNA

<213> B.fragilis

<400> 335

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gagggagatt	gctggagtg	gcacgataat	tccgcacggc	atctttgctt	tttatattcg	180
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<210> 336

<211> 1380

<212> DNA

<213> B.fragilis

<400> 336

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gtgaaacaag	aggaacttga	gggagaaaatt	atgtcttatt	atcagcatat	acaaccttct	180
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cgatcaaaag	agtggaaaca	ccttcgtaat	cttttttttg	ataaatggta	tcacctgttg	420
gcaaataatg	aataataatta	ccaaatagaa	cgtatcaaca	atctttgtga	gagattctat	480
cgcttacaga	aaaatattgc	agatcaactt	ccccacgag	gcaatgcccg	tttaatgtgg	540
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tctatcgaa	atgccgat	agtaatgatg	tcagattttg	aaatgcctcc	tttaaacgaa	1260
gaactttcag	aggaaataaa	aaaaataaag	caaaataaga	ctcatttata	cgccctctct	1320
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<210> 337

<211> 1644

<212> DNA

<213> B.fragilis

<400> 337

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ctttttgtag	tacgcggaat	cgcagtctac	aatcaggcat	tacgcaaaga	tggacgttct	180
tctgcccg	cagataagtt	tatctttgac	gcattgttca	ctaccattac	aaatgccaac	240
tttgataaac	actccattat	cgagaaaata	aagaaaggac	tggagctaaa	gaaagatcta	300
agtaaccaag	tcacaataga	acatgcgccc	gacgaatgta	cttgggtatgg	tgacgaaact	360
gagtttgaag	agaaagccca	aacggtgggg	gtactgcgaa	cttctgacga	agacattcga	420
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tataacttag	gatatgagaa	tccggagata	tttgcattca	tgcaatatgc	tttggctgaa	540
ttgacccg	aagatattac	tgtggacgaa	ctgataaacc	tcacactcgc	tacgggtaac	600
catggtgtgc	aggctatggc	ccaactcgat	actgccaata	ccagccatta	cggaaatccg	660
gaaatctccg	aagtaaacad	tgggtgttca	aacaatccgg	gtatccttgt	cagtggacat	720
gacttgaaag	atattgaaga	acttttgcaa	cagactgaag	gtaccggtat	cgacatatac	780
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ttggcacttg	gagtgaaaaa	gattcattta	gggcgcagcg	ttcctgcatt	cttatctcct	1560
aacgtgaagc	aggtactgat	cgataatttt	ggaattggcg	gtatcagtac	agcagacgaa	1620
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<210> 338

<211> 510

<212> DNA

<213> B.fragilis

<400> 338

acaaagaaga	ttatgtcatt	gttactaccc	gatagtggcc	tgatattctg	gatgtcctt	60
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gtggaaggcc	gtaaaacct	cattgacgaa	tatttgagg	tagccagaga	agcaaagcc	180
cagttgtcac	gactgaaaga	ggaggggcga	gctattgtgg	ctgccgctaa	caaggaacag	240
ggacgtatca	tgaagaggc	tatgcaggaa	cgtgaaaaga	ttattttacga	ggcccgcaaa	300
caagctgaaa	tagctgctca	gaaggaactg	gatgaagtga	aacgacagat	tcagattgaa	360
aaagacgaag	ccatacgtga	tatccgtcgg	caggtagctc	tgctttctgt	ggatatagcc	420
gagaaggtca	ttcgcaaaaa	tctggatgat	aaacaagagc	agatgggaat	gattgaccgt	480
atgcttgatg	aagtattaac	gaagaactaa				510

<210> 339

<211> 570

<212> DNA

<213> B.fragilis

<400> 339

cagaagaaga	tggaagtcgg	aataatttca	atgcggtatg	cgaaagctct	gatggcttat	60
gctgaagaga	gaggagcggg	ggagaggctt	tatcatgagc	ttgtcacact	ggcgacagat	120
ttccgtactg	tgaagggtatt	ttgtgccgtg	cttgacaatc	ctattgtttc	tggttaacgaa	180
aagtttaatc	tgatctgtac	ggcagccgat	ggggaccata	aaccgagtga	agaattttatt	240
cgtttcatc	ggttggtact	caaggagaga	agggagacct	atctgcaatt	tatgagtctg	300
atgtatctgg	atctttaccg	gaagaagaaa	cacatcggtg	tagggaaact	gatcactgct	360

gttccggtag	acaaagctac	agaagagcgt	atccgacaaa	ctgctgcaca	tattttgcac	420
gcataatagg	agttggaaac	agtgggtgac	ccttctatag	aaggcggctt	cgttttcgat	480
attaacgatt	accgactgga	tgccagtatc	gctacacagt	tgaagaaaag	caaacaacaa	540
ttcattgata	agaatcgaag	aattgtataa				570

<210> 340

<211> 1437

<212> DNA

<213> B.fragilis

<400> 340

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aagtgtaatg	gtgctttctga	tgggcataat	tatcgtatgt	ttctgtatga	atcagcacta	120
ttgatattgc	tttcttttatt	gttcgtgaca	gtcctgttat	tcacttttaa	gttggagata	180
gaagatcttt	cggagacttc	attaaaggct	ttattttacat	ggcaaaactc	gtgggtaccg	240
attttgggtt	cttttgggtt	atttctgggt	atcggactat	ttccggggcaa	gttgtttgcc	300
gctattcctg	tgacacaagt	tttccatcgt	tttactgcac	atcgttttgt	ttggaagcga	360
tcattgcttt	ttatacagtt	tgcggaatt	gcattttatt	taggcctgtt	gatgggtatt	420
cttttacagt	atcatcaggt	gatgaccctg	gacatgggat	ataaggtcga	taatttggca	480
gttgggtggt	cgccatatag	agaaattgat	aaaatggacg	gtattctccg	aggactgccc	540
atagttgagg	agttttgttaa	tgcaagtacg	attattttatg	gtggctacat	gggtcaacct	600
tacacagatg	cacatgggaa	ggaattttatg	ggacgtatcg	aatttgttga	tgaacattat	660
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caaagtgcgt	acatgccaca	ggctcctgta	gcactgatga	gtaatttgga	atggatgaat	900
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aacacattga	tgaaagaggg	ttttccgaca	gtagatattg	tattccgttc	tgcccgctcag	1020
gagattgata	agcaatatca	agaggtccgc	cgtttccgta	atgtcgtgat	tatagcttct	1080
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cgtttgggtt	ccgggaatat	tttctggacg	gcactaagtg	ctgttctggt	cggaaatagta	1260
tttgcatata	ttgtaagtaa	taaattggctg	gaacagtttt	ctgaccgggt	atcagtcaat	1320
gggggacatt	ttcttgcgt	gatcataatt	atcttgttgt	tgatcatagg	aagtgtcatc	1380
gggaggtcct	ggaatgtggc	taatgagaat	cgggtgaaca	gtatcaagaa	cgaatag	1437

<210> 341

<211> 288

<212> DNA

<213> B.fragilis

<400> 341

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aatcttagct	ataatgttaa	ggagtcagat	ttgagacaag	ttatggaaga	gtatggagta	120
gtagaatcag	taaaactgat	cacagaccgc	gaaacaagaa	gatctaaagg	gtttgcgttt	180
gtcgaaatgc	cggaatcttc	agaagcaagc	aatgccatta	aagaattgaa	cggagcagaa	240
tatgccgggtc	gtccgatggg	agtaaaagaa	gctttgccaa	gaaattga		288

<210> 342

<211> 921

<212> DNA

<213> B.fragilis

<400> 342

cctttttaatg	tggatccgct	aattttattca	cttttacttg	tatggtatga	attaaaagtt	60
atacctttgc	gcccgatttt	taatttataa	agattggata	tggctggtta	tatatcagat	120
gacacaagaa	aagtgcagac	tcatacgcta	atcgaaatga	agcaaagagg	cgaaaaaata	180
tctatgctta	catcgtatga	ctacacaatg	gcacagattg	tcgacgggtc	cggtatcgat	240
gtaattcttg	taggcgatcc	cgcacgaat	gtgatggcag	gtaatgtgac	tacacttctc	300

attaccctgg	atcagatgat	ctatcatgga	aaatcggttg	tacgtggtgt	aaagcgtgca	360
atggtagtag	tggatatgcc	ttttggctct	tatcagggtg	atgaaatgga	agggcttgct	420
tcagctatcc	gcataatgaa	ggagagtcac	gccgatgcac	tgaaactgga	aggtggtgaa	480
gagattatag	atactgtgaa	acgtattctg	agtgccggta	tccccgtgat	gggacatctt	540
ggattgatgc	cacaatctat	caataaatat	ggtacataca	cggttcgtgc	caaggatgat	600
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atgttgggta	tgaataacgg	tttccgccc	cgttctctcc	gtcgttatgc	cgatctttat	840
acggtaatga	ccgatgctat	cagtcactat	gtttcagatg	taaagaactg	cgacttcccc	900
aacgagaaag	aacaatatta	a				921

<210> 343

<211> 1332

<212> DNA

<213> B.fragilis

<400> 343

gatgaaaaag	tttggtttat	gaaaatccat	ttaaagttac	tcacagagcg	ctattggttt	60
cgtctcggac	taagcctctg	tttcgccata	actgcggctc	tgtcttatgc	cgacagagac	120
ttcatttgga	tgggattgag	cctctgtttg	ctactattca	gcatttggtg	gcaactttca	180
ctttaccgta	ttcatacca	acgagttctt	ttcatgattg	acgccctcga	gaacaatgac	240
agcgccattc	acttcccga	agagcagata	atgcctgaga	cccgagaggt	caaccgtgca	300
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tattacgaac	tgataatgga	ctgtataaac	accggtgtac	tcgttctcaa	tgaaaatgga	420
gcggtttatc	aaaaaaataa	tgaagcgctt	cgctgctcgc	gattaaatgt	gtttacccat	480
atccgccaac	tgaacaaagt	ggatatacag	ctgatgaaga	aaatagaatt	ctgccgtccg	540
ggagataaaa	tacaaactat	tttcaacaat	gaacggggta	caatcaattt	atccattcgt	600
gtatcaggca	tcaactgttcg	tgaagaacaa	ttgcgcattc	tcgcttttaa	cgacatcaac	660
agtgaattgg	atgaaaaaga	aatcgattcg	tggatacgac	tgacacgtgt	attgactcat	720
gaaatcatga	attcgggttac	tcccatcacc	tctcttagcg	aaacactact	atcgtttggc	780
gatacccggg	atgaagaaat	acgccggggc	ttacaaacaa	tcagtactac	gggaaaaggc	840
ctgctctctt	tcgtggaatc	ctaccgccgt	tttaccgcgt	tcccgacccc	ggaaccatcc	900
ttatttttatg	taaaagcttt	tattgaccga	atggtagagc	tggcacgcca	tcaaaaacaaa	960
tgtgacaaca	taacattcca	tatagatatt	gtcctgctgc	atctgattgt	gtatgccgac	1020
gaaaatctga	tttcgcaagt	agtaattaat	ctattgaaga	atgccatata	agctatcgat	1080
gcacaggccg	atggaaagat	tgaataaaaa	ggacgatgta	atgctgctga	agaaatattg	1140
attgaaataa	aaaataatgg	ccttgccatt	ccttcagata	tagcagatca	tatattcatt	1200
ccttttttta	ccaccaaaga	aggaggtagt	ggtatcggat	tgagcatttc	acgtcagatc	1260
atgcgtctgt	cagggtggaag	catcactctg	ctgcaaggca	aagaaactaa	atttattctg	1320
aaattttaat	aa					1332

<210> 344

<211> 723

<212> DNA

<213> B.fragilis

<400> 344

aacctgatgg	ttatgattat	gaagtgggtg	aatttttaatt	ccattattgg	catggcagta	60
ctatcgtctg	tgtttttacac	agaaaacgtc	gctgcacaaa	ccgacaaaaa	cgataccaaa	120
caaaagatag	ataccatcca	gacaacacag	ccggaatata	gcaaatatga	caaacgtatt	180
caccgttttc	gtaaagggat	gaattcactt	atacctacac	acaacaaaaat	acaatatgcg	240
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gaaacggatc	tgttcttcgg	cttcataccc	aaacatgact	cccatcgggc	taagatgacc	360
atgaccttaa	aacaaaatta	catgccttgg	agcctggagc	ttgggaaagg	atthttcaacc	420
gaaccttttg	catgtggtat	ctatthttta	actgttttcg	gacacgaatt	ctgggtacac	480
gagcctagcc	gttatccgga	aggatactac	gatttctcgt	ccaagatacg	cacacacatc	540
tttctgggac	aacggctgac	atacgatata	gatagagaac	gccggttctt	tgcaaaatct	600
gtgactctct	tttatgagct	gagtacctgt	gacctattat	tgatcagccg	cgtaaccaac	660

agttacctgc gggctcggga ttatctgagt ttatccttcg gacttaaatt ccaatggctt 720
tag 723

<210> 345

<211> 255

<212> DNA

<213> B.fragilis

<400> 345

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aatgagttcg	ctcattcaca	gtttgtattg	gataatgatt	attttctttt	tactattttcg	120
aatggtacac	gtattgaaac	gccttttttc	attaagttat	tcagattggg	atataaacgt	180
tctttgaaag	aatcccaatt	gcgatgttcc	atttgggtcc	atcctgcttc	tgccagtgcc	240
agaccgcggg	gatag					255

<210> 346

<211> 1269

<212> DNA

<213> B.fragilis

<400> 346

ttgtcttttt	ctctctttta	tcgtaatcat	ttagtagctc	gttcgggatt	tattggaaga	60
aaagtagtat	ttttgcgtca	ttatatctta	aaatattcaa	tcataagaa	aatactttta	120
ctcggatcgg	gcgaattggg	caaggaatth	gtaatttctg	ctcaacgtaa	aggtcaacac	180
atcattgctt	gtgattcata	tgccggggca	cctgccatgc	aggttgctga	tgaatgcgaa	240
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attatcgctc	ccgagattga	agccattcgt	acggaacgtt	tatacgattt	cgaaaaagaa	360
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ttggaagaac	tgaaggaagc	cgctgagaaa	atcggtttcc	cttgtgtcgt	gaagccttta	540
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tacttttcgg	aactgtctcc	acgtccacat	gatacgggaa	tggtgacatt	ggccggaaca	960
caaaatctga	atgaatttga	acttcaccta	cgtgccgtat	tggggttgcc	cattccggga	1020
ataaaacaag	aaagaatagg	agcgagtggc	gttattctgt	cgccgattgc	cagtcaggaa	1080
cgtccgcagt	atagaggtat	ggaggaaagt	accggagaag	aggatactta	tctgcgtata	1140
tttggtgaagc	cgtatacacg	tgtgaatcgg	cgtatgggag	tagtgctttg	ctatgctcca	1200
aacggttcgg	atctggatgc	tttgcgtgat	aaggcaaagc	ggatagccga	taaagtagaa	1260
gtatatataa						1269

<210> 347

<211> 645

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (97)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 347

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gtaatcaatg	ggcatgaaat	cgttcagaac	tttcgnttgg	atcagtataa	agggaaaaaa	120
tacgtagtat	tcttcttcta	ccgatggac	ttcacttttg	tatgtccac	cgaactgcac	180
gcatttcagg	aaaagctcga	agagtttgaa	aaacgtgatg	tcgctgtggg	aggttggtcg	240

gtcgactctg	aatattctca	cttctcttgg	ttgcagatgc	ccaagaacga	aggaggtatc	300
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gtgctggccg	gaagctatgc	ccccgatgaa	aatggcaatt	gggtatgcga	agggacaccg	420
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aacgacttgc	cgctgggacg	taacgtggat	gaagtattgc	gcatggtaga	cgctttacaa	540
cattttgaaag	agtatgggtga	ggtttgtccg	gccaattggg	cgaaaggcaa	agacgccatg	600
aaagctaccg	aagacggagt	agccaactat	ctgagtaagc	attaa		645

<210> 348

<211> 234

<212> DNA

<213> B.fragilis

<400> 348

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atacgggaata	aaagacatta	ttacgtatta	aaaaagtctc	ttaaataattt	gccattttaa	120
aataaaaggtt	taccttttga	cccgaatca	agaacgcttg	atggcaatgc	actcttagct	180
cagctggtag	agcaattgac	tcttaatcaa	tgggtccagg	gttcgagtcc	ctga	234

<210> 349

<211> 900

<212> DNA

<213> B.fragilis

<400> 349

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cagataaatg	atgattgtta	ccgagttccg	gaaagttggg	atgaactcac	cgaaaagcaa	120
ttgagctacc	tgggttaatct	tacacaaagc	gatattccca	tcgaagaact	gaaggtagac	180
atgatgctat	attgtctcaa	tgcacatggt	tgccggtatc	gggatatcta	tcgccatcaa	240
gtaaagatca	gcattgggac	tcccggcaat	aaaatccctt	tccggacaca	caagaagaaa	300
tattttgcttc	ttcctgaaga	agtcaatcgg	ctggccaaac	tcttcaactt	tctgttgatg	360
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cgcttcgaac	agttcatgca	cctgcaacac	tatcttgacg	ccataaatca	ggacccggaa	540
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aatggaaaga	gtaatggctg	tgtctttgat	tcgcaaatgc	gtcttttaga	ctccctcgca	780
cagtcagaca	tgaccaaaaa	gcctgaaata	aaaaaaggat	tcctgatoga	tgccctgtat	840
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<210> 350

<211> 498

<212> DNA

<213> B.fragilis

<400> 350

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gacttatata	attttaatga	taaactatca	tccgtatccg	gcatgatcct	gattgcagtt	180
gatggttgtg	aatctgaatc	aaaacgaaac	gaatccgatg	cgcttaataa	caatgatata	240
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gcaaaagaat	gcaaagctat	cgcaaaacaa	attcggaacc	atatcctgca	agaccccgcg	360
atttcagaat	tcattgacga	taccattcaa	tttaatggta	ttgggcccga	tggtgataat	420
ttctatggcg	tagtactgac	attttctttg	gttcaacctg	aaacctattt	cattgatcaa	480
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<210> 351

<211> 204

<212> DNA
<213> B.fragilis

<400> 351

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<210> 352

<211> 714

<212> DNA

<213> B.fragilis

<400> 352

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tttacattta	taaaacaaga	ctgcaaagaa	gagaaattat	taacagaagt	ttctcgccac	660
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<210> 353

<211> 480

<212> DNA

<213> B.fragilis

<400> 353

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cacaaaggaa	gcaaactgta	tattgaagcg	agattcacaa	cccggaaagta	tgaacaaat	360
gacggccaga	aacgaaccgt	ttctgaaatc	gtagccgaaa	gtattgaaat	gctcgatccc	420
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<210> 354

<211> 609

<212> DNA

<213> B.fragilis

<400> 354

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609

<210> 355

<211> 1260

<212> DNA

<213> B.fragilis

<400> 355

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<210> 356

<211> 471

<212> DNA

<213> B.fragilis

<400> 356

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<210> 357

<211> 312

<212> DNA

<213> B.fragilis

<400> 357

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<210> 358

<211> 312
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<400> 358

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<210> 359
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 <212> DNA
 <213> B.fragilis

<400> 359

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<210> 360
 <211> 969
 <212> DNA
 <213> B.fragilis

<400> 360

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<210> 361

<211> 789

<212> DNA

<213> B.fragilis

<400> 361

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<210> 362

<211> 3750

<212> DNA

<213> B.fragilis

<400> 362

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<210> 363

<211> 462

<212> DNA

<213> B.fragilis

<400> 363

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tattgttatt	gccatgagag	atatacccat	gaacctaaaa	atgatgaaga	gatgcaaaaa	420
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<210> 364

<211> 1098

<212> DNA

<213> B.fragilis

<400> 364

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<210> 365

<211> 351

<212> DNA

<213> B.fragilis

<400> 365

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<210> 366

<211> 1299

<212> DNA

<213> B.fragilis

<400> 366

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 <211> 969
 <212> DNA
 <213> B.fragilis

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 <211> 192
 <212> DNA
 <213> B.fragilis

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<210> 369
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 <212> DNA
 <213> B.fragilis

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<210> 370

<211> 3057

<212> DNA

<213> B.fragilis

<400> 370

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<210> 371

<211> 840

<212> DNA

<213> B.fragilis

<400> 371

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<210> 372

<211> 342

<212> DNA

<213> B.fragilis

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<210> 373

<211> 222

<212> DNA

<213> B.fragilis

<400> 373

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gaaatagctg	ggtatgacta	taaacaagat	cagaaaggat	ctaatatgaa	attaagaaaa	180
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<210> 374

<211> 1080

<213> B.fragilis

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gttgtggaaa	aaacttttcc	atatcataata	attatgtcca	cggtagctaa	tacgaaggat	900
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ggtgacggta	agattcgcgt	gagttattatg	tcatgtgccg	atcgtgaaga	tgccaaccgt	1020
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<211> 2025

<213> B.fragilis

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gtgggtactga	atacagataa	cataattttat	ggaggaaacg	gcttgtcaga	tgatagtgtg	1920
aagcattttca	cattgccccga	tcctttgtat	aagaaagaaa	agaaagaatg	gttgaaactc	1980
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<210> 376

<211> 1146

<212> DNA

<213> B.fragilis

<400> 376

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ctggatggcg	gtgtttatct	caaaaatgat	aataattttg	gtaatggagt	tgaattcagt	180
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agtataaaag	agatcagccg	caaaaacttt	agtgtttttc	aaggacgatt	tcaattcatt	1140
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<210> 377

<211> 516

<212> DNA

<213> B.fragilis

<400> 377

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ccctctcttt	tatctgaaat	cggaccggcg	gatataagga	tgcctacatt	cagtatctca	180
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aaatatcagt	tccgtattgc	cggttccgcg	aacctaaacc	agaatcaccg	ctgggaaaat	420
ggattctatt	tcacttcccg	aaagcatttc	aattacttct	tggaaatgtt	cgagcaggca	480
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<210> 378

<211> 582

<212> DNA

<213> B.fragilis

<400> 378

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aaatggatga	cccttattaa	ggaagatatt	tcgggtagga	aattgggtgt	aatccgtgat	180
caggcattcg	attcggaggg	aactgtggag	atttactctc	gcgaagtgac	tattaagaca	240
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aatggtgctt	atcgtggatt	attagagcaa	aaactgttgc	catctatcac	ccctaaagag	360
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cgggaatatg	ctgaagataa	tcttaaactg	aagaaattca	gacgtgagaa	ttttaatgaa	480
aatcgtacgg	gggtagctcc	ttttgatcat	ccaaagaaag	tatatgatga	attcattaag	540
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<210> 379

<211> 1227

<212> DNA

<213> B.fragilis

<400> 379

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ttaattgcat	taagtgtatc	tcactgttta	aatgatcttt	tgcaatctgt	catttcggct	120
gtatatcctc	tttttaaaga	agatctttcg	ttaagtttcg	ctcagattgg	attgataacc	180
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tcgtctgttc	tccatccgga	agcatcccg	atcacctttt	tggttcggg	agggaaaagg	420
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<210> 380

<211> 195

<212> DNA

<213> B.fragilis

<400> 380

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cggaaatgtt	tccttagaac	cctgcagata	gtgaacaaga	ttcatgtatt	cacactgggtg	180
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<210> 381

<211> 2484

<212> DNA

<213> B.fragilis

<400> 381

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aaggagtttc	aggcatttgg	ggaaacctgc	aaggatttga	caatacgata	tattaaatca	540
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aaagaggtct	ttgccattgc	actgactcaa	gagaagggtg	ccgatgccat	tgatttatcc	2460
gtaaagaaa	ccagccagga	atga				2484

<210> 382

<211> 198

<212> DNA

<213> B.fragilis

<400> 382

cagattatat	acataacact	aaatatcgga	tgccggttat	ttttgttatc	caaagatgaa	60
aaacaatcgt	taaatatattga	attatctcgg	gaagaaatag	aatatttctt	taaaccttat	120
cctgcagatg	agacggaggc	atacgagata	tgcaatgatt	ttataaagaa	aatatcaaca	180
gataaaaagta	ttctgttaa					198

<210> 383

<211> 213

<212> DNA

<213> B.fragilis

<400> 383

tatataatat	attatcagcg	ttttattttg	ctttgggagc	agggggtcgt	gggttcgaat	60
cccgtacccc	cgacaggaaa	taagagtaat	cacacatgtc	aatgtgggta	ctcttatttc	120
atttttgtgct	atggtggaat	tccgataata	cggaaatgatg	caactggaac	agagcgacgc	180
cttttacatt	ttcaaataaa	actcccggtt	ttaa			213

<210> 384

<211> 696

<212> DNA
<213> B.fragilis

<400> 384
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 agccaaatag atgccttccc tgttttaaaa gcacgacttg gcaaaagtct gccacaattt 120
 gtttatactc taagtcogga taaacagact gctactctgc aaataatgaa cttatatcaa 180
 ttaccacaac taaaacaatt ttgtgactca gtcttttcgg tgattaacag agaacatgta 240
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 cttctgtcat acttatcgca tgatgcttat acattatata tcaaaactga tttaaaaatc 360
 agttcgtact caaaacggta caatgagcaa aaacatccgg aaacctatga agagatcaaa 420
 aatttacctg acggttcttt atttgctatt cgggattctt tcgtagaggg aaaccgggac 480
 aaagcagaca ttataaaagg atcagttaca gtattggtaa atgaatccac ttattccgga 540
 gcctcgacat ttgcactctgc cattaataaaa tctcatgcag gaaaagttct tggcgaaacc 600
 ggctgcccaa ctgtatatatt tggcaattac atgtcattca cattacccaa ttcccatta 660
 gaattattata tctcactcaa caaattttat gaataa 696

<210> 385
<211> 552
<212> DNA
<213> B.fragilis

<400> 385
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 aagcaattca gtattcgtct ggggaagagt aagatgaagg ctctcgttaa ggaagagaaa 180
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 ggtacagata ttaatactcc gattgaaacc ggtgatatga gtatggacag acgccactgc 360
 attattaatg tgaagcgtaa cagacaagga aaattggttt atactcttcg tgatgccccca 420
 agcctgaccg gaactttctt gatgaacgag atcttggggg ataaagaccg tattcgcat 480
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 gaagaaattt ga 552

<210> 386
<211> 210
<212> DNA
<213> B.fragilis

<400> 386
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 cttcatgaag gaaaggccac acccaatatc tattataacg tttttgccga tggtagcag 120
 ctctgcgaaa tctcctatga cagattaatc gctatacgtat atcttattaa ccaaattgag 180
 aaagaaaaga aaggagaatg ccatgaataa 210

<210> 387
<211> 513
<212> DNA
<213> B.fragilis

<400> 387
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 agtgattata gatttgagaa aacattatcc ctatcaaaag ggtacataaa taaagctaaa 120
 aatccaaccg cggatatatt aatgaagatg tgtggtatat ataccgacat atctactgaa 180
 tggctgctta gaggtgaagg tgagatgttg agggagaaaa gagaagacct tggccttcat 240
 cgggctgagt cagcatctac agatgaaaac tctttaatct ataagatgta taaagagaaa 300
 gacgatgaaa ataaaaccct aatcaagcag aatgccgttt tagaggaacg catccgccaa 360
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 ttttccgac taccattagt agactacgaa gaagattatc cgcccgtaga acgtccttca 480

agttccaaac atccgtagc aggaaaagcg tga

513

<210> 388

<211> 579

<212> DNA

<213> B.fragilis

<400> 388

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ggatatacat	ggacaattgt	ttctcgttta	ggcgatatgc	ttaacgaagc	tgaagcccta	120
tttgggtgaac	gagataaaaag	atatacaata	cttgggtattg	agttagctaa	tataaaacaa	180
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tatgaatttt	gttctaaatt	actaaactat	gattctgagt	tgattaaaaa	agcaagaata	480
atagaacctg	acattttcttt	tatcaacaaa	gagatattac	taaatatatg	tcctaagata	540
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<210> 389

<211> 333

<212> DNA

<213> B.fragilis

<400> 389

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gtattttgata	agggtgtgtat	aggatctctt	ctatccatcg	actatagact	actctacact	180
ttatcatttc	tacattcatt	attgggttga	ggctttccga	tagatttaat	ggcgggttcgt	240
ctggccaaaa	aacagcacgc	gtctggttca	ttcgctctgt	gtgataatcc	aaattatata	300
ctactcctct	ctctatacgt	atcgtttcaa	taa			333

<210> 390

<211> 246

<212> DNA

<213> B.fragilis

<400> 390

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accgatgaat	ttttccgttt	catcaccacc	cccactccgg	aacgggaaga	gttcctggca	180
ttgtactgct	cttcgacctc	ttctgtgtcc	ggtaccatta	tacaaactaa	ttacaatgca	240
ctatga						246

<210> 391

<211> 321

<212> DNA

<213> B.fragilis

<400> 391

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ctgcctgccg	gtgaacgcag	ctacttctgt	gatatttgca	gaaatcatca	tcattctcct	180
atctacgaag	cataccatca	gggacgcctg	caaacaaaat	tcgaactccg	aaaaactgtg	240
atcaagttag	ccaaggccgg	aagtccggcg	gccgagccac	ttgctgataa	atacatgaaa	300
gaacaaatca	tcaacgacta	a				321

<210> 392

<211> 201

<212> DNA
<213> B.fragilis

<400> 392

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gcagaggact	gtttatggga	gatcgactc	ttcagtaacg	gattcgttta	tcacgctctg	120
cagaagttcc	ggatctttat	agaggaaaag	gactttaacc	ataccgtcct	ttacaactcc	180
catttccatc	tcaattttcta	a				201

<210> 393

<211> 1125

<212> DNA

<213> B.fragilis

<400> 393

aaagagtgtc	aacaagacta	taaattttatg	agaagcaatc	ggttttattaa	acgcctggac	60
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attgcagtag	tattcgactt	caacgagaag	atggataagt	ttatggaacg	gagtgcgccg	180
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agtcggtgtg	ttgtatttat	tgctgtcata	ttcttcacct	ctaaactggc	tgaaaactcc	300
gagattattg	caatgttttc	taccggatg	agtttttaac	gtatgttgcg	tccttacctg	360
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gattacaata	agacaggaaa	cggtttttcg	ctggataaat	tcgtagataa	gaaactggta	600
tcccatttga	ctgcccgtag	cattacttat	gatactactg	cggttaataa	atggaccatt	660
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catttgggaa	taggacttgg	actgagcttt	tcatatatcc	tgttccagac	cgtggcatct	1020
acttttgccg	taaatggaaa	tatgcctccg	atgatcgcca	tgtggattcc	taatttactg	1080
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<210> 394

<211> 246

<212> DNA

<213> B.fragilis

<400> 394

ggtttaagtc	atcttcattc	ttttttatct	tccattttcg	gatttgggtct	tgcgggcgtt	60
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gccagtgtga	atgcacatta	catctgggtat	tactttgcgg	caatcggttt	ggttgcagca	180
attgctttgc	ttatttttgc	aaaaatcact	gatttcatcg	ataaaaagaa	gaaaactaac	240
gtctga						246

<210> 395

<211> 1521

<212> DNA

<213> B.fragilis

<400> 395

aacaacaacc	aacgtatgat	gaaccaagaa	ttattaatga	gtcccaaccg	tttggtgact	60
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aatgaaatcc	gcatgggtcaa	ttttatgtat	cctgctgcgg	atggacggct	aaaaactctg	180
aattttgtga	taaacaatgc	ttcctatctg	gatgccatcc	tgacttgcgg	tgaacgggta	240
gatgggtcga	gtctgtttcc	tttcatagaa	gccggaagta	gcgatctgta	tgtaatacca	300
cgttttcgca	ctgcattcgt	cgatccgttt	gcagaaatac	ctacactcgt	gatgctttgc	360

tccttcttta	ataaagatgg	ggaacctttg	gaaagctctc	ccgaatatac	tttgcataag	420
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gtagagatgc	gttcaccgga	tggtctagcc	gatctttatc	aattattggc	aggtcttgca	1200
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gttaatgtaa	atatccatca	gaaagaaaat	gcagacaagt	tgaaagcttt	agcccaactt	1320
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tacaatgtat	tcagtcctgc	tatgatcgat	ggtattatca	gtcgattacg	aagctataat	1440
gatgccactc	tacgcaaaga	tatacaggac	aaaccggaag	agatgctggc	actggtgagc	1500
aaattcttcc	attgtggata	a				1521

<210> 396

<211> 570

<212> DNA

<213> B.fragilis

<400> 396

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gtaaaaaata	atattaaacg	ttttccatca	gattttatgt	ttgagctaac	gaaggaagaa	180
ttcgacagtt	tgaggtgcag	tttttagcacc	tcaaaaagag	gcgggacccg	atatatgcct	240
tatgctttca	ctgaacatgg	agttgctcaa	ctttcttcag	ttcttaacag	cgatttggca	300
attgagatta	atattcaa	cataagggca	tttatagcag	ttcgtcagtt	aatctccaat	360
cctccggttg	atagagtcca	taaactgaaa	gaagaaatca	aagcattaaa	agattacatc	420
gaagaagcat	ttactgacta	caacgatata	aatgatgata	cgcgcagtca	attggaatta	480
attaatcaaa	ctttggcgaga	attgcaagcg	aaaaagaaag	cggaagaaaa	acctcgtaac	540
ccaatagggt	ttatcaaacc	taaacactaa				570

<210> 397

<211> 231

<212> DNA

<213> B.fragilis

<400> 397

caaaaacgcc	actccggaat	agaccagatt	gtctgctgtc	accaggtact	cttctttgtg	60
atggacaaga	ccgcagaggg	ctatgatgaa	agcacatccc	aatacggaa	aggagaacat	120
atagacgggtg	acatggggaa	taaaccaa	actttgcaaa	gccggcataa	gcgactggtc	180
atgtatctcc	ggtttcagca	gattgattat	tacaaagaca	gtggacaata	a	231

<210> 398

<211> 1002

<212> DNA

<213> B.fragilis

<400> 398

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aaactggctg	gagcaggaaa	agcatttctg	tttattatag	attataaaca	agaatgttct	120
tttatagaga	aagtggatga	tattgattca	tcggagctac	tctacaatct	gaacgggttt	180
acaaaactgca	cgtctgttgt	tacaccttcc	agatacccaa	taatattggca	gccccaacct	240

atttcttttaa	gccaatataa	aagatcgttt	gatattatac	ggaaaaatat	cttgagtggg	300
aatagcttct	taacgaatct	cacttgcatt	acccccgtca	acactaatct	aggggttaaaa	360
gatatatttt	atcattctcg	ggccttatac	aaactttggg	tgaaagagac	ttttgtcggt	420
ttttctccag	aaatatttat	togtatagaa	aatggaagaa	tcagttctta	tccaatgaaa	480
ggaacaatag	atgcaacttt	accttctgcc	acaagattac	tgatggagga	tgaaaaagaa	540
gcagcagagc	atgccacaat	cgttgatctg	atacgaaatg	atttaagtat	agtggcagat	600
aatgtatctg	taaccgcgta	togtatgta	gatacactct	ataccaatca	tgggtcccata	660
ttgcagacca	gctctgaaat	aagtggaggt	ttaccgaaaa	actatgttga	tcatctggga	720
gaaattcttt	tcagacttct	tccagccggg	tctattacag	gagctcctaa	gtacaagaca	780
atagaaataa	tagagcaagc	agaagaatat	gagagaggat	tctatacagg	catcacggga	840
tactttgacg	ggagaaaact	ggatagtgcc	gttatgatcc	gctttattga	agagcagaat	900
gggcaaatat	tttttaaaag	tgggggagga	atcacctgca	aaagtgattt	ggaaaatgaa	960
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<210> 399

<211> 537

<212> DNA

<213> B.fragilis

<400> 399

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ctgtgtgctt	gtcgttcttc	ttctctacat	tctaataaat	tcaaagagaa	tggaactttt	120
cagcataatt	acaatgaact	caataccggg	accgggacca	ttgcctcaca	agtcaaaacc	180
actaaagacg	aacacgggtc	atcctggaag	atcacgtacc	attttgacac	ggcacaaaaca	240
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cagagtaaaa	ccgcgcagga	aagtaatgac	actgtacact	cttcgaacag	ctcttcaaag	360
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aaagtagcaa	ccgggtacgga	tgatggcata	agaaacggcc	tcagtatcgg	gatacctttg	480
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<210> 400

<211> 828

<212> DNA

<213> B.fragilis

<400> 400

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ttatttcgtag	catgcaataa	tggcaaagga	caacagccct	ctgaagaaaa	tgaagacccc	120
aaggccaaag	agattctcca	aggcatttgg	cttgatgatg	aaactgaaac	tcccttgatg	180
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cagagtgaat	attctttttg	gttccattct	ctggctgata	atattatcaa	gotccataag	360
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tatacagaag	tactaagaa	ggacagtgtg	gtaatgttcg	atggcggtccg	ctacagagcc	480
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atcagtatgg	acaatatatta	ctatgacaat	gtaatgcata	tatgtgtgta	tgaaggcaaa	600
aaaagtttat	atgccaagga	cattaccaag	caaagtgttg	tagatgtaat	tccaacagat	660
tttctgcaac	aggccattct	atctgatatg	aattttacag	gaattgaccg	caaaggctat	720
cattatcaag	cactcgtctg	tattccggaa	agtcgggtat	gcaatcttgt	gaatcttacc	780
atcagtttgc	atggaaaact	aaatataacg	gctgcaaaaat	ataaataa		828

<210> 401

<211> 381

<212> DNA

<213> B.fragilis

<400> 401

aatcatttta	atactttaaa	ttatttaatt	atgggcttag	atatagcaat	tgtttcagct	60
gtagttgaga	ttattacact	gatttttttc	ttcgttttat	gtcgaaatgt	ttccaaaatc	120

aaaaaagaga	ttgttagcaa	tgacaattta	cctggatatgt	ttgccatgta	tatatccttg	180
ggagaaacgg	acaaagcaaa	aaaaatattg	tataaggcga	ttagtaaaga	accggaattt	240
atcgcagcat	tctgctacaa	tggcaataat	tcagcacagc	aatctacatt	gaaaagaaaa	300
tataaaccat	acttggaaat	ccttggactt	gagttagatt	ttgaattggt	aaataagttc	360
atccaagaaa	gagaaaagtg	a				381

<210> 402

<211> 1413

<212> DNA

<213> B.fragilis

<400> 402

gtaatcatta	agaatagaat	attaatcatt	ccggcttttct	ttcttcttcc	caaaagaaga	60
agaaagggca	aagcccctaa	aatttttaaat	aagatggcaa	caaaagagta	cttcccgggt	120
atagggaaaa	ttaaatttga	aggtaaagac	agtaagaacc	cgatggcatt	tcgctattac	180
gatgccgaga	aaatgattaa	cgggcgtagt	atgaaagatt	ggttaaagtt	tgcaatggca	240
tggtggcata	cactttgtgc	cgaaggcggg	gaccagtttg	gaggcggaac	caaacagttc	300
ccatggaacg	gtgaccctga	tcccgtgcag	gctgccaaaga	ataaaatgga	tgccggtttc	360
gagtttatgc	agaaaatggg	catcggtgat	tattgcttcc	atgatgtcga	tctggttacg	420
gaagccgaca	gcatcgaagc	ctatgaggcc	aacctgaaag	agctggttgc	ttatgccaaag	480
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acggatcaat	ttccgattga	caacttcgaa	ctgacacaag	ccatgatgca	gattatccgt	1080
aacgacggat	tgggtaacgg	cggtaaaaac	ttcgatgcca	aaactcgccg	gaactctact	1140
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gaaagtgcag	ccaatctgct	caatgagtct	ccttaccaga	aaatgttgtc	cgaccggtat	1260
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ctggttgcct	atgccaaagc	caacggagag	ccgaagcaga	ccagcggcca	acaggaactg	1380
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<210> 403

<211> 597

<212> DNA

<213> B.fragilis

<400> 403

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actttgggtg	ctgccatttt	tctcagtggt	actatcctat	ttagttcatg	tgtaggatca	120
ttcggactgt	ttaatcgtat	ttcttctctg	aaccagtcta	ttggtacgaa	atttgtaaat	180
gaacttggtt	ttcttgcttt	aaatatcggt	ccggtatatg	gcgttgctta	tctggcagac	240
gctttgggtta	tcaattctat	tgagttctgg	agtggcacca	acccgatggc	taatgtaggt	300
gatgttaaga	aagtgaaagg	tgagaatggt	gattatttag	taaagactct	tgaaaatggc	360
tattctatta	ctaaagaagg	tgaagattca	gctatggagt	tgatttataa	taaagaagca	420
aataacttgg	atgttggtgc	cgatggaggt	agcacagagc	tattgaaaat	gaacaatgac	480
ggtactgctg	aaatgaactt	accgaatgga	gataaaatga	atgtaactct	tgatgcacaa	540
ggtatgatgg	ctgcacgtca	ggctacaatg	ggcggactgc	tctttgctgc	acgttaa	597

<210> 404

<211> 1533

<212> DNA

<213> B.fragilis

<400> 404

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tcggtcaagg	cgagcctggg	agatgcagaa	acaggtaaat	gtgtcgcttc	tgcgttcttt	120
ccgaaaacag	aggcgggcat	cattgccata	cgccccggat	gggcagagca	agaaccggaa	180
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gccaaagaca	tcaaagccat	cggcattctc	tatcagatgc	acgggtctgg	gtgtgtggac	300
aaacggcaac	gcacactgcg	tccggccatt	atctgggtgcg	attcacgtgc	ggtctcctat	360
gggcagaggg	cattcgaggc	aatcgggtgag	aagttctgtc	tggcacattt	gcttaattct	420
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gaacgaatgc	tgcataatcg	ggcaaccggg	tgcggtatac	acggcgtaga	cttcaacagg	1140
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ggcatcgaca	ttatggaaga	gatgggcatc	ccggttaaaa	agatccatgc	cggacacgcc	1260
aatatgtttc	tgagttccgt	ttttcgcgag	acactggccg	gtacgacggg	agccaccatc	1320
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atatataaag	accatgaaga	agcattcgcc	actctcgata	agctgacagt	cgtagaaccg	1440
gatgccggca	aacaacagga	atacactgat	gcttacgcac	ggtggaaaca	atgtctgact	1500
cagtcctatgc	agacagaaac	agagaataag	taa			1533

<210> 405

<211> 255

<212> DNA

<213> B.fragilis

<400> 405

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agggtgccat	tagggcagat	tgaaagttta	aaaaaagaac	tgtatagtgt	ctttagtatc	120
aataatcgaa	cctcttggtg	caataaaact	aaagggtataa	cttctcccag	catagaagta	180
ggtgaagctg	ttgagactgt	atttctaaaa	tatggtattg	aaaattgttg	ggaaattaca	240
gagatcaaat	tatga					255

<210> 406

<211> 237

<212> DNA

<213> B.fragilis

<400> 406

tcagaggata	accaatccca	tatctattta	ctttgctttt	ccagatctct	gacagccgga	60
atgcacatca	tcaaaattga	ggtaaataca	attgctatcc	cacaacagat	aaaaatattg	120
gctattccta	aactatcagc	aataaaatccg	gtaatgaaca	acccaatgat	agaaggcaat	180
aagctcacgc	tgtcaaaaaag	agaaaacaca	cgtcctaaat	atgccgggtt	aaactga	237

<210> 407

<211> 1158

<212> DNA

<213> B.fragilis

<400> 407

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agtaatgccc	gtgccgggtct	gattacaaca	gaccacgggc	aaatacaaac	ccctatatatt	120

atgccggtag	gtacaatcgg	cagtgtgaaa	ggagtacatc	agactgaatt	gaaagaggat	180
attcaggcac	agatcattct	gggaaataca	tatcatcttt	atttgccgcc	gggactggat	240
gtactcgaag	aagccggtgg	attgcataag	ttcaatggat	tcgaccgtcc	gatgctgacc	300
gatagtgggtg	gttttcagggt	gttttcctttg	tccggtatcc	gtaaattgcy	tgaagaaggg	360
gccgaattcc	gttcgcataat	tgatggcagc	aagcatatct	ttactcctga	aaagggttatg	420
gatatcgaac	gtatcatagg	tgccgacatc	atgatggcat	ttgacgaatg	cccaccgggg	480
gattcggatt	atgcatatgc	caaaaaagtc	ttgggattga	cacaccgctg	gctcgacaga	540
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atcgtgcaag	gatgtgtata	tcccgcacctg	cgtaaacaat	ctgcagaata	catagcttcg	660
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tacgagatga	ttgagttggg	gaacgagata	cttcccaagg	acaaaccacg	ttatctgatg	780
ggagtcggca	caccgggttaa	tattcttgag	ggatattgaac	gtggagtaga	tatgttcgac	840
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aacatgcgta	ataaaaaatg	ggaagcagac	ttctctccta	ttgaagctga	cggtgcttcg	960
tatgtagaca	cattgtacag	caaagcatac	ttgcgcattt	tattccatgc	gcaggagttg	1020
ctggccatgc	agattgcgtc	tatccacaat	ctggcgctttt	atttgtggct	ggtaggagaa	1080
gcacgcaagc	acattatcgc	aggagacttt	tcaacctgga	aacctatgat	ggtgaaaaga	1140
gtgtcaacaa	gactataa					1158

<210> 408

<211> 1068

<212> DNA

<213> B.fragilis

<400> 408

ctaaaaagta	aaaaacagggt	aatgaaaaag	tttttccgat	ttcaattatg	ttgtatttgt	60
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tcggagatgg	aaaattttatt	atacgattat	cacattgcca	aagcgatggg	agagaacatg	180
cctggtgggtg	agaactataa	aaaggcattg	tacgtcgaag	cagtattcaa	aaagtatggg	240
acaacagaag	aagtttttcga	ctcatcaatg	gtatgggtata	cccgaatac	aaaaatatta	300
tcggaaatct	atgagaaagt	gaacaaaaga	ctgaaagcgc	agcaaaatgc	catcaaccat	360
ctgattgcat	tacgtgacaa	taaacctaag	atgtctgctc	cgggtgacag	catcgatggt	420
tgggcatggc	agcgaattgc	tcaattaaca	gaggctccat	taaacaataa	atttacgttc	480
actctacctt	ctgatacgaa	cttcaaaaaa	cgcgatgtgt	tgctttggaa	aatgcaatat	540
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tatgaaaacg	acacagtgac	ccatagttgt	gtgaagcaca	tttttaaatc	tggcattcaa	660
aatattcgtc	tccaatcgga	tacaatgaat	atcaaggaga	taaaaggatt	tatcttttgt	720
ccgctatctg	aggaatcaat	aacacttctg	gtcagtgata	tttcattgac	ccgttatcat	780
gcaaatgatt	caataacaca	gataggtaga	gattctctaa	aaactgattc	aataaaaagaa	840
aaaagtaaa	acgattctat	tcagaagaaa	actcccaaag	acactattca	agcatcatca	900
ccccatcaac	gtacgaatcc	gaacgatctg	aatcgtccta	ataatgatgt	ccggcctatt	960
aaaccggaac	aacgtgaaaa	agagatgcag	atagaaaaag	agaaacagca	attggaaaaga	1020
caacaaagga	ccaatccaag	gaggccatta	cgtcgtcaga	ataattaa		1068

<210> 409

<211> 183

<212> DNA

<213> B.fragilis

<400> 409

ctcttaaatca	atgggtccag	ggttcgagtc	cctgaggggtg	tacaaaagga	gattataaat	60
aatctccttt	ttgttttttg	tggcattttg	aaatattgtt	ttatctttgc	caccgcaaaa	120
attaatttga	tgaaaacaac	ttatcagttt	aacatactcg	tcaatcattt	ggagctggct	180
tag						183

<210> 410

<211> 402

<212> DNA

<213> B.fragilis

<220>
 <221> unsure
 <222> (276)
 <223> Identity of nucleotide sequences at the above locations are unknown.

<400> 410
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 tttgatttaa aagcgttttag aaaacgattt ggtttaaaac aggttgaagt ggctcattta 120
 ttcaattgtg ggcagagcaa tatttcagat attgagactg gaaaaagagg gcttgaagag 180
 tatcaaaca gaattctctt cgataaatac ggagaagagg tagttaaaga gtacttaata 240
 cctgagagtg ccattcatca agggaaatata aacgngata atataaacgg gcacaatgtc 300
 actgtaaata aagcagactt tgataaactt attagcttgt taaacaaaag ggatgaacaa 360
 atagatagat tattgcgtat tattgaaat ttaataaat ag 402

<210> 411
 <211> 621
 <212> DNA
 <213> B.fragilis

<400> 411
 gagaggaaca atattatgac attaaagcaa gctcagaac tgtacgatga ttcagtgcag 60
 gcaaaaatga ctcatgccga ttattgcatg actcaatcgc aacttgaata tatcggtaga 120
 actatgtggg gattcacccc agacaaacaa gcaaaggtgt tattcaccaa agtaggaaag 180
 aggggtgtcg tagttattgc gtcacgagaa gcatttatta aagagatagg aaaacctgtt 240
 atctgcaaat gttcgggtatg cgatatgtat tatttagctt atagaaagtc ggtcgtatgct 300
 cacgatgaat taaatgcccc atgtccaaaa tgtgattctc ttggttgtga ttcagatatt 360
 gtacattttg aaacaagccg caaatttttg ctaaacgaga agatcgtaa aatccttact 420
 cccaataaag accctgaacg agtggaagct atgtacgatt ccgctccgga agattttcct 480
 gcacaatatg agatgtttgct tcccgatgga aagaggtgta cagattgtgt gcgatgtgcc 540
 acatgttgca gcgtatttgg tcaaaaagaa agtgccacta tttgccagtg gcacccctcg 600
 agatattcag cgggagaata a 621

<210> 412
 <211> 690
 <212> DNA
 <213> B.fragilis

<400> 412
 cattcactaa atagctttta taccacatgt ctaattttta aacggcaaaa catgaaaact 60
 ccatctttta ttctgatgac aattatttta tgtaatctca gtatcccaat aaatgctcag 120
 atactaacct cccgccagca aaaggaagat tttagacct tatatagctt actacatcag 180
 gtacatccgg acttatttgt gtatcaaaca caaaaagaat ttgaaaagaa acatgattca 240
 atatatagtt cgttgaataa agaacgaaac ctttctgatt ttactttat agtctctcca 300
 tttgttgcac ctgttaaaga tggtcatact aatttcacaa ttcttgctac tcaagacaga 360
 attacctatt tgaataatgg agggctgact ctgcctttac gcttaaaaat agtagagaat 420
 aagataattg ttgattttcc tctaatatcc tgttcaatac aggaaaatga tgaaataata 480
 tgtatgaata atataaatag tcaaacata ttaagccaat tgtatctctt actgggagct 540
 gaaaaaggaa acgctattaa ggaaaatcaa ttgaccagtt atctttctac tttgctatgg 600
 tataaatata attgggggtga aaatatgatt ttacaattaa aagaggaaaa aagatatgga 660
 aagaatcatt ggatgggtatc agccaaatag 690

<210> 413
 <211> 477
 <212> DNA
 <213> B.fragilis

<400> 413
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ttcctgttca	cggatgaaat	aagttttat	tcagtcatca	atcactcagc	cgttatcagc	120
cttcaccggc	ctaatacctg	gagaaacctg	cctatcacct	atatgggagt	ttctccagat	180
gtggaagcgg	acgacactca	agccgggtacg	ctatataaac	agacccttac	catccgcctg	240
aaacgcacag	gactgacaga	ttcagaactt	cacatcctgc	ggactatcaa	tgtacgtggg	300
tgcgtagtaa	gatgcaagga	tgcgaatggc	aatatccgat	tatatggaag	caaagagtac	360
ccgcttctgg	gaaccgtgat	agagaaaaca	ggaaccaaag	cctccgacct	ctccggaatt	420
gaagccactt	tttccggaaa	aggcgccctat	cctccactac	ctgttacaga	gttataa	477

<210> 414

<211> 243

<212> DNA

<213> B.fragilis

<400> 414

aaaggatcaa	aaatgggaac	aggatttacg	gaatacgaag	aaagccttat	acaagcaatt	60
tgttcgttat	attatatata	gacgaggact	tataaacagg	gtgtgttcat	aggatgatt	120
cctaaaaaca	cacgtataac	cttgaatggc	atatatatga	tgaagttatt	aaataccggg	180
aacgctgttt	atattgaagt	aaaaggggga	attaatgtat	taacaattat	acatcaacaa	240
taa						243

<210> 415

<211> 609

<212> DNA

<213> B.fragilis

<400> 415

attatgccaa	aaaaagacac	aacctacgac	cgcacgaac	gctccctggt	caaagatcgg	60
ggtgaatccg	ctctccagtt	atcaccaaag	gagatggaaa	ttaagaatcg	gatgatgctt	120
tgtgttagta	agaaaatgga	aagcccatta	attgaagacc	aggagctcgt	tactttttctc	180
atgcacggat	gtggaggggca	agcggaaacct	gtttcccaat	cacaggccta	tcgogatatc	240
ggtatgatca	accggttggg	cggtaacatc	cagttggcgg	ccaaatcctg	gtatcgctac	300
atgatcgtag	aaggaggaaa	gaaggcat	caactcgcta	tcgacaacgg	agatgctaaa	360
ggagctgccg	ccgctctcga	caagataggt	aaatacaccc	gttccgacaa	agacgatgac	420
gcattcgact	tcagtcagct	tattccccca	tcttttgaac	cttctgacga	tgtgacgaca	480
cttgagggta	ttgaagtgat	agacaatctg	gagcaacgcc	gccaggaact	ccgcagcttg	540
tgcaaagata	tgttgaccaa	acaggcgaca	gatattcaaa	ccattgaaga	ggaggatatt	600
gaggaatga						609

<210> 416

<211> 363

<212> DNA

<213> B.fragilis

<400> 416

cgtactgcaa	agatggaaaa	tatttttggat	tctgcaaaaa	caattcaaga	aaaacgcaca	60
atattaaaaag	gtttatcaaa	gccgcttcaa	atttttgggtga	aagaggctgc	tattcctacg	120
gtaaaccgatg	gactgaaagc	gatatacgca	cagtctgggc	acaccgaact	taaaacgctg	180
aaacagtgga	ataaggaggg	caggagtatt	aaaaaagggtt	cccatgcttt	atgccttttg	240
ggtgcaccta	agaaagtaga	gacgacccaa	gtggaagaag	cacagggaga	agataatgac	300
ccaatgaatt	tctatccgat	ttgttttggta	ttctcaaatt	tgcaggtata	tgaaaaacag	360
tga						363

<210> 417

<211> 195

<212> DNA

<213> B.fragilis

<400> 417

attgcacaaa	attgtatttt	gtacgcacaa	tgtatcaatc	gtacaaaaac	gtaccatggt	60
------------	------------	------------	------------	------------	------------	----

tcgtacggat	ataaaccaat	tataatcaac	acattatgtg	ataagactgc	acaatttaca	120
cagttgcaca	aaaaaggagt	accgtttttg	caagggggat	tagtttggtc	cggttaagtct	180
tgtttatgtc	cgtaa					195

<210> 418

<211> 759

<212> DNA

<213> B.fragilis

<400> 418

acaattaaaa	acacaataac	catgaaaaaa	attattttat	tacttgcttt	atgttttact	60
gcaataaatt	tctttgcaca	aaccacagat	ccgaatcagt	tgaagaatga	aggtaatgat	120
gctttgaatg	caaaaaatta	tgccgttgct	tttgaaaaat	acagcgaata	tctgaaattg	180
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gctacattga	cggaaggat	caaagctggt	ccgggcaatg	ctactattga	aaaattatat	420
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gaagagaact	ataaacatgc	caactgatgtg	actagtaaga	agtggaagac	tgacgcttta	540
tatagccttg	gagtgtttatt	ctacaataat	ggagccgatg	ttctacggaa	agcaactcct	600
ttagctagtt	cgaacaaaga	aaaatatgct	tctgaaaaag	caaaggcggga	tgcggttttc	660
aagaaagctg	ttgactatct	gggagaggca	gttactttat	caccaatag	aactgaaatc	720
aaacagatgc	aagatcaggt	aaaagcgatg	attaagtaa			759

<210> 419

<211> 369

<212> DNA

<213> B.fragilis

<400> 419

aacatgaaaa	agaaaaaaga	aactccaatg	catcccgttg	tggaaaatat	ccgtaaaata	60
attatggata	aaggaattac	ccaagttgct	gcatctgaac	ttgtgggtac	ttctgcatct	120
caaattagta	aaattttgaa	tggaagaagta	caaattagca	tttgccagat	ttcaaatttt	180
gcaactaatc	ttggaatgga	gataatagac	gtattttacat	atcctaataa	atatgtaaaa	240
gcagaagaca	ggaatgataa	taaagaacct	attgaggcag	ttctccaaat	taaactcaga	300
aaagataaaa	aagatcaagt	actaaagttg	atatttgggg	aacataattt	agaaatatta	360
aacaaataa						369

<210> 420

<211> 1077

<212> DNA

<213> B.fragilis

<400> 420

acaattagaa	aggagggtg	cttaatggcg	gtatataatc	gaatccctga	ccggtttact	60
aacctggata	tccgcgatac	cctgaacgct	tatgggtggaa	gtgtgggcga	taactcgctt	120
aactatttct	ctgctgctgc	acacattaac	atgtggagca	aacgtaaacc	ggtgaaaaga	180
aatatcatgt	ttaatacggga	ggacccgaac	tggttccgtg	ccgattccgg	aaactacggt	240
atcaatgtcc	cccgtgcagc	ggatattgct	ctactgaccg	gaacttacac	ctatgatata	300
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accgtaccat	tactaccat	gcttccctcc	ggacttatcc	ttgcttccgg	cagtgccact	420
gttgtgaagt	tgatgctgaa	atcacttgat	tcaacatata	atgttgtccc	ggccgatata	480
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tccctggcagg	gtgaaacgac	acaatcctat	tacagcttga	acgcagagga	cggttttgat	720
gagtcgaccg	ttgatattgt	caccccgcat	gccgatgttt	actcgttcgg	catccttgga	780
cttagcatta	tcgaagcgag	aaagatatct	ttaatcggtg	cggcgattat	caactccgga	840
agtctctttc	aagagggccg	cttaataagc	agactggaca	ataattacta	tttaaagtct	900

gtaaaagtgc	ttgcgacccg	tgcaagtgc	gggtgttactg	ttgccgagaa	agcacaaagc	960
ataacatctt	ccactacacc	gacacgctta	ggaaacgact	ggatggcagg	tgagtccgtc	1020
aacttcagaa	caccgggtctc	taggtcttca	ccggggggcgg	gaggcgagca	cgtcgtc	1077

<210> 421
 <211> 252
 <212> DNA
 <213> B.fragilis

<400> 421	
accctcggaa	ataccggatt
tcaaaactaca	aattaaaagt
gctcaggaaa	gaataaaaaa
gaacaagagt	tagtcgactt
aacaatgaat	ga
	60
	120
	180
	240
	252

<210> 422
 <211> 996
 <212> DNA
 <213> B.fragilis

<400> 422	
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caaaaatata	taactttgca
gtattccccc	gtcaagggtgc
gcttttagcaa	aagaattggt
attatgttca	acggtagcga
ttcctccact	ctgttatattc
gccggacact	cactgggtga
gacggcttaa	aattgggttta
ccttctacaa	tggctgctat
tctgttaccg	ctgaaggaga
gtaatttccg	gatctgtacc
gctaagcgtg	cgcttccgtt
gccaaagtag	aattggaagc
gtttatcaga	atgtagatgc
gttgctcagt	tgactgcttc
ggtgctaccg	acttcacaga
atcgactcta	cagtttcggc
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	120
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	240
	300
	360
	420
	480
	540
	600
	660
	720
	780
	840
	900
	960
	996

<210> 423
 <211> 474
 <212> DNA
 <213> B.fragilis

<400> 423	
tgcattatga	agaatttaga
gagttcgcaa	ggcagtatca
gaaggccggc	tgattgtccg
aagaaagaac	tgacagaacg
aaacttactg	tttctgccgt
tggatcaaga	aacggatgga
ggaattgaca	aatgtaccgt
cacaaagtag	ctctatacta
	60
	120
	180
	240
	300
	360
	420
	474

<210> 424
 <211> 336
 <212> DNA
 <213> B.fragilis

<400> 424

cataccatga	acctatcttc	ttttaaaactg	accaatatta	acgaattgat	atccgtatac	60
aaagagaatc	cggagcgctt	taatcgcttt	tataacgcag	tgtacctgct	gctggatggc	120
attccggaat	gcggaagtat	tcgtgtaatg	gatcactgtg	aggcgctctc	ctatgacttg	180
tttataaagt	gtgcatgttg	gattattcag	gaagagacgg	aacagaaaga	gttgacggat	240
gcattacttg	agttttcggg	tgattataca	attattcgcc	ggtgcgcgaa	gttcgtaaaa	300
tccaaatcct	gggttcattt	ctactcacga	cgatag			336

<210> 425

<211> 1320

<212> DNA

<213> B.fragilis

<400> 425

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tttgcgga	ttggcggtga	tgttacttgt	gttgacacca	acagcgaaaa	aatagaggcg	120
cttaaaaagg	ggattatccc	catttatgaa	aatggattgg	aagaaatgg	catccgcaat	180
accaaagccg	gtcgactaaa	atttacgact	tcactggaaa	gttgccctgga	tgatgtagaa	240
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aaaagtaccg	tacctgtagg	tacagcatgc	aaagttcgtg	atgctattca	ggaagaatta	420
gacaaacggg	gtgccaaaat	agaatttgat	gtagcttcca	atcctgagtt	tctgaaagag	480
cgtaatgcag	tcaatgactt	tatgagtcct	gaccgtgttg	taatcgggtg	ggaatcggaa	540
cgtgcagaaa	aattaatgac	taagctatat	aagccattca	tgctaaataa	tttccgcgtg	600
atattcatgg	atattccctc	tgccgaaatg	accaaataatg	ccgcaaactc	aatgttggct	660
actcgatatca	gtttcatgaa	cgacatcgct	aatctgtgtg	agttagtagg	agctgatgta	720
aatatgggtgc	gtagcgggtat	cggttcggat	acccgtatcg	gacgtaagtt	cctttatcca	780
ggcatttgggt	atggtgggtc	atgtttcccc	aaagacgtaa	aagctttgat	aaagacagca	840
gaacagaatg	gatatcagat	gcgtgtgtta	caggcagtag	aagaagtga	cgaaaatcag	900
aaaagcctgt	tattcgacaa	actggtaaaa	caatataatg	gaaatctgga	aggtaaaaca	960
gttgcattgt	ggggattggc	attcaaaccg	gaaacagatg	atatgcgcga	agcacctgca	1020
ttggtcctaa	ttgacaaaact	gttgaaagcc	ggctgcaaag	tacgggccta	tgatcccgcga	1080
gcagcaaatg	aatgtaaaag	acgaatcggc	gaaaccatat	actatgcacg	cgacatgtat	1140
gatgcgggttt	tggatgctga	tgctttgatg	ctggtaaccg	aatggaaaga	atttcgtctg	1200
ccttcgtggg	ccgttgtgaa	aaaaacaatg	tcacaacagg	tagtcatgga	cggacgtaac	1260
atztatgata	aaaaagaaat	ggaagaacag	ggtttttattt	accattgtat	cggcaaataa	1320

<210> 426

<211> 501

<212> DNA

<213> B.fragilis

<400> 426

aacaaaatga	aaaatgtatc	gagcgcaaaa	agcgagaggg	ctaaagccgt	agtgttaagt	60
aatgtagcta	ataagaagaa	tgaaacagcc	cctctaattg	tgctgccatc	ccttccaacc	120
gagaaagaag	aaacgaaaga	acagggtttcg	gccaaagtgg	aaactcccgt	tcaaacttcc	180
aagaaagaga	gttcttccgt	agtagccgca	cccaataagc	gtctaagtat	tgatgaactg	240
accgataagg	cggagcggtg	ttatctgctc	cgtcagaaat	atcaagaagt	gagagaaaag	300
cggaaacagc	ttgaaagctt	tactatctca	catgataaaa	ataatgccca	acttactttg	360
gtagacgcaa	aagggctttc	catttctaca	agtaatcccg	ttgcaattgg	taagttgtta	420
tctgattgga	tgttagattt	aaataatcac	ttggcgaaaa	ccgaagaaga	aattcgttca	480
gaattggaac	ggctaaatta	a				501

<210> 427

<211> 249

<212> DNA

<213> B.fragilis

<400> 427
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gacaataaag gtttaagaat gaccactacg atagtcgatg ttaaagatga tccgctcggc 120
tcaatcgttg gctttgggac tgaaaaagtt tgccggagatg atgcatttgc caaaacaatg 180
ggtttaccag gtaagtatat ggcagtgtgcc ttttttatag atagagaaga actaaagaaa 240
tacctttaa 249

<210> 428
<211> 525
<212> DNA
<213> B.fragilis

<400> 428
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cctgatttca caatcgaatc tacgtcagat gcacagtaca attttgattt gaccgactta 180
aaaggtaaat atgtgctgct tagtttttgg gcaagttagc atgcacagtc ccggatgcaa 240
aacgcaagtt tgagcaatgc gcttcgatca acttctcaag atgtggaaat ggtttccggt 300
tcatttgacg aataccagtc ggtatttcag gaaaccattc gtaaggacca aatagttacg 360
cccacctgtt tcgcggaaac taaaggcgaa agctccggct tgtttaagaa ataccgttta 420
aaccgggggt tcaactaacta tttattggat ggaaatgggt tgattatagc caaaaacatc 480
tctgctgcag aactttctgc ttatgcaaac aaaatcaaag gttga 525

<210> 429
<211> 564
<212> DNA
<213> B.fragilis

<400> 429
tatcatcaga aacgaatgaa ttatatacaa acagaaatag atgggtgtgtg gatcattgaa 60
ccgaagattt ttttcgatcc ggcgggatat ttcatggaag cattcaagca acaggaattt 120
gatgctacta tcggacagat aaattttata caagataatg aatctcaatc ttcattcggc 180
acgttacgcg gactccatta tcaaaaagga gcctatagcc aagccaaact agtgcggtgc 240
atcaaagggtg aagtgtctgga tgtggctgtc gatttaagaa agtcatcacc tacatttgga 300
aagcatatca gcgtattgtt aagcgacgaa aataaacgcc agctttttat tccccgtggg 360
tttgcccatg gatttttagt gaaaagcgaa atagctatct ttacttataa ggtagataat 420
atatatgccc cccaatctga ggcttctatc ctatacaatg atccggcatt ggctatcgac 480
tggcctattg ccgatttctca acttgtcatg tcagagaaag acaagcaggc aggagccttt 540
cggaagcag aatattttga atag 564

<210> 430
<211> 621
<212> DNA
<213> B.fragilis

<400> 430
ggagataaga atatggaatc aaagtttcat gaactgaaaa acaggctgct gaagaatatt 60
gaccagacgt ccgaatctag gctttatatg gatatacagc tggctcaaaa ctgcgaaact 120
cttatgtcta ttatcaaaaa ggatatcgga tatctggcaa aggaaggat cctttccccc 180
ggcatagcag aagattttta ggacgtattt ctatctgccg gcataaaatg taactccgga 240
ggctcatccg gatatatgtt aatatgggac ggcaactgccg ttgatatttc cggaactgcc 300
acggctgtaa tctggaaaag tgaacgagcc ttcatcaaag gacgcgcagc cgctttcctt 360
cttggagagg tctctgcaat aacctgtgaa cgttcgatgg tcattgcggc aggaagctcc 420
actatccttg ccgagggaga ttccgttgtt ggagtttcag gctatcatgc ctctgtaaag 480
gcgtcagact atgctactgt cgtaaatatg aactgtccca acattgacct tcgtgacaac 540
acccgccttt ggcttctgc acgcggaagc tttgcagccc gaaaaaattg tgatataatt 600
attaaaaaca aggaggaata a 621

<210> 431

<211> 225
 <212> DNA
 <213> B.fragilis

<400> 431
 ccaaaaaaga aggaaggaaa acctatgttt aaagatataa tcgaattaga taaacaagtc 60
 gtagaccgga tcgtagataa ggtccacgaa aacaatttag aaattgagat ggaaatggga 120
 gttgtaaagg acggtatggt taaagtcctt ttcctctata aagatccgga acttctgcag 180
 agcgtgataa acgaatccgt tactgaagag tacgatctcc cataa 225

<210> 432
 <211> 687
 <212> DNA
 <213> B.fragilis

<400> 432
 acagaaaaga atgacacaat gagtaatata cctgttatct ttcgtttttt aaaggacctt 60
 actgccaaca acaatcgcgga gtggtttaat gaacatcgga aagaatatga aatagcccgt 120
 ttagaatttg aaaatttcct ttccacagta attgcccgt tttcactttt tgatgaaagt 180
 attcgtggta ttcaacctaa agaatgcact tatcgcatct accgggatac ccgcttttct 240
 tccgataaaa ctccctataa gaatcatttt gggggatata ttaacgcaa agggaaaaaa 300
 tcctatcaca gtgggtacta tatacatata caacctgagg gttgcatgct ggctggagga 360
 agtttatgct tgccttctaa tattttgaaa gcacttcgcc agtctatcta tgataacatt 420
 gatgaatata gttcgatagt ggaggatcct gaatttcagc aattcttccc cattgtaggt 480
 gaagatttcc tgaaaacagc tcccaaagga ttcccgaaag attttaaata cattgattat 540
 ttgaaaccta aagaattcac ttgtgcttat tccgtcccg acagtttctt ttgactccg 600
 gatattctgg acaaaataga agaagtgttc cggcaattta aacgttttgc cgactttacg 660
 aatttcacta tcgatgattt tgagtaa 687

<210> 433
 <211> 342
 <212> DNA
 <213> B.fragilis

<400> 433
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 ttaaagcaat atgcataga aatagaagga ggatatattt gtcatatctt tcctttcagc 120
 gaagaaatag agtctgtaga atggtttccg ggtgtcatat tactgactcc acaagaagaa 180
 tcagatataa atactttgtt taactttact aatatagaaa aacaaagtat ttatatccg 240
 aaagttacca tagatatgaa atggcgggct tatttattat atcctttcaa ttttgttaca 300
 atgcagcctg tcgccgaaac tctgcacaga caattgcagt ag 342

<210> 434
 <211> 1074
 <212> DNA
 <213> B.fragilis

<400> 434
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 caggtgtttc acgctccatt tatcagcacg aatcctcatt ttgaacttta caaaatagta 120
 gagcgtagta aggaactctc taaagaacga tatccgcaag catcaatagt acgtagtttt 180
 aaggagttga cagaagatcc tgaaatagat cttatagtcg ttaacactcc ggacaatata 240
 cattatgaat atgccggaat ggctcttgaa gccgggaaaa atgtagtagt tgagaaaccg 300
 tttacttcta ccaccaaaca ggggtgaagaa ttaatatgctt tggctaagaa aaaaggtttg 360
 atgctaagtg tatatcagaa tcgcagatgg gatgcagatt tcttaacggg acgtgatatt 420
 cttggccaat ccttattagg acgttttgga gaatatgaat ctacatttgc tcgttatcgt 480
 aattttataa agcctaatac ttggaaagag accggagagt ccggtggtgg attaacctat 540
 aatttggtgt cacatctgat cgatcaggct attcagcttt ttgggatgcc tgaagctgtt 600
 tttgcagatt tgggtatcct gcgtgaagga ggaaaagttg atgattattt tataattcat 660

ctgttacatc	cttcgttggc	accaaattgtg	aaaatcacct	tgaaagcaag	ttacctgatg	720
cgagaagccg	aaccacgttt	tgccttacat	ggaacactag	gttcgtatgt	taaatatgga	780
gtcgataaac	aggaagctgc	tctattagct	ggtgaaatac	ctgaacgtcc	gaattgggga	840
gaagaatcag	agcaggaatg	gggattatta	catacagaaa	taaattggaaa	agaaatctgc	900
cgaaaatatc	cgggcatagc	cggaaattat	ggtggctttt	atcagaatat	ttatgaacat	960
ttatgttttag	gacaaccatt	ggaaacacat	gcacaagata	ttttgaatgt	gatacgaata	1020
atcgaagcgg	cttatcaaag	ccatcgagat	aataaaattg	tcaatcttaa	atag	1074

<210> 435

<211> 546

<212> DNA

<213> B.fragilis

<400> 435

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atggttataa	tcgctatatc	aatttatatta	ataaagataa	tatgtactcg	ttacaaccaa	120
aactcagatc	agatactccc	tcctcccaat	atgcactcta	ttcaggagag	tgcatccatg	180
catttggtaa	gaataggaca	gttgcctcac	ccaggacctg	gatattgtta	ttacgaatta	240
ggaggaatga	gatatcaagc	gctaacagga	tttgacattg	gcgtacacga	aggatatgca	300
aaagcagagc	ttaataatcg	gtatgataaa	tatgcggttg	gagtctacag	agaaggagat	360
cacaaattaa	tgggatacgt	tcgaagagaa	caaaatagag	agctttatga	atttatgtta	420
aataataatt	gtatagctaa	agctaaattt	cgaatatgga	tacaccaagg	agaaatctat	480
ggagcagctt	acataaaaga	agaatggaaa	tcttcattag	gctttaagtc	tgacattaaa	540
atttag						546

<210> 436

<211> 525

<212> DNA

<213> B.fragilis

<400> 436

aaactaattg	aatgttgaa	cgaaaaaaga	actcaaagaa	ttatgaaaag	taaattcctg	60
atatttttgt	cggcagtagc	catgctgtta	ttatttagca	attgtggaag	caaaacaaca	120
agtaatgatc	aggccactac	cgaagtgaaa	gacactgtca	cttcaaaaga	agaagctgta	180
cgggatagtg	tatctatctt	gggagaccag	gtatatgata	tagtgaacac	agctcccgaa	240
tttccggggag	gaatgaaagc	gtgtctcgag	tttctctaca	agaatattac	ttatccggca	300
caagctattg	aaagtaagca	ggaaggtcag	gttgtgatac	agtttgttgt	taccaaaaat	360
ggtaaaatta	ttgatccgaa	agttgtgaaa	agtgatatctc	catcacttga	cgcagaggcc	420
atacggatca	taaattttaat	gcctgactgg	actccgggaa	aacaaaaaaa	tggtcaggaa	480
gtgaattcac	ggtttacact	tccagtccgt	tttacctta	aatga		525

<210> 437

<211> 438

<212> DNA

<213> B.fragilis

<400> 437

accatgtatg	atattgtagc	gcagaggcct	agactgtttt	tagcaaagaa	agatatcact	60
tgtaaaaaat	tgctggctat	gatttttatg	tcagaggcga	cgcttaaagg	caaattgaat	120
ggtacaagaa	cgctagatct	taatacaata	atatccattg	caatacggct	tgaggatctt	180
tctgttgaat	ggcttcttcg	tggcgaaggt	gatatgttta	aatctagttc	tggtgtttct	240
attttatctt	catcagtacc	tatatttaca	ggggagacct	cgtttatata	cagtatgtat	300
aaagaagaaa	gagaagaggt	taaaacttta	ttaaagcaaa	atggtatatt	ggaagagcgt	360
attcgtcagc	tcgaggatga	caatagatta	ttaagagatc	aagttgtaac	agaattaaac	420
ctaaatacta	aactgtag					438

<210> 438

<211> 369

<212> DNA

<213> B.fragilis

<400> 438

aagatgcatg	atattgtaac	gcaaaggcctt	aatcaattttt	tagttgaaaa	gaatattact	60
tataaagaat	tatctgggtat	gattctttatg	tcggaacgt	cactttgtag	aaagttgact	120
ggttcaagga	gtcttgattt	gcatacatta	atatctatag	tagcatgctt	gccagatgtt	180
tcttccgagt	ggcttcttag	aggcaaaagg	agggtgtgta	attcttcttc	gagcattagt	240
tccgatgtct	tagtagaaga	acttaaaatg	gaaaaataacc	tattaaaacg	aaaaattcaa	300
gttcttcaag	aattgttgga	gtttaagatg	gaaaaaatca	gagctgagaa	tggtaacata	360
aaaaaatga						369

<210> 439

<211> 912

<212> DNA

<213> B.fragilis

<400> 439

cagaaaagtg	accattatgt	ttcttctttg	ttatatagtg	ttttcattta	tcatatggta	60
agaaaaagtt	caataaataa	atacgagtta	gacgtcagaa	aggggttaca	agaactcttt	120
gacaaatgtc	gacacaatat	gaagcattct	ggggatttat	tattatgtca	acaaaatggc	180
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caacaagtca	attttatttc	gtttaatgga	ataggaaata	ttactgatga	caatgattat	300
tataaaaaag	aaggaaataa	ctttttttat	ggttaattctg	agtttgaagc	tgatattatg	360
agacaacata	ttacctatat	gaatatatgg	gaaaattctt	actttttacg	ggatttact	420
caagtggtaa	acgtgttaaa	tggtttaaat	tataattgga	atttgacatt	caagaatctt	480
aagcccaatc	aaaaaagcga	acaaataaga	gaaggataaa	taaaattatt	agatctatcc	540
cccaacttcc	aacgtatact	taaagatgca	tatgtcggac	aaatacgaaa	tgctgtcgct	600
catacacaat	accattgtat	tcaaggagga	atcttatatg	acaactactc	accatcaagt	660
aaatattcta	tcctgcaagg	tctttcttat	gaagaatggg	agaagaaata	tgtctactct	720
tttttcatat	ttataggtat	attccaaatg	ttaaaacaaa	tcacaaacga	attttatctt	780
ccttgttccc	aattaacctt	tgcaaaggga	gttccaattc	aaataccact	ttcggacaac	840
aaaggatatg	cagagactta	tttatatccg	aatcaaaaag	gagatatattg	gagatttaca	900
agaataattt	ga					912

<210> 440

<211> 213

<212> DNA

<213> B.fragilis

<400> 440

gcataatcgcc	taaacgagaa	acaattgtcc	atgtatatcc	atcatttgat	ggtaaaggac	60
cacaagagaa	aatattatta	tctatcatat	gaaaagagat	tcataattat	aattaattta	120
gtttctgcta	aattacaaaa	tagtaatgga	ttaaaaaaga	aaaagcagag	taatagctct	180
gctttaatat	gtttctacag	aaatatggcc	taa			213

<210> 441

<211> 246

<212> DNA

<213> B.fragilis

<400> 441

cgggtggcgag	aaacttctgt	taataatttc	tcttctttgc	agtcttgttt	tataaatgta	60
aatgagatca	aggtacgttt	tgggggtgct	cccgggttag	tgatgaccaa	gagctggcgg	120
gatggataca	ggccttgtga	agatgcgatg	tctttaaaag	aatcacttgc	atccatcggt	180
atgactactg	taaaagtacc	atttggcgaa	agtaaattcg	atactccctt	cagcaactct	240
tcataa						246

<210> 442

<211> 210

<212> DNA
<213> B.fragilis

<400> 442

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ttcagcttgc	ttctgaaagg	ggtgaaacta	ccgactatgg	tttgctacgc	ttccggttta	120
ccggattctc	aagaagtgca	tgttagccaa	aaggatgtat	atgctgcatt	cggtcggtat	180
ttacttcgat	ttgctttcaa	tgtggaatga				210

<210> 443

<211> 216

<212> DNA

<213> B.fragilis

<400> 443

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gaaatgaggg	gagaaatatc	tattcaggaa	cttagtcgga	aaattaacct	cagcgccgaa	120
gacgttgac	ttgcggtagg	ttggttagcc	agagaaaata	atatttttat	tcagagacac	180
aactacctgt	tatacgtcag	tcatgatgct	ttctga			216

<210> 444

<211> 807

<212> DNA

<213> B.fragilis

<400> 444

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ggaggcttta	ttaaaggctt	tgccattttg	ggagttattc	aggctttatt	ggaacatgat	120
attaaaccgg	atattatctc	aggagtcagt	gccggggctt	tggccggagt	attttatgcc	180
gatggcaacg	aaccctatag	ggttttggac	tacttttccg	gacataaatt	tcaggacttg	240
acaaaacttg	taattcctaa	agtaggctta	tttgctttgg	gagagtttat	tgattttttg	300
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attgccatgc	gttcttatca	ttttatgttt	cgttgccaata	cgtttccgga	gcgagacaat	660
tgcgatttac	taattgaacc	ctacaacctc	gaggggtata	gcaatactga	acttgaaaag	720
gccgaagaga	tttttgaaca	aggctataac	actgcttctg	aggttctgga	ccaactaatt	780
gaagagaaag	gaaagatatg	gaaataa				807

<210> 445

<211> 1221

<212> DNA

<213> B.fragilis

<400> 445

agggacgcgg	acagtttaca	acttttttgc	caacactttt	gttataattg	gataataaac	60
ctattttatc	caatgaaagt	acacgaatat	caggcaaagg	agattttctc	cacttacgga	120
atacctgtcg	agaggcatgc	tttatgccat	acggcagatg	gggctgtggc	tgtttatcac	180
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ttggagatga	ctataaaagg	ttatcccgtc	accaagattc	ttcttagtga	ggctgtcaac	360
attgcagccg	aatattacat	cagtttttacg	atagaccgta	atacgcgctc	tgtcacgctg	420
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aatggagccg	gtctggctat	gacaactatg	gatatgatca	agctttatgg	aggaaatccg	900
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cctattattg	tgccggttac	aggcactaat	ggaaatatgg	gacgtgaatt	attgcgtaag	1140
aataaccgtt	ttcaagtggc	ccagacaatg	gaagaagcta	ctaaaatggc	tatagaatca	1200
ttaaagaaag	aatcgatatg	a				1221

<210> 446

<211> 1443

<212> DNA

<213> B.fragilis

<400> 446

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gatatcacia	ctgaccggga		gacctctacc	gttgaagtag	ttcccaaagg	gaaagaggct	180
ccaattaagt	ttgttcccag		agggcggaat	aacaacatga	tgtatgacat	tatgaagaag	240
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gatagtgtcc	tcgtatatcg		taaataccgg	gataaggaaa	cccgaaaaat	catcaaagaa	360
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atttttaatc	aggacactca		gcccagactg	gtacaagtaa	aggcaaagga	agcaacctgt	540
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gccgtaaacg	gatggccgaa		agatatctac	ttttccgtca	ccaactgtca	gcttaccacg	1380
cttgacaaag	ggacaggagc		tactaaaaat	acaggtttaa	cctcagaaac	agaagaaaaa	1440
tga							1443

<210> 447

<211> 645

<212> DNA

<213> B.fragilis

<400> 447

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gaagtcaaac	gctataacgc	ctcccgcgga	aaagccacac	agttgactaa	tgccccggca	120
tccggactga	tccgccttga	aaccgtctca	gaaaccgaac	gcttttcaat	ggctcaggat	180
gctgatagac	tgactgcata	taacaaggcc	gttgaaaagt	ggcaagatag	tgtggcccgga	240
caattacgag	ccggaatagc	cggccgcagt	atgcgaatag	cccgtgaact	tgagccacgg	300
gcctacaccc	acaaatacgg	tattatcaac	cgtcttggtt	tctccttccc	tcgacatgga	360
atctacatcc	acaagggcgc	cggcgaaggt	caggggtggc	tcacggttc	caaatggaat	420
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aaatcactcg	gacgacagaa	tgaaggcaac	cgccgggcct	acgaatgggt	tgaccctgta	540
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<210> 448
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 <212> DNA
 <213> B.fragilis

<400> 448
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 gacgagtctg aactctactc ggaatggaat gctgtttcac tccgttccct ctctgctccg 360
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 gaaacaatcg tagacgatgc tctttccatt tttccattt gtgtatccat tccatcacat 480
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 <211> 222
 <212> DNA
 <213> B.fragilis

<400> 449
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 aacaatcaga cgtagtcttt cttcttttta tcgatgaaat cagtgtattt tgcaaaaata 180
 agcaaaagcaa ttgctgcaac caaaccgatt gccgcaaagt aa 222

<210> 450
 <211> 450
 <212> DNA

<213> B.fragilis

<400> 450

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caaaagtggg	gcaattttca	ggaactttcc	atatcctttc	ctgatccatt	agggctgggt	180
tctcccctct	ctttaggatt	ggctgttttt	gcagagttag	catgttcaat	ggcctttatt	240
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tttgttattc	atgccaatga	tgtttttgca	atgaaagagc	tggcgtagt	atatctgatt	360
atttttgttt	tgatgtatat	tagtgggtccc	gggaaatatt	cagttgatta	tgtgatagga	420
cgacaactca	aaaacaaacg	aaaattgtaa				450

<210> 451

<211> 240

<212> DNA

<213> B.fragilis

<400> 451

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gtaattccat	ttggaaccga	tgaagccacc	ctgaccttcg	ccggcgccct	tgtggatgta	120
gattccatgt	cgaggggaagg	agaaaccaag	acgggttgata	ataccgtatt	tgtcgggtga	180
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<210> 452

<211> 666

<212> DNA

<213> B.fragilis

<400> 452

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aaaactcata	tgtattggca	tgaaggtatt	cgcattacgg	actgggttta	tatctatttc	180
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ttaaagaccg	gatataattat	ctgtgtatca	tttaattctaa	ccggtgcatt	gggtaatatc	360
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aagtaa						666

<210> 453

<211> 1005

<212> DNA

<213> B.fragilis

<400> 453

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agtactctca	agaactctat	cactgagaag	gattctaaaa	tcacccaact	tgaagagcaa	840
gtgaagaatc	tgaagaacgg	tcctacaccg	gggcatgccg	gtctgactcc	tgaacaagag	900
cctgaaggta	gcggaaccca	ggaagagtta	tctgcttttt	gtgaccagaa	cgcaggaaac	960
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<210> 454

<211> 1407

<212> DNA

<213> B.fragilis

<400> 454

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gatgctcaga	tgcaggaaat	cattacttcg	gggggatggt	tacaatgtca	ttcgggcagt	180
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<210> 455

<211> 192

<212> DNA

<213> B.fragilis

<400> 455

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acggactcac	ctgccatcca	gtcggtttcct	aagcgtgtcg	gtgtagtgga	agatgttatg	120
ctttgtgctt	tctcggaac	agtaacaccg	tcacttgcac	gggtcgcaac	gacttttaca	180
gacttttaaat	ag					192

<210> 456

<211> 789

<212> DNA

<213> B.fragilis

<400> 456

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actacttatg	gggagtattt	ggaaaagcta	tccccaaaac	acggacggga	aaaggatttt	120
aatgactttc	tgcaaatagt	cgtttgTTTg	ctctcaatgg	gacgtaagga	agaactttat	180
ttcaaaacga	taaagcccta	tgacaaaaca	gaactggatt	tgTTTTcaca	ggctTTTTgcc	240

gcacttggtta	tgcagatgga	caggcaacca	ctggtagacc	cgttcggaga	ctattttcaa	300
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atgaaccaat	tgattacagc	tcctaaagta	aatgatcagc	ctaaacaggg	agatcggagg	420
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tggcatcggt	ggttgattat	cgttgatagt	gtaaccaaga	taccgaccgt	ttatgaagtg	660
gaagccggaa	taataaacca	accgcctgca	tgtgcggatg	atttaaagcc	tttaccgggtg	720
acagggatca	tacagccggg	aaagaacatg	attcccgcca	attttgtacg	ttataccctt	780
aaatgttag						789

<210> 457

<211> 366

<212> DNA

<213> B.fragilis

<400> 457

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gtcctacta	actcacacag	attagcgatg	tcgttcatga	aactgatacg	agtagccaac	120
attgagtttg	cggcatattt	ggtcatttctg	gcagagggaa	tatccatgaa	tatcacgcgg	180
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tccacaccga	ttacaacacg	gtcaggactc	ataaagtcac	tgactgcatt	accctctttc	300
agaaactcag	gattggaagc	tacatcaaat	tctatTTTtg	caccccgttt	gtctaattct	360
tcctga						366

<210> 458

<211> 903

<212> DNA

<213> B.fragilis

<400> 458

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gaatacggaa	caaagtgtgg	gggcggaaca	tcacccggca	aaggaggaa	aatgatagac	180
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<210> 459

<211> 1761

<212> DNA

<213> B.fragilis

<400> 459

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aataataatc	actgtatcta	caatggagat	atttcacaaa	acggttgtgg	aaaaatggct	180
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<210> 460

<211> 195

<212> DNA

<213> B.fragilis

<400> 460

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atgctttcct	ctatttttaa	cagtgaagtt	gtaattgaga	ttaacaaaag	attatatcga	180
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<210> 461

<211> 777

<212> DNA

<213> B.fragilis

<400> 461

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cgttttctcc	gggaaggaaa	tacagttggg	attacggggc	gtagagaaga	taaactacaa	180
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cttttaacca	atgtaatatg	atttaccaat	gtagtggatt	gggcttttca	cttttttcag	420
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caacagattt	atcgcgccat	ccttcgaaga	agaaaagttg	cgtatgtttc	gaagagatgg	720
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<210> 462

<211> 1419

<212> DNA
<213> B.fragilis

<400> 462

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aatccccaaa	tggtagcgga	tgattatcgg	tttaagtcct	taactgaaat	atggctaggc	180
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gtggaaaacg	gtgagatacc	tttatcggaa	atggagcgtg	tctgtcagat	ggttgaagat	1380
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<210> 463
<211> 774
<212> DNA
<213> B.fragilis

<400> 463

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caagcggcca	ttccggatag	cggaaactgg	atcagccatc	atcttctgac	atcagacggg	180
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<210> 464
<211> 393
<212> DNA
<213> B.fragilis

<400> 464

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gttcggagta	atacagaacc	tccggctaga	gttttggaga	atttagctaa	gtatctaccg	180
aatttaaacy	cgacttggct	tttaaccgga	gagggagaaa	tgattcaaga	taaatccact	240

cctgagatgc	cgataactct	tgtttcggta	aatgaatata	aaagtcgatt	gcagcaaagt	300
gaggtaagat	tggaagctct	aagggctcag	gtggtattaa	aagataaact	actagccgga	360
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<210> 465

<211> 597

<212> DNA

<213> B.fragilis

<400> 465

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catgcttcta	cttttgcata	tcgggtatgat	gatttttttg	cataccttcc	gattgttgct	180
atgttcgtgt	taaaacttac	aggagtaaag	agccgtagta	actggaaacg	aatgctcgtc	240
tctactgcat	tttcttatat	attaatgggg	gccatagtgc	ttacaatgaa	atcactggcg	300
ggggttcttc	gtcccgacgg	ttccgatttc	ctttcattcc	cttcggggca	tacagctacg	360
gcttttacgg	ctgccacact	actgtataaa	gaatatgggt	tcaagacccc	cctagcgggt	420
attgctacct	tcttgccggc	agttgtcacc	ggattcacaa	ggcagttgaa	taatcgccat	480
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<210> 466

<211> 1599

<212> DNA

<213> B.fragilis

<400> 466

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gctcaattat	cccaatcggt	tacacgtgta	tattcggacg	gaagcgatgt	gttctggaca	180
cacgagcaga	ttgagaaact	aattaaaatt	ttccccgaag	gacaaattgt	tactgtgggtc	240
gacgaaaaga	tagtcggctg	tgcactctct	atcattgttag	aatatgataa	agtgaaaaac	300
gatcatacct	atgccccagg	cacggggaag	gagactttca	ataccatttc	ttccccagg	360
aatatcttat	atggcatcga	ggtctttatc	catcccgaat	atcgcggtt	acgaactagct	420
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gatctcgact	tattgaacga	actacacact	tacggcagcg	ttcgcaacct	gaaggacagg	1560
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<210> 467

<211> 420

<212> DNA

<213> B.fragilis

<400> 467

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ttccatgtga	gttggagcac	tgttgacaat	actctccgaa	atgcaaaaac	aaaattaggt	180
ttaagtaaa	tgactgagtt	gggggcatgg	tggttctgca	ctaattacgg	aattagtttt	240
gatctatctc	ctattgccag	gcaatgtaca	gcaggagtta	tcttactctt	gttttccctt	300
ggagaagtga	caacagtaac	aaatatatca	tataccatgc	aaagagtaag	aagaccacgt	360
acagagtatc	gcacccgtcg	acacgaaaact	tctatatatc	aaccatatat	tattaactaa	420

<210> 468

<211> 1293

<212> DNA

<213> B.fragilis

<400> 468

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<210> 469

<211> 396

<212> DNA

<213> B.fragilis

<400> 469

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cgtgagcagt	tgatcgcacg	cctggccggt	cgttttaggtt	ttgccaagat	tccgtccgat	180
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gcagcaagag	gtatatgtgt	tttgttaggt	gtgaagtca	tgccccgtga	gtacgagttg	360
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<210> 470

<211> 1296

<212> DNA

<213> B.fragilis

<400> 470

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gagttcactg	atgccgatgg	caagaccaa	cgggcaaata	cacagggttac	agttgttgcc	1260
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<210> 471

<211> 348

<212> DNA

<213> B.fragilis

<400> 471

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tatctcgaga	ctcaagacag	tttcggagaa	gaaggactga	aaagagttct	taaccatgct	180
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gattccgtcc	ggattttcac	caaccttgaa	gaagccaagc	gattcgggtg	tgaaaataaa	300
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<210> 472

<211> 768

<212> DNA

<213> B.fragilis

<400> 472

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ctgatggact	acgttgtacc	gctggaagag	aaacaaaccg	gagtagccca	tcgggcagcc	720
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<210> 473

<211> 2322

<212> DNA

<213> B.fragilis

<400> 473

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<210> 474

<211> 267

<212> DNA

<213> B.fragilis

<400> 474

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<210> 475

<211> 1530

<212> DNA

<213> B.fragilis

<400> 475

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<210> 476

<211> 591

<212> DNA

<213> B.fragilis

<400> 476

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<210> 477

<211> 204

<212> DNA

<213> B.fragilis

<400> 477

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<210> 478

<211> 960

<212> DNA

<213> B.fragilis

<400> 478

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<210> 479

<211> 360

<212> DNA

<213> B.fragilis

<400> 479

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<210> 480

<211> 216

<212> DNA

<213> B.fragilis

<400> 480

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ttaaaaaaat	acggttttcca	gttaggagat	aaagtaaagg	tagaaatcag	caaaaataag	180
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<210> 481

<211> 3450

<212> DNA

<213> B.fragilis

<400> 481

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<210> 482

<211> 546

<212> DNA

<213> B.fragilis

<400> 482

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<210> 483

<211> 1275

<212> DNA

<213> B.fragilis

<400> 483

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<210> 484

<211> 237

<212> DNA

<213> B.fragilis

<400> 484

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<210> 485

<211> 1062

<212> DNA

<213> B.fragilis

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<211> 4932
<212> DNA
<213> B.fragilis
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<211> 393

<212> DNA

<213> B.fragilis

<400> 487

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 <212> DNA
 <213> B.fragilis

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<212> DNA
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<211> 1242
<212> DNA
<213> B.fragilis

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<212> DNA
<213> B.fragilis

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<211> 312

<212> DNA

<213> B.fragilis

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<211> 615

<212> DNA

<213> B.fragilis

<400> 495

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<211> 195

<212> DNA

<213> B.fragilis

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<210> 497

<211> 951

<212> DNA

<213> B.fragilis

<400> 497

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<210> 498

<211> 627

<212> DNA

<213> B.fragilis

<400> 498

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<211> 2049

<212> DNA

<213> B.fragilis

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cattggacag	caattgccaa	gctcggacaa	accacatatt	ttgatcgtga	tgaaataggt	1980
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<210> 500

<211> 477

<212> DNA

<213> B.fragilis

<400> 500

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aatccttata	cccaagagga	atatgaaagc	atgggttagta	gtggcatatg	gaatggagga	180
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aacttgcccta	aaacgggggt	ggatagctat	gatctaattgt	atcaaggcgg	gtttgctata	300
gggtataagg	ccgggttattc	gggatctaca	ttggatgaca	tagggattgg	tgcatggagt	360
gcttttagctg	tcattttctgc	cggtagtga	atcggggggtg	tcaatagtga	tatgatatgg	420
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<210> 501

<211> 360

<212> DNA

<213> B.fragilis

<400> 501

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gccccaaaaac	ctttcgtacc	cattccggat	actgaagaac	cgggaagtcct	gaaagtcacg	180
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aaaacagttt	ctcagaaaaat	agaaacgact	cgggccaacg	acccggaatt	taccattcat	300
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<210> 502

<211> 660

<212> DNA

<213> B.fragilis

<400> 502

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ctggcacagg	aaaaaacaaa	tctcgggtga	tacctggtac	ctatgtgtgt	gtataatggt	180
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aacagaaaag	agcagatgga	atattataaa	ttggtgagaa	atgtgaagaa	agtgtatcct	300
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cggcaaaagg	atcaaagttc	ttatgaactg	gtaaaagcat	ttatgggacc	ttttaaagca	540
ggattctatc	aaacatttgc	cgctcttttc	ggagccagtt	taaaaaaaca	atatgacccc	600
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<210> 503

<211> 927

<212> DNA

<213> B.fragilis

<400> 503

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acagcttttc	tgattcctta	tcagatcact	acaggtggaa	caaccggtat	cggtgccatc	180
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gatatcatta	tcatacagttc	atgctatctt	atctttaacg	actggcgcag	agtgatattc	600
ggtttcgtta	ccttgtttat	catcggtttc	gttctggact	atgtagtcaa	cagcgcccg	660
caatcggtac	agttctttat	cttttcgaaa	gattatgcaa	agattgccga	ccgcattacg	720
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gtaaaagtat	tagttgtact	tgccatacaa	cgtagtcac	tcgatatttt	ccgttttagt	840
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<210> 504

<211> 228

<212> DNA

<213> B.fragilis

<400> 504

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accgatgcc	ataatataaa	gtatttcata	accggtgttt	ttataaattt	tctatccgct	180
tctgtatctc	ctttattttt	tcctgtcttt	gttttatttt	cattataa		228

<210> 505

<211> 438

<212> DNA

<213> B.fragilis

<400> 505

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ttatgggtga	agaataattat	attagctact	ctgatgatgt	tgtttctgat	tggtgttata	180
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cattctatga	aattcgggaag	tttctctgta	accaactatc	tattgataga	atatggaaaa	360
gggaaatatg	cttctgtact	tccggtgaaa	gaaaaggaat	ttatggaact	gattgaaaaa	420
acaagaaact	taatttag					438

<210> 506

<211> 636

<212> DNA

<213> B.fragilis

<400> 506

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aaaataaccg	agctgaaccg	gataagtata	gaagagttta	agaagctga	taaattgcct	180
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cccagatgc	ataagacagc	tttgggagcc	gagtttacag	tggattggaa	gtatgttaat	360
aacgcagttg	aaacggttga	taacctccgg	agtgaaggat	atgtggtata	ctctgtcgaa	420
caggcggaag	ggagtatcat	gttggatgag	ttaacactgg	accgttcgaa	gaaatatgct	480

gtagttatgg	gaaatgaagt	aaaaggagt	cagcaggagg	ttattgacca	ttcggatgg	540
tgtattgaga	ttccccaata	tggcacaaaa	cattcattga	atgtatcgg	aacagcagga	600
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<210> 507

<211> 1347

<212> DNA

<213> B.fragilis

<400> 507

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<210> 508

<211> 252

<212> DNA

<213> B.fragilis

<400> 508

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tatcttttta	ccggaagg	gcagggactt	aagatcgccg	ccgttagcgg	gcatcacatc	180
cgattcccgg	acggaaggcg	ccgtgccgtt	attcaaggat	gggagttcaa	ccgcatattt	240
tccatcaatt	aa					252

<210> 509

<211> 249

<212> DNA

<213> B.fragilis

<400> 509

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cctgtaaagt	tgaaaaagag	caattactct	gataatattc	cgttttgggg	tgcaaagata	120
atcaatttta	ggctaagtca	gtcatctgct	ttctcttttt	gtccaaaacg	gggttgcctt	180
ttattacctg	gatcacagac	aatgagagag	aatttgtgtc	actctgccgt	cttgaaagaa	240
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<210> 510

<211> 957
 <212> DNA
 <213> B.fragilis

<400> 510
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 atcacttgca ttgcccgtag agcacatctg caagcaatac aacaagacgg gctcaaattg 180
 aaatcagatt tgaaagggtga acatgctcta cggataaatg cctgcacggc agaagaatat 240
 aacggaaaaa ctgatgtgat atttgtatgt gtcaaagggg attccgtaga ctctatcaca 300
 gagcttatca agcgggcagc ccacgaccga acgattgtaa ttcccatatt gaatgtatac 360
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<210> 511
 <211> 600
 <212> DNA
 <213> B.fragilis

<400> 511
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 tgtcatcacg atattccgga gacagcagag actcctgaag gcaatgcata cctcaaatac 180
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 aatgcggaag ccaacatggt gaaactcctc cacgaaactg aaggaaaaga caaccgtaga 360
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 atcataaaag gcgaaataat caaagaaaaa agaggtgatt ccggattcgg atacgatccg 480
 gtattcgttc ctgaaggata cgaccggacc tttgcggaat taggtaatga aattaaaaat 540
 caaatcagtc atcgtgcttt ggctgtgaac aaactatgtg aatttcttcg ttcgatctga 600

<210> 512
 <211> 1482
 <212> DNA
 <213> B.fragilis

<400> 512
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 aatgcatatt gtcaaagtat accaagggaa gtgacattag atgaagtgat aaacagacta 120
 tctctggaat catcatcggc taaaatagaa ttacttaact tccaaaatga cttattgcga 180
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<210> 513

<211> 579

<212> DNA

<213> B.fragilis

<400> 513

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<210> 514

<211> 1521

<212> DNA

<213> B.fragilis

<400> 514

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caagccgctt taggaatgca cgccgaactg gctaaaagcg gagacatgaa aaacgtgaac 1500
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<210> 515
<211> 447
<212> DNA
<213> B.fragilis

<400> 515
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ccattagaga actatgtttc tgttttcggg aaattatgta ccgaacaatt gacgaattat 300
gatcttgtgt tttttggaga tttatattta gtcctttttt tggatgtaaa tgttcgggtc 360
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gaagaacggt ataggaaatt ggaatga 447

<210> 516
<211> 1374
<212> DNA
<213> B.fragilis

<400> 516
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caagccatta ttgaccgtat gccacacctac tggacaaaat ggggtgatact atgtgtaggg 180
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<210> 517
<211> 1824
<212> DNA
<213> B.fragilis

<400> 517
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gtgtttttca	taaaaagtac	ggattgtacc	cataaggatg	aaaaagaaat	ctcttttgag	1740
aaagcttctg	ataggcttat	aatgaaaata	aaacaaagac	aggaaaaaat	aaaggagata	1800
cagaagcgga	tagaaaattt	ataa				1824

<210> 518

<211> 255

<212> DNA

<213> B.fragilis

<400> 518

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ataatgggat	atgattccat	ccgggaaagt	cctttgatga	tcgtgatgaa	gctccaccgg	180
tgggttaagg	atgataaccg	tccgccaggt	aaaatgattg	taagtatttt	tacctttttt	240
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<210> 519

<211> 315

<212> DNA

<213> B.fragilis

<400> 519

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agagacatcg	taagttttat	ctttgatgcg	gaagtaaaac	gcggagcacc	tatctggaaa	180
atagtacgtg	ctttacattt	tggcacctat	gcgggaatgt	tttcaaagat	cgtcactttt	240
atcgctgccc	tgataggaac	ttcattacct	gtcacaggat	attggatgta	tctgaaaaga	300
aaaaaattac	tatag					315

<210> 520

<211> 1617

<212> DNA

<213> B.fragilis

<400> 520

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aagtggaaac	aatgggcaga	aaaacaacag	gtatttcctt	ttgaatacag	accatggact	1560
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<210> 521

<211> 1017

<212> DNA

<213> B.fragilis

<400> 521

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aagaatgcag	taatcttggg	acactattac	cagaaaggcg	aaatacagga	tattgccgac	180
tacattgggg	acagtctggc	tttgggtcaa	attgcagcca	aaaccgatgc	ggatattcct	240
gtgatgtgtg	gcgttcattt	tatgggagaa	accgcaaagg	tgctttgtcc	ggacaagaag	300
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<210> 522

<211> 1425

<212> DNA

<213> B.fragilis

<400> 522

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aatgtggcca	tgccctcgca	agatccgggt	gagccgttta	taatcaaact	acaagttaag	1380
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<210> 523

<211> 915

<212> DNA

<213> B.fragilis

<400> 523

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ccggaattat	ttaatctttt	cggcatctca	atccgttatt	acggactatt	gtgggctatc	180
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<210> 524

<211> 735

<212> DNA

<213> B.fragilis

<400> 524

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<210> 525

<211> 1884

<212> DNA

<213> B.fragilis

<400> 525

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<210> 526

<211> 1125

<212> DNA

<213> B.fragilis

<400> 526

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<210> 527

<211> 2208

<212> DNA

<213> B.fragilis

<400> 527

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<210> 528

<211> 1194

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (130)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 528

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<210> 529

<211> 1584

<212> DNA

<213> B.fragilis

<400> 529

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<210> 530

<211> 786

<212> DNA

<213> B.fragilis

<400> 530

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<210> 531

<211> 2679

<212> DNA

<213> B.fragilis

<400> 531

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<210> 532

<211> 1800

<212> DNA

<213> B.fragilis

<400> 532

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<210> 533

<211> 1413

<212> DNA

<213> B.fragilis

<400> 533

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<211> 687

<212> DNA

<213> B.fragilis

<400> 534

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<212> DNA

<213> B.fragilis

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<211> 285

<212> DNA

<213> B.fragilis

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<212> DNA

<213> B.fragilis

<400> 537

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<211> 1689

<212> DNA

<213> B.fragilis

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<211> 2433

<212> DNA

<213> B.fragilis

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<211> 1119

<212> DNA

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<211> 2898

<212> DNA

<213> B.fragilis

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gaatttccgg	ctgatgccgc	cagcgatgcg	attcaagcca	ctgtacttgc	cgacgaacgc	2820
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<210> 543

<211> 753

<212> DNA

<213> B.fragilis

<400> 543

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aaagataaca	ctgtggcgat	tataaaagag	tatgagccat	tgtttaatgg	gcgcctgaag	180
tggattagt	aaaaggacaa	tggcttgtat	gatgcgatga	ataaagggtt	tcaaatggca	240
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tattatgttg	ctcagaacga	tatatctaaa	atagttcggg	attggaaatc	agggggacaa	420

cgtcctttct	gtaaaggggtg	gcatccggct	catcctacat	tttatgtgaa	gaaggaagta	480
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cttcgtttga	ttgataaaga	gcatattaaa	ttatattatc	ttcctgaacc	tttagtcagg	600
atgcgattag	ggggaactac	aagtaagaat	ctatctaata	ttaggaaagg	aaatcttgaa	660
tgtataaatg	cttttaaaaa	gaacggaata	aaagtgaagta	tgttatatcc	tttatatcgt	720
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<210> 544

<211> 636

<212> DNA

<213> B.fragilis

<400> 544

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aacggaagca	atccggtacg	cgccgggactg	aaaccgttac	tgggatttga	cgtatgggaa	540
catgcttact	acctcgacta	tcagaaccgt	cgtgccgacc	acgtaaacaa	actgtgggag	600
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<210> 545

<211> 381

<212> DNA

<213> B.fragilis

<400> 545

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<210> 546

<211> 852

<212> DNA

<213> B.fragilis

<400> 546

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gaagccacta	acctgatccc	caaacctatg	gtggagatcg	gtggtaaacc	catcctctgg	180
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aaagtgtggt aa

852

<210> 547

<211> 1125

<212> DNA

<213> B.fragilis

<400> 547

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atcgggcaga	cggtcggatt	gacggtggac	tggtataaga	gataccggga	agaagaggta	1080
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<210> 548

<211> 186

<212> DNA

<213> B.fragilis

<400> 548

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gtaataatag	ggatattatt	atcccaagca	ttgtcttcat	tgccacagga	cataaaaact	120
aaaaaaaaata	gactgagaaa	gagtgggtaca	aaatacttca	taatgttttag	gttaggttat	180
aatga						186

<210> 549

<211> 1434

<212> DNA

<213> B.fragilis

<400> 549

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<210> 550

<211> 324

<212> DNA

<213> B.fragilis

<400> 550

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gatcacgcc	ataacgat	agccgtcgac	tggaaagaag	cccttgaaaa	agaagggttg	180
aaagtagatg	tacgtatgca	ggggttgggc	gaaatacccg	ccatccaaca	actgtttatc	240
gatcatgccc	aatttatgct	aaagcatgaa	atggtggata	taatgaagaa	aaaagccaaa	300
tatgcaaaag	acaaaagacga	atga				324

<210> 551

<211> 1503

<212> DNA

<213> B.fragilis

<400> 551

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gtcatgatgt	accacggatt	tccacgtgca	tcacaagctg	aaaaattaga	aaagctggag	180
cctctgtctc	cttctctgcc	ttctgtcagt	gaaattactt	ctcgctgcc	cgaaggagaa	240
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<210> 552

<211> 519

<212> DNA

<213> B.fragilis

<400> 552

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gacttcttcc	gtgttttccg	ttatcagggg	gccaaaccga	gaaactccgg	aacaattagc	480
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<210> 553

<211> 1044

<212> DNA

<213> B.fragilis

<400> 553

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caactttcag	atatattact	taatataagc	tcttttcaaa	aattagtcga	tagaaactat	960
cgaacggcaa	gaaaaatatc	ttcttgggat	aacagggtca	aagatattat	aacaattcct	1020
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<210> 554

<211> 1161

<212> DNA

<213> B.fragilis

<400> 554

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<210> 555

<211> 1668

<212> DNA

<213> B.fragilis

<400> 555

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<211> 1788

<212> DNA

<213> B.fragilis

<400> 556

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<211> 774

<212> DNA

<213> B.fragilis

<400> 557

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<210> 558

<211> 468

<212> DNA

<213> B.fragilis

<400> 558

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<210> 559

<211> 1227

<212> DNA

<213> B.fragilis

<400> 559

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<210> 560

<211> 423

<212> DNA

<213> B.fragilis

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<210> 561

<211> 756

<212> DNA

<213> B.fragilis

<400> 561

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 <213> B.fragilis

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 gtggataaag atttgttctc tggcctcgga tggctgttga gagaagataa gatctctact 180
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<210> 564

<211> 1329
 <212> DNA
 <213> B.fragilis

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 <212> DNA
 <213> B.fragilis

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<210> 568
 <211> 1488
 <212> DNA
 <213> B.fragilis

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<213> B.fragilis
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<210> 570

<211> 285

<212> DNA

<213> B.fragilis

<400> 570

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<210> 571

<211> 900

<212> DNA

<213> B.fragilis

<400> 571

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<210> 572

<211> 1437

<212> DNA

<213> B.fragilis

<400> 572

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<210> 573

<211> 1899

<212> DNA

<213> B.fragilis

<400> 573

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<210> 574

<211> 312

<212> DNA

<213> B.fragilis

<400> 574

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<210> 575

<211> 207

<212> DNA

<213> B.fragilis

<400> 575

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<210> 576

<211> 723

<212> DNA

<213> B.fragilis

<400> 576

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<210> 577

<211> 207

<212> DNA

<213> B.fragilis

<400> 577

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<210> 578

<211> 1230

<212> DNA

<213> B.fragilis

<400> 578

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<210> 579

<211> 249

<212> DNA

<213> B.fragilis

<400> 579

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<210> 580

<211> 1320

<212> DNA

<213> B.fragilis

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ggtgtacgta	cggggatcga	tgccctcgag	accgacggag	ctttctggag	gatattcgac	420
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ggaggagaca	atacctgggtg	tgacgggatt	atgggagtga	tgtagtggtg	gacccctggc	720
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aacgccgggt	tgggtgatta	ttttgttttc	taccgtgggc	agccggatga	ccaactgacg	840
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gtcattatat	ttttgattct	gttactggta	cctgccatca	atctgagctc	gatgaccat	960
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gtcggactgt	tgttctgtct	gatcatatct	tattgttggg	gaggtacgct	ttttgccgat	1140
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tctactttta	tttatgcatt	actttttctg	tgtggcactga	atctgctgag	tagtggatgg	1260
ccggccctgga	gggcatcgcg	gatgtctatt	ataaatgctc	tttagcgaaa	gcttaactaa	1320

<210> 581
 <211> 288
 <212> DNA
 <213> B.fragilis

<400> 581
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 agcaatattt tattacatat atatattacc cataccaaca tcgtattgaa cgcattaaaa 120
 aaacacccca tcaatataca aaagacaact acccccatg agattatgta ttccggacaa 180
 ttcttttttct cataccttct gaataacata acagcaatca ttccatatag acaattaaga 240
 acaacaaccc ctgcatatcc aaaatcaaga tatggatctg cgatataa 288

<210> 582
 <211> 579
 <212> DNA
 <213> B.fragilis

<400> 582
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 cgaccggaga acttcgacaa catttaccgg ctgacgtcgg acgataaatt attgggtgcc 180
 tggcgggcct tatggatatg cgacaaactg tgcaggcaga agccggagtg gctgatccct 240
 ttcaggaag agctgaccgg aaggttgatg tcccgcgggc acgatggctc gaaacgactg 300
 cttctttcca tactctacca tgcaccgcga acgaagggtg cttccgtggc tctgctcaac 360
 tctgcctgg acgccatgct gtcgccccaa gagagtatcg gcgtgcaatc gctcgccatc 420
 cgaatggctt accgcctgtg cgagcccgag ccggagtgtg tgtatgagct gcgtaccata 480
 ctggagagta cagagaccga aatgtattcg accgccgtaa aatcggctgt acggaacaca 540
 ttgaagaaga ttaaccagaa gaataaaaaag aaaaaataa 579

<210> 583
 <211> 801
 <212> DNA
 <213> B.fragilis

<400> 583
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 ctggcatcgg gcaccgaaat ggtgacagtg gccatgaaac gtgtcgacat ggagagcaca 180
 gaagacgaca tgcgtgaaaca tattgtacat ccgcacattc agttgcttcc caacacatcg 240
 ggcgtacgca acgcggagga agcgggtgtt gccgcacaaa tggcacgcga ggcttttcgga 300
 accaactggc tgaactgga gattcatccc gaccgcgcgt atctgctgcc cgactcgggtg 360
 gagaccctga aagcgactga agaactggtg aaactcggat tcgtcgtgct cccctattgc 420
 caggcagatc cgggtgctctg caaacaactg gaagaagcgg gagccgccac ggtaatgccg 480
 ctgggagcac ctatcggaac caataaagga ctgcaaacca aggagtttct gcaaatacatt 540
 atcgaacagg ccggtatccc ggtagtgggtg gacgccggaa tcggagcacc gagccatgog 600
 gcggaggcta tggaaatggg tgcacggca tgcttggtta acacagctat cgccgtagct 660
 ggcaaccgga tagaaatggc aaaagccttc aagcaggcag tagaagccgg acggacggca 720
 tacgaggccg gactgggtat gcaggccata gggttcgtgg cggaagcaag ctcaccactg 780
 acggcatttt taaacgaata a 801

<210> 584
 <211> 330
 <212> DNA
 <213> B.fragilis

<400> 584
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 ctgatagaat cctacatatt ggacgcaaaa gaacaaaata tcaagacatg caaagattcg 180

ttggcagcgt	acatagagga	aaaagaactt	tttgggaaaa	tgagaaatgg	agtattcaaa	240
ccattagttt	tcagcacaat	caggaattac	gtcaacgaaa	tctggaataa	gatggaaaaga	300
aagaaaaaga	accaagaagg	aaagcgctga				330

<210> 585

<211> 1281

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (1074), (1086)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 585

aagaaaaaca	agagacatga	catccttatg	aaaaatat	ttaaagattt	aaaaagtaaa	60
gaccacaaac	gctatctggg	aggtttggac	gtcttcagat	atattgggtcc	cggtttattg	120
gttactgtag	gtttttattga	tccgggcaat	tgggcttcta	atattgcggc	aggttcagaa	180
tttgggttact	cactgtttatg	ggtggttacg	ctgtccacca	tcattgctgat	catattgcaa	240
cacaatgttg	ctcacttggg	aatcgtgaca	gggctttgcc	tttcggaggc	ggcaacgcag	300
tatacgccca	agtgggtatc	gcgtcccata	ctggggacgg	ccgtacttgc	ttccatctct	360
acatcactgg	ccgagattct	gggagggggc	atagcgctgg	aaatgttgct	cgacattcct	420
attgtctggg	gggccgttct	gactaccgtt	tttgtttcca	tcattgctttt	tacaaattca	480
tataagaaaa	tagagcgctc	catcattgct	tttgtatcgg	tgatcggtct	gtcgttcctc	540
tatgaactct	ttttggtgga	tattgactgg	cctatggcag	tagaaggggtg	ggtgacgccg	600
gctataccta	aggggagcat	gtcattattt	atgagtgtgc	tgggtgctgt	ggtgatgcct	660
cacaatcttt	tcctacattc	ggaggtgatt	cagagccacg	aatacaataa	gcaggatata	720
gcgtccataa	agaaagtgtt	gaagtacgaa	ttgtttgata	cgctcttttc	aatgattata	780
ggatgggcca	tcaacagtgc	catgattctg	ttggcagccg	ctaccttctt	taaaagtggc	840
attcagggtg	aagagctgca	gcaggcgaaa	tcattgctcg	aacctctgtt	gggaagtaat	900
gcggctattg	tttttgcttt	agccctgctt	atggcggtga	tctcgtctac	gattaccagc	960
gggatggcgg	cggatcttat	tttcgccggg	atctttggcg	aatcatacca	cattaaggat	1020
agccactctc	aggtaggggt	tatcctgtcg	ttgggcattg	cattgctact	gatnttctta	1080
tcggcngatc	cgtttaaggg	tctgatcacc	tctcagatgg	tgctgagtat	ccagttgccg	1140
tttacgggtt	ttttgcagg	cggctctgac	tcctcgcgta	aggtgatggg	cgattatgtc	1200
aatagtaaat	ggagcacgtt	tgtgctttat	accattgccg	tgatagtga	agtgttgaat	1260
ataatgttgt	tgttctcgta	a				1281

<210> 586

<211> 288

<212> DNA

<213> B.fragilis

<400> 586

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gaatttgtaa	aaagcatgat	ggaaacaaaa	acggtagtca	gaacggcccc	ccagacaata	120
ggaatgtcga	gcaacatttc	cagcgctatg	gccccctcca	gaatctcggc	cagtgatgta	180
gagatggaag	caagtacggc	cgtccccagt	atgggacgcg	ataccactt	gggcgtatac	240
tgcgttgccg	cctccgaaag	gcaaagccct	gtcacgattc	ccaagtga		288

<210> 587

<211> 1347

<212> DNA

<213> B.fragilis

<400> 587

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ttctcgtcga	tgaatattac	ggcgagtatt	ctattgtttg	tcacagcgat	tgccgctgcg	120
gtaatcgcta	actctccggc	agcatcggtg	tatcaggagt	ttttgtcgca	tgaacttcat	180

tttcgcatcg	gaggettttaa	tttacttttcg	catgcgggac	acaatctgac	gatgattgag	240
ttcattaatg	acggtctgat	gacgatttttc	ttcttaatgg	tcggactgga	gattaagcga	300
gagttactgg	taggcgagct	ttcctcgttc	cgtaaagctg	cactgccatt	cattgccgca	360
tgtggcgga	tggtagtgcc	tgttgtcatc	tattccatgg	tttgtgcccc	gggcactgaa	420
ggcgggcaag	gactggctat	ccctatggca	accgatattg	ccttttcttt	gggagtgtct	480
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tcggcttccg	accgtgtcat	cagtcacctt	cagtcgcttg	aggataacct	gcatggtgca	960
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gccaaactcg	gtgttttata	cggtaacgga	atggcgggta	tcttgggata	cctgggtttg	1320
cattgggtct	tgcccaaaa	aagataa				1347

<210> 588

<211> 1014

<212> DNA

<213> B.fragilis

<400> 588

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aatgaacaat	ctgattcctc	aggactatta	aagagccaaa	taactgacat	cattaattat	180
tccaaaatca	attttgatga	aaactttaat	aatacagaac	tttataagaa	cttgatttta	240
agccctaaat	gggaaaatgt	ttctatgggt	cttcagaaac	aagacacact	ccattttatgt	300
gttcctctgc	tagcacagga	caatcctgaa	cacaattcct	attatctatt	tatttcaaat	360
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attataaatg	ctcctattac	cagagccggg	attatagatg	ccgggtggat	ccccgaagtt	480
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gcttttcttg	agttcctaca	cagcaaattg	cttaaagaac	atggcaatga	aagttcctcg	600
gatagtctct	catctgggtg	cgattatagt	cggctgactg	aagcagaaaa	gcgcttctt	660
atgcgacatc	cacaagtaat	taaaaaat	catgataacg	caagaaaagc	tagtgaagca	720
gctaataaat	ttccaggaca	gcacaatgga	gagggcgatg	cggtaagaca	tgtttattgg	780
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gaacaaaatc	cgggacaaga	tattgcagag	aagaatatgg	atctatttaa	taactccatt	900
ggttatcaac	tgggagatct	agcaaaaacaa	aataaatggg	cagaagaacg	tttatttaag	960
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<210> 589

<211> 429

<212> DNA

<213> B.fragilis

<400> 589

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aaccctttta	atcatatacg	tatgaaacag	aagaaaagac	cggcatcaca	aactgaagcc	120
atgaaactga	gatggaaaaa	acggattgtc	tttgagaaa	gatacactga	aatgtgtgcc	180
gaatggattg	cggagcgcct	ggaagcgttg	accgaccatc	tgcaatacgg	gcacgcagcc	240
atcgcttatc	agaagcagaa	cggagacttc	aggttggtga	aagcgacact	gatctactat	300
gaagcgggaat	tccacaagaa	gtatgatccc	acaaaaatag	aaggcgagct	agtctactgg	360
aatgtggacg	aacagcgatg	gacgacattc	cagggtggaga	acttcatgga	gtggagaccg	420
atcgatatag						429

<210> 590
 <211> 2484
 <212> DNA
 <213> B.fragilis

<400> 590
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 ggagtagaag aagttcaaac gattaaaggc ggggttgaag gtctcgtgat tggcgaggtg 180
 ctgacttgcg tggaaacatcc caattcagac catttacaca tcacaaccgt aaatttgggt 240
 aacggcgaac ctactcagat tgtgtgcgga gctccaaacg tagctgccgg acagaaagtc 300
 gttgttgcca ctttgggcac gaagctctat gatggtgacg aatgttttac tattaagaaa 360
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 ggaacttcac atgacgggat catcgtattg ccggaagatg ccgtaccggg tactcttgcg 480
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 aacacttctg tctacgaatt gaaggcttat gtggagaata ttttcaaacg tttaggattg 1980
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 aaagcttttg atgttgataa tgaagtctat tacgctgatt taaactggaa agagctgatg 2160
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 aatcttgaag ccggaaagaa atcttatgct gtcagcttct tgcttcagga tgaaagccag 2400
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<210> 591
 <211> 192
 <212> DNA
 <213> B.fragilis

<400> 591
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aatccggggt aa

192

<210> 592

<211> 579

<212> DNA

<213> B.fragilis

<400> 592

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tatacgggtt	tccttatatt	tataggtcca	tgggctacgg	aacaatcgcc	aacagagata	180
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atcaccggca	tctcttcagt	tgctgttttt	atactgatat	cgggactgag	cctactcttg	480
aaaaacatag	taggagaacg	gaaattacga	cttgaaatac	tcttcatacac	caatctgttt	540
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<210> 593

<211> 723

<212> DNA

<213> B.fragilis

<400> 593

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aatgcgcttt	tctggatata	caacgggcta	cttgtcccgg	tagtagttct	gttgttacta	180
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gccgaacaag	aattgggacg	ttcacgtaca	tttgtcaagc	tgggtcccat	gctcggacta	480
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tcaatggcct	acaatatgca	agtagcattt	gccaccactg	tagtaggtat	ggttatagct	600
gctatcggag	tggtcaccc	gcaaatccgg	caacgttggt	atgcccggtga	aataaacgac	660
cttgaattta	tcagtaaaac	cctaattccat	ggcacgaaac	aaacttctac	acaaccagaa	720
tga						723

<210> 594

<211> 948

<212> DNA

<213> B.fragilis

<400> 594

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cttgccggcca	aaatgcccg	tgccagccgt	accaagctaa	agtctctgtt	gagcaaacga	180
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<210> 595

<211> 1806

<212> DNA

<213> B.fragilis

<400> 595

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<210> 596

<211> 489

<212> DNA

<213> B.fragilis

<400> 596

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<210> 597

<211> 411

<212> DNA

<213> B.fragilis

<400> 597

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<210> 598

<211> 3981

<212> DNA

<213> B.fragilis

<400> 598

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<210> 599

<211> 522

<212> DNA

<213> B.fragilis

<400> 599

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<210> 600

<211> 288

<212> DNA

<213> B.fragilis

<400> 600

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<210> 601

<211> 1812

<212> DNA

<213> B.fragilis

<400> 601

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<210> 602

<211> 1788

<212> DNA

<213> B.fragilis

<400> 602

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<210> 603

<211> 717

<212> DNA

<213> B.fragilis

<400> 603

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ggaatgttac	acatgcctcc	tcctcccaag	gggggtggtcg	gagtgacacc	ggcagtaacg	600
ggcagtggtg	aagcatgcga	agttctcaaa	atcatttggtg	gattcggaga	ggtcctggca	660
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<210> 604

<211> 447

<212> DNA

<213> B.fragilis

<400> 604

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gcaaagctct	gtggcaaaac	ctgggtaaat	gattcggaga	agaatgatgt	agacgagtg	180
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gacgatacga	tggaaggat	tgtttttgac	tatggagtga	acgggggtgac	ttatttcgat	360
aacgtgtggg	tacgtgagca	taatctgtcc	gggaagctga	acggaaaggt	agttgtattt	420
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<210> 605

<211> 1779

<212> DNA

<213> B.fragilis

<400> 605

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agtgtttctc	cgaatttgga	atatgataag	cctatttcca	agcctttacc	tttattgcca	1740
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<210> 606

<211> 789

<212> DNA

<213> B.fragilis

<400> 606

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ggttggtttc	tgattaagtt	aattagtaac	tttgctaaac	ttaacagttt	aacaaaagaa	180
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gctctttttg	aagagggact	ggatattctg	catctcagaa	aaccggaaac	accggctatg	300
tattcagagc	gcctgttgac	actgattccg	gagaaatacc	acaaacggat	tgtcacgcac	360
gaacacttct	atctgaaaga	agaattcaac	ctgatgggaa	ttcatctgaa	tgcacgaaat	420
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gtgaaagatt	tcggattcgg	aggtgcagta	gttttaggag	atttatgggg	caaattcgac	720
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<210> 607

<211> 330

<212> DNA

<213> B.fragilis

<400> 607

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cgattcaata	tgaccgaaat	tttctccaaa	gaagattata	cgatggtaaa	gaatcccga	180
caagagaaca	tggagattat	cacaaaagaa	ggtaaagaga	ttaaagcata	tactccatcc	240
gaacagaaag	aatcatccgg	taaaccgagg	aagaaagtag	gtgtagccta	tgaactcgag	300
aatggaaaga	tcattttatg	cctgaataa				330

<210> 608

<211> 924
 <212> DNA
 <213> B.fragilis

<400> 608
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 gggttcgggca ctgcgttata tccgatcacc aaaggagtca gtaagcagtt gcttccgata 120
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<210> 609
 <211> 1437
 <212> DNA
 <213> B.fragilis

<400> 609
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 tttgtacctt acgtagtgcc gggcgacgtg gtagatttgc aggtaaaaag aaaaaagaat 180
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<210> 610
 <211> 507
 <212> DNA
 <213> B.fragilis

<400> 610

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ctttgcacgg	caatagcatt	ttcggcatgc	aaatccaata	aagccggaca	ggacaccgca	180
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<210> 611

<211> 945

<212> DNA

<213> B.fragilis

<400> 611

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<210> 612

<211> 261

<212> DNA

<213> B.fragilis

<400> 612

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aatctgcaag	gaatttcacg	tctggtgacc	ggaatgcctg	tgtcggatgt	cattacgaag	180
cttgaaggga	tccgggtgtg	ggctcgctct	acttcatgtc	ccgaccaact	atgccgtgct	240
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<210> 613

<211> 618

<212> DNA

<213> B.fragilis

<400> 613

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<210> 614

<211> 894

<212> DNA

<213> B.fragilis

<400> 614

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<210> 615

<211> 360

<212> DNA

<213> B.fragilis

<400> 615

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<210> 616

<211> 291

<212> DNA

<213> B.fragilis

<400> 616

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ctcagccacc	gggtggcacc	cctttgtctt	tacggaggca	aagtaagtga	aaaagaaaat	180
aagaagaaag	taaatcgggg	attatttcat	cgcggagtca	tgcggaattt	gtttttgccc	240
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<210> 617

<211> 357

<212> DNA

<213> B.fragilis

<400> 617

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tatttacttt	catttatccc	caaacacacc	tatacgaata	tgaaagtaca	agtgaacaac	180
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gaaaacggtg	tagccatcgc	cgtcaacaac	cgaatgatac	cgcgtccgca	atgggacgga	300
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<210> 618

<211> 2730

<212> DNA

<213> B.fragilis

<400> 618

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aagctggaca	acgagctcga	ggtggaagat	ctcaaggaa	tcgtgaagaa	atttaaagct	600
gccgtaaaag	cacaaacagg	caaggacttc	ccgacttggt	catacgaaca	gctttgggga	660
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<211> 1419
 <212> DNA
 <213> B.fragilis

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 <211> 591
 <212> DNA
 <213> B.fragilis

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 aattttctatc atccggaagc tgaagggggc attgcctgga atgatccgga tttgaatatc 480
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 <211> 423
 <212> DNA
 <213> B.fragilis

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 acctcagtca gtatccccat ccggaatcac cgtctgaacc tcggaacctg gcaagggatc 360

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<210> 622

<211> 471

<212> DNA

<213> B.fragilis

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<210> 623

<211> 1311

<212> DNA

<213> B.fragilis

<400> 623

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<210> 624

<211> 291

<212> DNA

<213> B.fragilis

<400> 624

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<210> 625
 <211> 462
 <212> DNA
 <213> B.fragilis

<400> 625
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 aatacatttg tgtttataaa taacgatgga tcaatatcaa tagaaacagt ttcaagatct 360
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<210> 626
 <211> 1188
 <212> DNA
 <213> B.fragilis

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 <211> 936
 <212> DNA
 <213> B.fragilis

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 agtaaagtaa agaaaagtag agcaaaggaa aataaagaat taccctctc agttcccccc 660

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<210> 628

<211> 801

<212> DNA

<213> B.fragilis

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<211> 765

<212> DNA

<213> B.fragilis

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<210> 630

<211> 582

<212> DNA

<213> B.fragilis

<400> 630

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<210> 631

<211> 2871

<212> DNA

<213> B.fragilis

<400> 631

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 <211> 1146
 <212> DNA
 <213> B.fragilis

<400> 632
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<210> 633
 <211> 1935
 <212> DNA
 <213> B.fragilis

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<210> 634

<211> 228

<212> DNA

<213> B.fragilis

<400> 634

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agcaacatgg	gacgatggga	cgactccatt	aataacctga	tttccctcca	ggctatcaaa	180
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<210> 635

<211> 1353

<212> DNA

<213> B.fragilis

<400> 635

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gcaaaaaaat	taacattagt	agaacaagga	tactattata	cttttatcag	tgtattgtat	180
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<210> 636

<211> 186

<212> DNA

<213> B.fragilis

<400> 636

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aaaatcataa	acacttattt	tctaccattt	tctttaatcc	gaagtattca	tttgagtatt	180

atttga

186

<210> 637

<211> 918

<212> DNA

<213> B.fragilis

<400> 637

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gaagataaaa	tacagaaata	cagaaaacaa	ggttacaaac	ttcctccacg	caaggtattg	180
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gaaatattga	cttattaa					918

<210> 638

<211> 1011

<212> DNA

<213> B.fragilis

<400> 638

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<210> 639

<211> 849

<212> DNA

<213> B.fragilis

<400> 639

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gcaggatatct	ggttccccggc	ccgtcagttc	atgaaaatcc	agccggcaga	ggcattgcac	840
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<210> 640

<211> 441

<212> DNA

<213> B.fragilis

<400> 640

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gagccatcaa	gcaccaacaa	cacctcgttt	ggagcatcag	gcactacttt	cttcattaca	180
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gaagccggat	cggcccccat	cttttggtta	atgaccggaa	catccactct	ctcgccccat	360
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<210> 641

<211> 1092

<212> DNA

<213> B.fragilis

<400> 641

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<210> 642

<211> 288

<212> DNA

<213> B.fragilis

<400> 642

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ggtgggtcata	attttaagga	agggaaaagt	gtcgggaatac	atcttgagcc	tggtccggat	180
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<210> 643

<211> 699

<212> DNA

<213> B.fragilis

<400> 643

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ggtctatttta	tgatatctct	taaagaaggg	tcaggagtaa	aagaaatctt	agtatgtccc	600
tctatttttaa	tacgttcacc	cgtattgaca	tttacacttt	cacgactatt	gacccctatc	660
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<210> 644

<211> 723

<212> DNA

<213> B.fragilis

<400> 644

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gatgcgatgg	aacaatacgt	tgccgcaacc	agtatagaaa	aagataaagc	taaactggga	300
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gaaatgtcta	aggagaatgc	ggaacagctg	ctcaattctg	tgatgcaaga	tgaaaaaggg	660
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<210> 645

<211> 192

<212> DNA

<213> B.fragilis

<400> 645

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aaaaaagatc	tatttgatca	ttacatcatt	ttctcgattt	cttcgaattc	cgtgcccata	180
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<210> 646

<211> 1068

<212> DNA

<213> B.fragilis

<400> 646

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<210> 647

<211> 651

<212> DNA

<213> B.fragilis

<400> 647

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<210> 648

<211> 984

<212> DNA

<213> B.fragilis

<400> 648

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gcgggtggccg	gaaaatcgaa	ggtggatgat	gaagtgttgg	ataatctgga	agaggtagtt	180
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gcagtagcta	ataacgctga	tgtggtgatt	attgatacag	caggacgttt	gcacaataaa	660
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atcggattgg	gtgaggggat	ggaagaccta	caggtgttcc	gcaagaaaaga	atttgtagac	960
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<210> 649

<211> 1200

<212> DNA

<213> B.fragilis

<400> 649

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<210> 650

<211> 369

<212> DNA

<213> B.fragilis

<400> 650

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<210> 651

<211> 1848

<212> DNA

<213> B.fragilis

<400> 651

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<210> 652

<211> 282

<212> DNA

<213> B.fragilis

<400> 652

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gctgggtttg	gtattattaa	taagaaaggt	ttggacgctg	ctttgaatga	tgcggttgcc	240
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<210> 653

<211> 840

<212> DNA

<213> B.fragilis

<400> 653

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<210> 654

<211> 207
 <212> DNA
 <213> B.fragilis

<400> 654

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aacagaaaaa	atactactga	aagacttgag	ttgaagaagt	acaacccaat	tctgaaaaga	180
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<210> 655

<211> 3390

<212> DNA

<213> B.fragilis

<400> 655

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<210> 656

<211> 1479

<212> DNA

<213> B.fragilis

<400> 656

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<210> 657

<211> 2543

<212> DNA

<213> B.fragilis

<400> 657

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<210> 658

<211> 996

<212> DNA

<213> B.fragilis

<400> 658

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gatgcacgag	tatatgcgca	tgcccctaaa	agttacaaga	attatctgct	tcattgtaccg	180
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gtttatgaag	agattgataa	attggaaaaa	acaaagttga	atgtgaaaga	gtacagtaaa	900

cgtcaggaag aatatcggtt gtttgcgtta gctgcattct tatgtatatt gcttgaggta 960
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<210> 659

<211> 870

<212> DNA

<213> B.fragilis

<400> 659

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<210> 660

<211> 1365

<212> DNA

<213> B.fragilis

<400> 660

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 gattcagaac agttgatgcg tcaattggaa gaagccggat atgatgtaac ccatgactcg 180
 gaaaaaccga caggagagat agctgttatc aatacctgtg gttttatcgg tgatgcaaaa 240
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<210> 661

<211> 1248

<212> DNA

<213> B.fragilis

<400> 661

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gtaattcgtg	tcgtgtctgt	acgagatcgg	gcagatgaga	ttattgaagc	tgtagatgct	180
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<210> 662

<211> 1005

<212> DNA

<213> B.fragilis

<400> 662

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ttggtagagt	cactgttaat	cggactactt	tctgatggac	acgtgctgct	tgaagggtga	180
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<210> 663

<211> 1257

<212> DNA

<213> B.fragilis

<400> 663

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<210> 664

<211> 303

<212> DNA

<213> B.fragilis

<400> 664

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caggaaagca	atgctatagg	aatacagga	tttggtactt	ttgaggtaaa	aaagaaagca	180
gaacgtattg	tcataaatcc	cgctactaag	ttgcgactgt	tggttccacc	caagttagta	240
ctggcggttta	agccgagtcc	tatattaaaa	gataagttta	aagaaacatt	tccgtatgaa	300
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<210> 665

<211> 441

<212> DNA

<213> B.fragilis

<400> 665

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gagggcagta	acgactttcg	tcgtgaccgt	gaagggaatg	taattgtgac	tcgtctgaat	180
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tctaattctg	ctcagaaaagc	tattaatcaa	gagattaata	aaatggctaa	atcggatggt	300
gaatctaagg	tttatacaga	ttacaatgaa	cagttccaag	tgattgcatg	gatgatattg	360
ctcttggttat	tgggtgaaat	gttgattctg	gaccgcaaaa	atccattggt	taagaacatc	420
aggttggtttt	ctaataagta	g				441

<210> 666

<211> 216

<212> DNA

<213> B.fragilis

<400> 666

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atcgacaacc	ggccggttta	tggtttctct	aaagacaaga	gatcaccatt	tcttgccctt	180
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<210> 667

<211> 1551

<212> DNA

<213> B.fragilis

<400> 667

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accgtcgcgg	cgcagagcct	ccctcccaca	caggaaactt	cgcaacatca	gcttagcttt	180
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<210> 668

<211> 201

<212> DNA

<213> B.fragilis

<400> 668

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agttccggga	cattctcccc	tatatgggta	agaaaacaaa	aagggatagt	tagcagaaaa	180
tgccattacc	tgtctttttg	a				201

<210> 669

<211> 435

<212> DNA

<213> B.fragilis

<400> 669

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catatcaatg	ggatgcctgc	tttgtcaagt	gcttccgaag	caaagaaaa	gtgtatgttt	180
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ttgaccaatg	cacgtaaatg	cctgaaaaca	gcacgttgca	ttactgatgc	gttgcgggaa	360
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<210> 670

<211> 807

<212> DNA

<213> B.fragilis

<400> 670

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gagaacgtcc	taatgattga	tgacgaaagc	ctgacccaat	atcttgatgt	tcaccagacc	180
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gtactcctct	cacaatgtga	cgacgaaacta	tttctattga	aaacccagaa	actacaccaa	300
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aacgcactaa	gggatgccaa	cttcatcatt	gtccgcaaag	acggaaacat	cgagctgtca	780
ccagagatcg	ctgcactggg	aatataa				807

<210> 671

<211> 1242

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (1135)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 671

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acctctcgac	gcctctactt	cggtgtctgc	ctggtacttc	cgttgttcac	gctctttttc	180
atggctacca	tattcggcaa	cgggcagatg	gaaaatatcc	ccatcggcac	tgctcgaccgg	240
gacaacacgg	ccacttcgag	agatattacc	cggcggatgt	ctgccgtacc	caccttccgg	300
gtaacccgcc	acttcgttga	cgaagccgag	gcacgcaaaag	cggtagacga	gaaagaaata	360
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ggagtgaacg	aacagcagat	agaaaccttt	ctactccccg	tgcaagccaa	caatcatccc	600
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ccttcggcag	tgatactctg	tatcttcccc	ttattggcgt	tggcgatgct	tccgcacctc	1200
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<210> 672

<211> 753

<212> DNA

<213> B.fragilis

<400> 672

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aagaatcccc	gtccgtgggt	aaagatgggc	atgaagctat	atatgatttt	tctgtatttg	180
tggattgcta	tgcacatatta	tgccatctgt	tgtgacgagc	gcagttataa	cggggcgctg	240
gctatgttct	gggtgggttat	ggccacgata	tgggtatggg	atgccatcac	cggatatact	300
actttcgaac	gtacatataa	atatgatatac	ctttcgtacg	tattgttgat	tttaccattt	360
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attaattggg	tgtttgtctt	tgtatgcgta	tctatcgga	tcttacttac	caccaccctg	720
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<210> 673

<211> 1503

<212> DNA

<213> B.fragilis

<400> 673

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<210> 674

<211> 1203

<212> DNA

<213> B.fragilis

<400> 674

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gtttatgggt	tgctctataa	ctatatgtat	gtccccaata	tctgacccga	cgctccgggtg	180
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gggtgccgtat tctctccccc gcagggactg cttgccgtgg ccatggccaa gcccgtaaac 540
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<210> 675

<211> 966

<212> DNA

<213> B.fragilis

<400> 675

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<210> 676

<211> 621

<212> DNA

<213> B.fragilis

<400> 676

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gaacgcctgg cgttatccct ctctcctaact ccggtttact tggccacctc acgtatctgg 240
gacgaagaat ttctgcaaag ggtattgcgc catcaagcca accgcggacc ggaatggacc 300
aatatagagg aagaaaaaga attgagccgc cactcttttg aagggcggtg agtgctgatc 360
gattgtgtaa ccctctgggt caccaattat ttctttgatc tcgaagcaga caccgacaag 420
gcaactgact ctgttaaagc cgagtttgac cgactgacac aacaggacgc gacccttatt 480
tttgtcacca acgaaatcgg tatgggagga acttcagaaa acctgatata acgaaagtcc 540
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atggaacggg gattcctgtg a 621

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<210> 677

<211> 1509

<212> DNA

<213> B.fragilis

<400> 677

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ggatgtatgg	tgattaagcc	ttacggatac	gctatttggg	agaaaaatgca	gcgtcagctg	180
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<210> 678

<211> 507

<212> DNA

<213> B.fragilis

<400> 678

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tggaatccat	ttgtgccatt	ttctctcttc	cggtaaccca	ttggaaagat	tgcaatcggt	420
gttcggacat	atcaatggga	tgcttgcttt	gtcaagtgtc	tccgaagcaa	agaaaatgtg	480
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<210> 679

<211> 345

<212> DNA

<213> B.fragilis

<400> 679

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ccatataggg	gagaatgtcc	cggaaacttt	tgcttctttg	cccagaaaac	cgggcttggg	180
aaggggaaga	gtctgtgttt	tcacttcgaa	gagccgatat	ttcgacaaa	agaagtaagc	240
atttactccg	aaagacggtt	gtgtttttca	aaaatgaata	agagttttgc	ccaatatctc	300
tatatgtttt	cttccattac	atatattgtt	cttatttggg	agtga		345

<210> 680
 <211> 1002
 <212> DNA
 <213> B.fragilis

<400> 680
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 gtcttgcaag ggcaggccga agctaccgag attcgcatca gcgggcaaact gccgggacgc 180
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 acgggcagct atgatttaca gacattcgaa atccatgctc gtcccaccaa gaaagtggag 960
 gggctgcgtc cgggaatgtc ggtactggta gaaatcaaat ag 1002

<210> 681
 <211> 411
 <212> DNA
 <213> B.fragilis

<400> 681
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 agtaagaagt atcattcaat aattaaagat tacgcagctc tgatagaaga tttaaaaaag 180
 aatccgcata taggggtaga cctgggaaac ggcatacgaa aagtacgaat ggctatagcc 240
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<210> 682
 <211> 498
 <212> DNA
 <213> B.fragilis

<400> 682
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<210> 683
 <211> 840
 <212> DNA
 <213> B.fragilis

<400> 683

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tattcggccc	atttgatggg	agcagggtgtg	catacctccc	gtgtgatccg	taattcaaag	180
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catccgatca	gttttgaaca	taactcagag	ttgagtgcct	tgagctggga	ggtttacgac	360
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tttgggtggcg	atattatttc	tatgggcatt	gtcttttcgg	ctaccatcac	cggacttttc	540
ctgaagcaac	agatgcagaa	gaagaaaatc	aatcattata	ttattttcat	tgtttccgct	600
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<210> 684

<211> 1743

<212> DNA

<213> B.fragilis

<400> 684

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<210> 685

<211> 576

<212> DNA

<213> B.fragilis

<400> 685

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gcagtgatcg	gcattatccg	ttcattgtctc	cctcaggagc	atgactggca	gaagttgctg	180
caccacctcc	aaagagagtt	aatggtagtt	atgagtcattg	tggctactcc	atccgccatt	240
cgcgataaga	atccgaatgt	gctgtcgcgc	ggactggcgg	ctttctgtga	gcaagagatg	300
gatacaatga	ctgccggact	gaaagagaac	ggttatttcc	tgttgcccg	tggcacacct	360
gtctctgctc	agttacagtt	tgcccgtaac	gtagcccgcc	gtgcagagcg	gcggctctgg	420
accttgaatc	ggcaagatgc	tgttccggaa	gatattctga	gctttatcaa	tcgtctgtcc	480
gatctgtttt	ttgtaatggc	acgttctgac	atgcaacaac	aggactggcc	ggaggaacgc	540
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<210> 686

<211> 783

<212> DNA

<213> B.fragilis

<400> 686

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tag						783

<210> 687

<211> 978

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (704)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 687

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cttctgtctt tgagttaa

978

<210> 688

<211> 399

<212> DNA

<213> B.fragilis

<400> 688

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atggccttatc	togaattaga	agcagaaaaa	gcagaactga	tccggactat	tgccaacata	180
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ttctgcgaac	aagaaagagt	aagaaccgga	gaaagcaagt	caagaccggc	cgaagaacta	360
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<210> 689

<211> 3255

<212> DNA

<213> B.fragilis

<400> 689

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<210> 690

<211> 1347

<212> DNA

<213> B.fragilis

<400> 690

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<211> 2466

<212> DNA

<213> B.fragilis

<400> 691

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<211> 870

<212> DNA

<213> B.fragilis

<400> 692

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870

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<211> 312

<212> DNA

<213> B.fragilis

<400> 693

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<210> 694

<211> 753

<212> DNA

<213> B.fragilis

<400> 694

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<210> 695

<211> 201

<212> DNA

<213> B.fragilis

<400> 695

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<210> 696

<211> 531

<212> DNA

<213> B.fragilis

<400> 696

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<210> 697
<211> 312
<212> DNA
<213> B.fragilis

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<210> 698
<211> 195
<212> DNA
<213> B.fragilis

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<212> DNA
<213> B.fragilis

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<211> 360
<212> DNA

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 <212> DNA
 <213> B.fragilis

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 <212> DNA
 <213> B.fragilis

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<211> 2367

<212> DNA

<213> B.fragilis

<400> 705

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<210> 706

<211> 1143

<212> DNA

<213> B.fragilis

<400> 706

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<210> 707

<211> 402

<212> DNA

<213> B.fragilis

<400> 707

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<210> 708

<211> 1929

<212> DNA

<213> B.fragilis

<400> 708

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<211> 870

<212> DNA

<213> B.fragilis

<400> 709

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<210> 710

<211> 579

<212> DNA

<213> B.fragilis

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<210> 711

<211> 597

<212> DNA

<213> B.fragilis

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<210> 712

<211> 2031

<212> DNA

<213> B.fragilis

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<210> 713

<211> 759

<212> DNA

<213> B.fragilis

<400> 713

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tggatttctt	taggcaggca	agtagcctca	gaattaacat	tgcactatga	caatataccc	660
caaaattcag	tactttggct	tcggaattta	tcaagaggga	gagaagaaac	cgtatttcga	720
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<210> 714

<211> 948

<212> DNA

<213> B.fragilis

<400> 714

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aagagcaaa	acgtttgcat	cggagctgtt	gtaaccacca	tactgtact	gatagggtcaa	720
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gaattttacca	aagcatgggc	aaacgaaatg	ggaagtaaaa	ttttccccga	cgaatatgca	900
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<210> 715

<211> 192

<212> DNA

<213> B.fragilis

<400> 715

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ctacccaaaac	tgttgctctc	catcgggtctt	cttaaagatc	cgttcgtcct	ttccctccgt	180
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<210> 716

<211> 2181

<212> DNA

<213> B.fragilis

<400> 716

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aacggagtct	cactgaaaga	tgccgtaggt	atcttcgggg	gaggatgtac	cggcgagatt	240
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<210> 717

<211> 1044

<212> DNA

<213> B.fragilis

<400> 717

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acgtcaacta	cagatttctat	ttatgctgtg	tttgcttatc	cggaaatgaa	atttttgagc	300
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ttggtaaaaag	atgattcgtt	atatttataat	catttaaacag	ataaggattt	gttgcagaaa	420
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aatgataaaa	tgtatacagc	tcattgcata	acggatcctt	cttataatga	tattagggtta	540
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<210> 718

<211> 798

<212> DNA

<213> B.fragilis

<400> 718

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<210> 719

<211> 1158

<212> DNA

<213> B.fragilis

<400> 719

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<210> 720

<211> 282

<212> DNA

<213> B.fragilis

<400> 720

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<210> 721

<211> 873

<212> DNA

<213> B.fragilis

<400> 721

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<210> 722

<211> 411

<212> DNA

<213> B.fragilis

<400> 722

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<210> 723

<211> 1068

<212> DNA

<213> B.fragilis

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<211> 564

<213> B.fragilis

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<211> 2172

<213> B.fragilis

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<210> 726

<211> 1560

<212> DNA

<213> B.fragilis

<400> 726

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<210> 727

<211> 1503

<212> DNA

<213> B.fragilis

<400> 727

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<210> 728

<211> 2013

<212> DNA

<213> B.fragilis

<400> 728

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<210> 729

<211> 1032

<212> DNA

<213> B.fragilis

<400> 729

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<210> 730

<211> 777

<212> DNA

<213> B.fragilis

<400> 730

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<210> 731

<211> 195

<212> DNA

<213> B.fragilis

<400> 731

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<210> 732

<211> 582

<212> DNA

<213> B.fragilis

<400> 732

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<210> 733

<211> 1026

<212> DNA

<213> B.fragilis

<400> 733

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<210> 734

<211> 351

<212> DNA

<213> B.fragilis

<400> 734

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<210> 735

<211> 1056

<212> DNA

<213> B.fragilis

<400> 735

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<210> 736

<211> 594

<212> DNA

<213> B.fragilis

<400> 736

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ctggtagaag	aaaagaatcg	gttgcgttac	accattttct	cgtcgatttt	gttaataacta	540
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<210> 737

<211> 2175

<212> DNA

<213> B.fragilis

<400> 737

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gccggacaga	aagcagccac	cgatgccgga	aacccttttc	tggcagagta	ttcaactcct	180
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ggaatggaag	aacagaaaaa	agaaatagat	gctattgtca	atcagcgttc	ggttcccgat	300
ttcgataata	ccatcgctgc	attcgatcag	agtggagagt	tgtaaataa	ggtagagtact	360
gtgttttagtg	gtctgaacag	ttgtaacacg	aacgatgaaa	tcagggtttt	taataaagag	420

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aataggggac	tatag					2175

<210> 738

<211> 738

<212> DNA

<213> B.fragilis

<400> 738

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aggatgttaa	taataggaat	agcaggcgga	acaggctcgg	gaaagaccac	cgctcgtaagg	180
aaaatcattg	agagcttacc	agctgggtgaa	gtagtattgc	tacctcagga	ttcatactat	240
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gctttttgaat	ggagcctttt	gtctaaacat	gttgccctcc	ttaaagaagg	caagtgtatc	360
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ccacgtgaag	tggtcataat	cgaagggtatc	ctggctttat	gtgacaaaaa	gctgcgcaat	480
atgatggatc	tgaaaatatt	tgtagatgcc	gatccggacg	aacggttgat	ccgtgtgatc	540
caacgtgacg	tagtggaag	gggcccgcact	gcagaggctg	taatggagcg	atatacgcgt	600
gtgctgaaac	ctatgcattt	acagttcatc	gaaccatgta	aacgctacgc	agattttgatt	660
gttcccgaag	gaggagcaaa	tcaagtagcc	atcaatatat	tgaccatgta	tataaaaaaa	720
cacatcggtg	ggccatga					738

<210> 739

<211> 1395

<212> DNA

<213> B.fragilis

<400> 739

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aaagatagcg	gagaactcgt	tgttctgact	ctttatagtt	ctacttctta	tttcatctat	180
cgtgggcaag	acatgggttt	ccaatacgaa	ctcagtgaac	aatttgccaa	aagtttagga	240
gtgaaattgc	gaatagaagt	agccaaaaac	gtaccggaac	tcacccgaaa	gttactaaat	300
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atctattgtg	gcgaagaagt	aatcacccac	caggtaattg	tccaacgaac	caatgggaaa	420
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attccttata	cagtggctga	taatgatgtc	gctaagttga	atgcgactta	ttatccta	660
ctgaatacca	gtctgtctat	cagttttgac	caacgcgctt	cctgggctgt	acgtaaagat	720
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ctactaaaaa	gcaatgaaga	atatttccact	gatccggtat	gcaaaaacgg	atatttccgt	1320
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aaaataaaaa	gttga					1395

<210> 740

<211> 1431

<212> DNA

<213> B.fragilis

<400> 740

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tttcccgccg	gtcctcattt	aggctccttc	gtagtgtcat	ggcgtgcggg	gagctgtcgc	180
gagttcgccg	atttggtagt	gtatgtaatg	cgtgcttttg	gtattccttg	cgggacagac	240
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tataatccta	aggcaaagg	ataccggaat	acgtatggct	taaactggaa	agatgtaaag	420
agacaacagg	gaaaaatgat	gcatccggcg	tttcgaaaac	ctctatatca	ggaatgtcacg	480
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tctttaaatt	atgtaattcc	gaaaggggta	gccttatttt	taaagaatca	tacggaggga	1380
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<210> 741

<211> 720

<212> DNA

<213> B.fragilis

<400> 741
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 catttcggcg tattgaggggt actgaatgat gatagcggtg accctgaaat gggattcgat 180
 acacaccctc accagaatat ggaagtcatt tctatcccc tgaaggggtta tctgagacat 240
 ggcgacagcg taaaaaacac ccggacaatc acaccggcg atatccaggt tatgagtacg 300
 gggaaaggta tcttccacag tgaatataat ggaagtgaca aagagcaatt ggaatttttg 360
 caaatatggg tattcccgag aattgaaaat acagagccgg aatataacaa ctacgatatt 420
 cgtcctttac tgaaaagaaa cgaacttgct ctaattatct caccggacgg taaagtaccc 480
 gcttccatta agcaagatgc atgggtttct atgggaacat ttgacgcagg aaagagtttc 540
 gaatacaagt tgcacagga aggtaacgga gtttatcttt ttatcatcga aggagatgtg 600
 gaagttgcag gcaaccgatt gtcacgacgt gacggcatcg gtctttggga tacaagagc 660
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<210> 742

<211> 1482

<212> DNA

<213> B.fragilis

<400> 742
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 agttgtatct ttgcaacctg caaacttaaa cccttcttta tgtataccaa caaacagatc 180
 tggagtgtca gttaccgat tctcctgagc ttgcttgccg aaaatgtcat caacgtcacc 240
 gacactgcct ttctgggacg tgtcagtgag atagccctcg gtgcttctgc catgggtggg 300
 cttttctata tttgtatttt caccattgcc ttcggtattca gcaccgggtc ccagatcgct 360
 attgcccgc gcaacgggtga agcacgttac ggcgatgtag gtccgggtcat gattcaggga 420
 gtcttggtcc tgttggtcat ggctctctcg ctcttcggat tcaccaaagc gttcggcgga 480
 aacatcatgc gctgctgggt ctcttccgaa agcatttatg atgccacgat ggagtttctc 540
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 gtggtactgg actatgccct gatattcgga cacttcgggc ttccggaaat gggcatcaaa 720
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 atcacgattg caatctacgg atcgtacatc attttcatcg gaatgtgggt gaaagctccc 1380
 atcgaatggg gctttacgat tgagattctg tactatacac tgttgctcgc cacaagctat 1440
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<210> 743

<211> 1269

<212> DNA

<213> B.fragilis

<400> 743
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 gagtttgccg gggagaatag gggagagcct gaaaaagttt tggaacacta taatgatagc 180
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gaagtttttg	aaaaaagatc	ctggaataaa	tatttgccat	ttgatgattt	ctgtgaattg	480
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tgccctgggtg	tgtttacatt	ggaaggatgt	atgcccatag	atataactgt	gcagaaagga	1140
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gggatgaagt	gggtggcagc	cggataccct	ttccagtgtg	gacgaaaagg	gagagggtgaa	1260
gtatcataa						1269

<210> 744

<211> 504

<212> DNA

<213> B.fragilis

<400> 744

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gaagtgatta	gcacctggcg	tccccgtccc	gaataccagg	gatggattga	tacactacat	180
ggaggtatcc	aggccgtact	tttggtatgaa	atctgtgcat	gggttattct	ccggaagtta	240
cagactacgg	gggtgacatc	aaaaatggag	acacgttatc	gtaagtcgat	cagtactaat	300
gattcacatg	tagtgctcaa	agcgcatatt	aaagaagtga	agcgtaacat	tgtgataatt	360
gaggcacgtc	tttataataa	agatgaggaa	ttgtgtacag	aagctctctg	cacttacttc	420
acttttccga	aggagaaagc	cagagaagag	atgcattttt	tgtcatgcga	agtagaagat	480
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<210> 745

<211> 1017

<212> DNA

<213> B.fragilis

<400> 745

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gaacggaatg	agggacaacc	attacctgca	ttgaccttcc	tccatattcc	gctaccggag	660
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cgtatcatcg	tattgaaaga	aggtaaacgt	gaattcgata	cttggcttcg	ggaaaaagga	960
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<210> 746

<211> 3165

<212> DNA

<213> B.fragilis

<400> 746

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attggtgcca	ctatcatggt	gaaaaactca	tcaaacggaa	ctgtcaccca	tatagatggt	180
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acagtagaga	aagaggtagg	taacaacact	gtaatcaatg	ttgaactgtc	cgatgacatt	300
caggccatcg	acgaggtagt	ggtcactgca	atcggtatca	agcagcaaaa	gaagaagatc	360
ggttacacaa	cccaacaaat	caacagtgcg	gtattgaatg	ccactcccag	tctgaatgtg	420
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<210> 747

<211> 1251

<212> DNA

<213> B.fragilis

<400> 747

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cggctttatc	aagaaaatcc	caaacatgtg	atgagcgtatg	aactgcttga	aaagtttattc	180
gagcaatata	tcaattcgca	aacctatgccg	caagtactct	tcacctggca	cggaggagag	240
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cgtggaagaa	gcatagacaa	ctgcatacag	actaacggaa	ccctgttgac	cgacgagtgg	360
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<210> 748

<211> 615

<212> DNA

<213> B.fragilis

<400> 748

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gcgttggata	atatttttgc	acgtaaaagt	gtgcgggctt	atttagacaa	ggaagtagaa	180
aaagaaaaaa	tagattggat	gctacgtgcc	ggtatggctg	caccatccgg	aaaagatatt	240
cgtccgtggg	agtttgtatt	ggtcacccgac	cgggttgcct	ttgattcgat	ggccgctgct	300
ttaccttatg	caaagatgct	gactcaagct	cgctatgcc	ttgttgtatg	tggagatgta	360
gctcaatctt	cctattggta	tctggattgt	tccgctgctg	cacagaatat	attattggct	420
gccgaagcac	aggggctggg	tgcggtatgg	acagctgctt	atccttatga	agaccgtatc	480
aggggtgttc	gtaaatatac	ggagcttccg	gggaatatag	tgccctgtg	tgtgattccg	540
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taccgataagt	tttaa					615

<210> 749

<211> 849

<212> DNA

<213> B.fragilis

<400> 749

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aatttaaacac	aacaggcaac	tcaggattta	gtgattgccg	aatctgcatt	agctattatt	180
gtcgtgccgg	tatatggagg	tcgtgtagcc	cctttggcca	tggatcgtct	ggcaagtgtg	240
cgcggaagta	atactccggc	ggttatcgtg	gtggtatacg	gtaaccgtgc	ttacgaaaaa	300
tcgttgatgg	aacttgatta	ttgggctatt	caacaggggt	ttaaagtgat	tgccggtgct	360
actttcatag	gagaacactc	ttatagtaca	gaaaaatatac	ccgtagctgc	cggacgtcct	420
gacgaacgtg	accttgctgt	ggcagccgat	tttggaagc	agatttcaga	taaaatagca	480
tctgctaccg	aaccggaaaa	attatatgcg	gtcgtatgtcc	gtaaaatccg	gcgtccgcgt	540

cagccttttt	ttccattgtt	tcgctttttg	cggaaagtga	ttgccttgcg	taaaagtgga	600
gttccccctt	cccgtactcc	ttgggtggaa	gatgaatctt	tgtgtactca	ctgcggtacg	660
tgtgcgaaaa	tgtgtcctgt	aagcgccata	gccaaaggtg	acgagttgaa	tacggatgcc	720
gaacgctgca	ttaaatgttg	tgctgtgtga	aagggatgcc	cacagaaagc	cagagtatat	780
gataccccgt	ttgccgtact	actgtcgcaa	tgttttgta	agcagaaaga	tccctgtacg	840
ttgggtttaa						849

<210> 750

<211> 906

<212> DNA

<213> B.fragilis

<400> 750

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tggattgtga	atatctgttt	ctattcttgt	gtggcttttg	ttgcctggat	ggtattgcag	120
gtgttttgcc	tgacttcttt	caaaattccc	tccaattcaa	tggaaaccgg	attgctttcg	180
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tcattgcgag	gagaagaagt	ggatatctat	cgtctaccgg	gtttcggatc	gtttcagcgg	300
gacgatgtgc	ttgtttttta	tttcccttat	caggatggga	gcgacagcat	cggatttgat	360
ataatgaagt	attatgtgaa	acggtgtatt	gccttgccgg	gtgatacttt	ggaaatacgt	420
aagggctatt	atcatataaa	aggaatcaca	gacagtgtgg	ggaatgtgca	ggcgcaacat	480
cggattgcac	gtgtcagaag	ggaagattca	catgggatcg	tgatggatgc	ttttccgtgg	540
gacggacgtc	tgggatggac	cattcaggaa	ttcggacctc	ttccggtacc	ggccaaaggg	600
caggtggtga	aaatagatac	attgtcttgt	ttgctttacg	gaagattgat	ccattgggag	660
cagaagaaga	gactgcggca	aaaaggagag	gcggtatgtc	tgggcgatag	tgcaataacg	720
gaatataagt	tcacagagaa	ttactatttc	gtatcgggag	ataatatgga	aaattccaag	780
gattcacgtt	attgggggaat	gttgcccgaa	tcataatattg	taggtagggc	atttacaata	840
tggcggtcgg	acgatccttt	acgtggaaag	attcgttgga	accgggtatt	taaaagaata	900
aatga						906

<210> 751

<211> 1278

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (524), (1246), (1269), (1270), (1271)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 751

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ctgctcgatg	ccgacgttaa	ctataaagta	gccaaaggat	tactgatac	ggtgaaggaa	180
aaggcactgg	gacagaacgt	gctcacagcc	gtaaaaccga	gccagttgat	ggtgaagatt	240
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cagccggcag	tcacctctgat	gtccggtttg	caaggttcgg	gtaagaccac	tttctcgggt	360
aagctggccc	gcatgctgaa	aaccaagaag	aacaaacgcc	cgttgctcgt	tgcatgtgac	420
gtttaccgtc	cggcagctat	cgagcagctt	cgcgtatttg	ccgaacagat	tgacgtaccg	480
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gcacgtgcc	agggatacga	tctggtaatt	gtcgaatcgg	ccggacgtct	ggcagtcgac	600
gaacagatga	tgaatgagat	cgctgccatc	aaagaagcca	tccagcccaa	cgaaattctg	660
ttcgtggtag	actctatgac	cggacaagat	gcggtcaaca	cagccaaaga	gttcaacgaa	720
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gacatcgttt	cgttggtgga	acgcgcacag	gaacaatatg	acgaagaaga	agctaaacgc	960
ctccaaaaga	agattgccaa	gaaccagttc	gacttcaacg	acttcctcag	ccagatgtcc	1020
cagattaaga	aaatgggtta	tctgaaagag	ctcgcttcaa	tgattccggg	tgtgggcaag	1080

gccatcaaag	atatacgatat	cgacgacaac	gctttcaaaa	gcatcgaagc	catcatctac	1140
tccatgactc	cggaggaacg	cagcaatccg	ggcatcctga	acggttcgcg	ccgtacacgt	1200
atcgccaaag	gtagcggtag	gactagtctt	caccgcgggt	tccagnggcg	ctctattggc	1260
atcagttttn	natatcac					1278

<210> 752

<211> 651

<212> DNA

<213> B.fragilis

<400> 752

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gcaagttatg	ctgccgagcg	gacgattcag	ttacctaagc	ccgacatgaa	tcgtgccgga	120
ctgctaatag	aagcgttatc	cgaacgcat	tctactcgtg	aatatgcttc	gaaggctttg	180
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gatcaccggt	ctgcgggttg	tgccgggtcag	gcctttgtca	acaatgcgcc	ggatcgttg	420
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ggagctatgg	atgcagggat	tgtttcgcaa	aacatctcgt	tgttctgttc	ggctgcacgt	540
ctggccacag	tcccgcgtgc	atcgatggat	ctggtagggc	tcaaagctgc	tttgaaatta	600
aaggatactc	aaatgccgat	gatgaatcat	ccggttggtat	attttaaatg	a	651

<210> 753

<211> 600

<212> DNA

<213> B.fragilis

<400> 753

aggaatttaa	tacgtacata	ttattgtcat	aagaaacggc	atacgaaagc	aattttgtat	60
gcccgttttc	tgtttaatca	aaaaaatatt	cgtattttgt	ttgcgaaaat	aaaaagaact	120
ctttatcttt	gcatcagatt	taaaatggta	atgaatacat	ttttggaaag	aagaaagaaa	180
atggaatcat	acaaccgatt	actagagcac	aacatcaaac	cgtccatgca	gcgaattgct	240
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gacacttcac	aacatgcccc	ttttctgtgc	aagcgttgcg	ggcgtattta	tgatttgaaa	480
tgccagggtg	agatgaaaca	agtggaaagg	cttcaaattg	atggacatga	agtaagcgaa	540
gtgcactact	attataaagg	tgtttgtaag	aaatgtttta	ataatatacg	tattgactaa	600

<210> 754

<211> 1023

<212> DNA

<213> B.fragilis

<400> 754

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tatatcctga	ctaattgatga	gatatccaga	attgtagata	ccaccgatga	atggatcatg	120
ggacgtatcg	gaatcaaaga	aagacgcac	ctgaatgaag	aaggactcgg	cacctcatat	180
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ggtttcttat	atgcattaga	aaccggggct	aactttatcc	gttcgggaaa	atacaaaaaa	420
gtcattattg	ttggtgccga	taaaatgtcg	tctgtgatag	actataccga	tcgtgccacc	480
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gccggtgggt	cagtttgttc	cccttcttat	tttacagttg	acaaccacat	gcattacctt	660
caccaagaag	gacgttacagt	atttaaatat	gctgtagcca	atatgtcaga	tgcatgtgag	720
tcgatcatcg	aaagaaacca	actgacaaaa	gatgaaatag	actgggtcgt	tcctcaccag	780

gccaatcaac	gtatcatcag	tgctgttgcc	caacgtctgg	atgtaccatt	agaaaaggtt	840
atgatcaata	tgaacacta	cggcaatacc	agtgcaggta	cgcttccatt	atgcatttgg	900
gatttcgaaa	ataaactcaa	aaaagtgat	aatttgattt	tcaccgcttt	cggagccgga	960
tttgectggg	gagctgttta	cgtaaagtgg	ggatatgatg	gcaagacaaa	taacgcatgt	1020
tag						1023

<210> 755

<211> 864

<212> DNA

<213> B.fragilis

<400> 755

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atggcccttc	ttgaagaatc	agacatcaaa	ctgagcacaa	ccaaacgtac	tttactcgta	120
caatcgctcca	actttccggt	tgaggctactt	tttctccgtg	acgatgatat	tccccaatct	180
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cccaaagaca	ttgaatatcc	cggtttgagt	tggtttaacg	gaaagaagat	agctacttcc	360
tatcccgga	ttttagatgc	ttttatgaaa	agtaacgggg	tgaaggctga	agtgcatgct	420
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gtcagttccg	gttctactct	agtcagcaat	cgcctgaaag	aagtggagggt	cgtaatgaga	540
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actgtgatgc	cgttggcaca	agatggttgg	tgctctgtac	atacagtgct	cgatgagaaa	780
cggttttggg	agatcatagg	taagctgaaa	gcgctgggag	cgggaaggat	tttgggtgtg	840
cctattgaga	agatgattat	atag				864

<210> 756

<211> 462

<212> DNA

<213> B.fragilis

<400> 756

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gagttgatcg	atacttatac	agcaggatatt	gtgttgaccg	ggacggagat	taagtcacac	120
cgtctgggta	aggcaagctt	ggtagatacg	ttttgctatt	ttgcgaaagg	cgagttgtgg	180
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cgtgaccgta	agttgctatt	gagcaaaaag	gagctgaata	aattggaaaag	agggacgaaa	300
gacgcgggat	tcaccattgt	ccctgtgcgt	ttgtttatta	atgaaagagg	tttggccaaa	360
gtgggtttag	ctttggctaa	aggtaaaaag	caatatgata	aacggggaggc	tttgaaagaa	420
aaagacgacc	gtcgtgatat	ggacaggatg	tttaaacgat	ga		462

<210> 757

<211> 477

<212> DNA

<213> B.fragilis

<400> 757

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tttgcctgta	acgatggagt	caaagcagat	caaaacaaaa	aagaggcaaa	gagcgggtgag	120
gttatcgtga	tgaataaaga	gatgtttatc	aacgatgtct	ttgattacca	gaattcaaaa	180
gagtggaat	ataaaggtga	taaacctgcc	attatcgacc	tgatgcaga	ttggtgcggt	240
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gtaatatata	aggtgaacgt	ggataaagaa	aaggaaactgg	ctgcactatt	caatgcaaca	360
agtattcccc	tctttgtatt	tatcccaatg	gagggcgaac	cccaactgtt	tcgtggagca	420
gcagataaag	ccacttataa	aaaagcaatc	gacgagttcc	tggtgaaaca	gaaatag	477

<210> 758

<211> 579
 <212> DNA
 <213> B.fragilis

<400> 758

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gaggtgccga	aaggatggaa	acgtccttct	gctgtgcatt	cttgcaatga	tgaacctttg	180
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gatcgttggtg	gtgcggtatt	gaccattatg	gaaatacaaa	aatgtgcac	ttttcaggaa	300
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aagtctgtca	atagtaagaa	tggggttaaa	aagatggctt	ttacttcgta	taaggcagag	420
cgtcatccgg	aaactaacga	attatctgct	ttgcaaaagg	ctgaatggta	tttgcagggg	480
cgtgaaaatg	tatattatat	cagttttacg	tcttgctcat	tgTTTTTTaga	actgctaccg	540
cagattaaaag	atattgtggc	gtcgttaaag	gaacttttaa			579

<210> 759
 <211> 1458
 <212> DNA
 <213> B.fragilis

<400> 759

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acagcagtat	ggattcccc	cgcttacaaa	gccgacgaac	aacaagacga	aggttatgca	180
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ggtacgaaag	aagaactgaa	agaaatgatc	gatgaattac	ataaaaaatca	tatttccggt	300
tatctggatg	tagtactgaa	tcataaggca	ggagggtgatt	tcactgaaaa	gttcatagtt	360
gtagaagtgc	atcccaatga	tagaacccaa	gcattaggaa	aaccgttcga	aatacagggc	420
tggaccggat	acagcttcca	tggacgtaag	gataaatatt	cagacttcaa	atggcattgg	480
tatcattttt	caggaaccgg	ttttgacgat	gccaaaaagc	ggagtggcat	cttccagata	540
caggggtgaag	gcaaagcgtg	gagcgaagg	gttgacaatg	aaaatggcaa	ctacgatttc	600
ttattatgca	atgatataga	cctggatcat	cctgaagtag	tcaccgaatt	gaatcgttgg	660
ggaaaatggg	tttccaaaga	gctgaacctc	gacggaatgc	gtctggatgc	catcaaacac	720
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gacggttatc	cttgtttgtt	ctacggagat	tattatgggtg	tcaaaggaga	aaactcacct	1140
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tggataaaaa	agaattaa					1458

<210> 760
 <211> 477
 <212> DNA
 <213> B.fragilis

<400> 760

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ataactatat	ttgccccctg	taaacgaggg	ctctatat	atcaaaagaa	aggaaaaatt	180
atggaaaaat	ttgaagattt	aatacagtca	caaagtcccg	ttttagtaga	ttttttcgca	240
gaatgggtgcg	gccccgtgaa	agcaatgaaa	ccgattcttg	aggatctgaa	acagcaggta	300

ggcgagaaag	cccgtattgt	aaaaatcgat	gtggacacac	acgaagaact	agctgtaaaa	360
tacagaattc	aggctgtgcc	gacttttatc	cttttcaaaa	agggagaagc	tgtctggcgc	420
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<210> 761
 <211> 1014
 <212> DNA
 <213> B.fragilis

<400> 761						
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agaatacagg	ttccttcggg	gttattgtat	ccacggagtt	tagttttatg	tgatagtaat	180
ctgatagtat	tcaatgaaaa	aatggatact	atgtttcaat	gcttccattt	gccggatttg	240
acttttcaat	atgggttttg	aacacagggg	cagggaccga	atgatttcgt	tctcccttct	300
attacccttg	tgaaatatca	aaagaacggg	tttgtcatgt	tagacggaat	taacctgaaa	360
catattagtg	tcaagaaaga	caaagctatc	gtacagactt	cgactttaaa	ttatggattt	420
aattgtttta	atgacttgat	aagtatttcc	gatagcagtt	attgttgtaa	tggaggtttt	480
gagaatgaaa	aagaatttag	gtttctttat	cctgacggaa	atcatgaatc	atggggagaa	540
tatcctgaaa	cagaggaacg	tttcggatct	gttttgagca	ggaatcaggc	gtatataaag	600
atgaccgtcg	ctaagcctga	taagagttgt	tttgtttcgt	tctaccaaca	tatacgccgt	660
ttcagaattt	atggtaaaga	tggagaatta	aaaagagatg	ttattttaga	tattcttccc	720
gggcaagaac	gtcctgaagt	ggatgattat	ttgagattca	tacatcctat	aagtgtctat	780
gcaacggaca	gttatattta	tacattaaat	ctggatatga	caacagagga	aattgagaat	840
cggaaaacta	ctcctaacat	ccaagtattc	gattgggaag	gaaagccact	tacacaatat	900
aaactcgatt	gttttattaa	cacttttgtc	gttgatgaag	ttgcaaataa	gatttatgga	960
gcttttggtg	aagacgaaga	tcataatttat	gtatttaatt	taccccgatt	atga	1014

<210> 762
 <211> 1050
 <212> DNA
 <213> B.fragilis

<400> 762						
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gatgtacctg	ataaggtag	tttacaacc	caggtaatga	atgatagtct	tttgacaact	180
atgcctgggtg	atattattgct	gattgacgat	tatttagttt	gggtctgatcc	tttctctgat	240
aacaaaatttc	tgcatgtaca	tcgttcttcc	gatggaaaat	atatcggttc	tatggggcaa	300
aaaggagaag	gtccacagga	atttgtaagt	cctttaatca	atcgtttttc	cattaatcgc	360
tgtattgctg	ctcatgatgc	taacgggaaa	accagaggct	atattatctat	tgacagttta	420
attgtcggaa	aagaaccttt	tatgtcttta	tcagattttg	atcggaatat	acgaatggct	480
aaattggacg	aacaactgta	tctgactgaa	accgaaaatg	gtgagaacga	ttattttaaa	540
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catatgggta	catataaaaac	ttacgataaa	gatcgtggac	tccttgcttt	tggtcctttt	660
aatttttctt	atttggcttt	gtataaaaag	gaaggggata	attttaagtt	attatgggaa	720
cgcattgectg	aaaaagaaaa	ctattctgtt	gttgatgggg	cgattaggtt	tgatcgtagc	780
gtgatgggag	tgagagatat	atgcatgact	aaagattata	ttgttactct	ggagcgtgac	840
cgggaagttg	atccgttgga	tgaaaggact	gtcggacgta	atgcaagtaa	atgtccccgt	900
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gtaatgcgca	ttgctgctga	cggacgaagt	aatgctctgt	atgtgatagg	agttaatcct	1020
gattttgcat	tggcgaaata	tgatttatag				1050

<210> 763
 <211> 1797
 <212> DNA
 <213> B.fragilis

<400> 763

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gtcatgtcat	ctctgtctca	agctgagaaa	ataatggaat	ctcgcccgga	tagtgcaatg	180
gctatttttcg	aacatatccc	aactccggaa	actcttcatg	gtaaagcgca	ggcggactat	240
agcctattga	tgacacaggc	tatggataaa	aactacataa	attttacttc	agattcgctg	300
attaaatttg	ctgttggtta	ttatggaggc	catactgaag	atcttgtagc	taaaggaaaa	360
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agctataagg	agtctttaac	ttattattct	ctagtaccag	actctctctg	tatgacatat	600
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tattatgata	aagcaattta	tattttcta	gcaaataaat	atgtagctgt	agggtcgttg	720
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cttaccaaac	atgatattga	aatttgctgt	ctattaagat	ttggtattga	acatgaggtc	1680
ttagggaagta	tttttctgac	ggagactgat	tcagtgacaa	aagctaaaag	acgtatgaaa	1740
aaacgactga	atctatctgc	ttcggatgat	ttggacgttt	ttttgctaaa	atattag	1797

<210> 764

<211> 312

<212> DNA

<213> B.fragilis

<400> 764

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gaagagaaac	tcgttgtgat	gaatagtttt	aaggaggcta	ttgaagcatt	acctgctaaa	120
atctctgtga	tccgcaaaat	tgaagtcgga	ttgaatatga	atccgggaga	aacctggaat	180
attgcgttgt	atagtgaatt	tgataatctg	gatgatgtga	agttctatgc	tacccatccc	240
gagcatgtgg	ctgccggtaa	gattttggca	gagacaaaag	aaagtcgggc	ttgtgtagat	300
tatgaatttt	ag					312

<210> 765

<211> 213

<212> DNA

<213> B.fragilis

<400> 765

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aaactgagaa	aaaacttcat	tgataatcaa	aagagacagg	gtacgccgtt	tgaacggaag	120
tgtaccctgt	ctttttatta	ttcttctaca	atatccagct	ccttgatgat	gtgtgaggca	180
cctgcatact	tatcaataat	aaatagagta	tag			213

<210> 766

<211> 864

<212> DNA

<213> B.fragilis

<400> 766
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acttcatgta tggattccgg agaaagcggg cctcagcagt gggccggtgt ggtgaaagtg 180
aatgatagaa tgggttatgt tacattcaca gatgctgccg gtacagagct gatccctact 240
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gcacctgttg gttcgttgag ttttgcatac ggatattcaa ctgtggcccc atttcagttt 480
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gctattgctg agcgtgcaac acgtacttcc agctttaagg cttatgaaat cagccaaatc 720
ttaagagaat atactctgaa gagtggacaa actaaacctg ctaaaataac tatagtagca 780
cagcaaaatg agtacaacaa taagtggaa gatacttcta ctatagagaa ggtatatgaa 840
atagaatata aaactgcgga ataa 864

<210> 767

<211> 393

<212> DNA

<213> B.fragilis

<400> 767
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gaagaagcga gtcgttccat caaccggttg attcctatct ctgcagatat tgatggcact 180
actttatttta ttgaatttac aaaggttata ggtaatgtgg atattacagt gaaagatgat 240
accaaaaaag aagttttattc atcttctgtg gatgtaactg ctgctaatac agctacttgc 300
ttctctattg ccgatttagc accgggaact tacctgcttg aatttaccaa ttcgaatggc 360
ggttatgtat atggacaatt tattgtagaa taa 393

<210> 768

<211> 714

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (613)

<223> Identity of nucleotide sequences at the above locations are unknown.

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cccacacccg gaatcattga agcagactct ttcagattac ccattttctt aatctgggac 120
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ttagcttctt cttcgtcata ttgttctctg gcgcgttcca ccaacgaaac gatgtcaccc 240
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ccaccgcggg tatcaccgtc gagcttggtc agcaccacgc cgtcaaagtc gaggcgttcg 420
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ttgatggcat tcntggcgat ggaaaccgga tctttgctgt cgatctccga gtacatcggt 660
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<210> 769

<211> 237

<212> DNA

<213> B.fragilis

<400> 769

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ctgaaagtga	agtcgtttta	gttggtgata	cagagtggat	cgttggttgt	tctagttttt	180
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<210> 770

<211> 1149

<212> DNA

<213> B.fragilis

<400> 770

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ctgctattgg	caggattggg	tgcttgttca	ccttcgggaa	agaaaacagg	agcggattcg	120
actgtcgcga	ctctgcgaac	ggcggaacaa	gtgaatttac	tgaataatct	acggaagggt	180
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aatgcacgtg	aaagggtaaa	ccactattat	gctccttatc	ccggacaggt	gtccgccgat	1080
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<210> 771

<211> 1560

<212> DNA

<213> B.fragilis

<400> 771

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gcccgtccac	tcgaagatct	gtttataagt	caggtgaagt	ttctcgctc	tgcactccca	1140
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aggctgggta	cagacacatt	cgacattaca	actcctttgc	ccatgaatct	ctctcaagct	1260
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atacttgtcc	ttcaaggcga	acgtgattat	caggtcacca	tgcaagatgt	cgaattatgg	1380
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ctgtttcagg	aaggagaagg	gaagtcaacc	cctcttgaat	acagccgtcc	ctcctctatt	1500
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<210> 772

<211> 1569

<212> DNA

<213> B.fragilis

<400> 772

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attctcttca	tggtagacga	catgggctgg	caagatacat	ccctgccttt	ctggacccaa	180
aagacacact	acaacgaggt	atacgaaact	cctaatatgg	agcgccttgc	caaacaaggt	240
atgatgttca	cccaagccta	tgccagcagc	atcagttcgc	ccacccgctg	tagcctgatt	300
acaggaacta	acgcccgcgc	tcacccgggtg	accaactgga	catatcccaa	aggccagcaa	360
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gccctacatc	cggacattgt	gaaaagttta	tctaaagagc	tgggtgacta	tttgcgcaaa	1500
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atcaaataa						1569

<210> 773

<211> 321

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (304)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 773

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gctgtaggca	cccatttggc	taaattactc	tcacgcgaga	aacaggacat	catcctgatg	180
gacgatgacg	aagagaaact	aagtacgttt	agttctaact	tcgacctgat	gactgttacg	240
gcctctcctt	cgtccatatc	aggactgaaa	gaggtaggca	tcaaagaggc	agacctcttt	300

attingcggtc actcccgatg a

321

<210> 774

<211> 1410

<212> DNA

<213> B.fragilis

<400> 774

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ggactgggcg	atatggcttc	gtccatgttc	tggaaactgt	tcgggtccta	tctgatgatt	120
ttttataccg	atgtattcgg	cttgccgtgt	gccgtggtag	gaaccatgtt	tctgattacc	180
cgggtatggg	attcggcttt	cgatccgac	gtgggagtga	ttgccgatcg	cacacagacc	240
cgctggggga	aatttcgtcc	ttatctgctg	tatcttgccg	ttccttttgc	actgattggg	300
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acctattctt	tgatgatgat	ggtatattcg	gctatcaatg	tgcccttatgc	ttcactgctg	420
ggagtataaa	gtcctgaccc	gaaagaacgg	aataccctgt	ccacttaccg	tatgactttt	480
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gttttcatca	gtatgtatcc	gctgtcggag	aagaagatga	gagaggtgac	ttcagagttg	1380
gagaagagaa	gaaaggctat	tcaatcataa				1410

<210> 775

<211> 1995

<212> DNA

<213> B.fragilis

<400> 775

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ttggcagaaa	gcgatttagc	agcctattcg	gctaattctat	atgatcaact	tccatcccac	180
actccaggcc	aatacagtat	gggagtattt	gcaacagaca	ataatagtga	caaccaagca	240
gcaagtaatc	caaacggttc	atltgtaaag	ggagaaacac	gtgtgggtca	aagtggaggt	300
gcttgggatt	ttgggaaaat	ccggaatgtc	aattatttca	tcaataaggt	acgtccccga	360
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gggtccgggat	ggccaggagc	aaacaaagat	tatttaaagg	acttcactat	caatattgat	780
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gtcggttaca	tccaacgcaa	tggaggtggg	aataccggat	ggactcgtag	tatgatgcaa	1020
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aaaacttatg	aagcagttgc	aaccaatcgt	gatccacgac	tgattttataa	tactttatta	1140
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tcagtaaaaa	agggattagc	aacagatgcc	gcacaaggac	ctacactccc	atcaactaca	1320
gcctgtgtca	tattccgtgc	agcagaggca	tacttgaatt	atatggaagc	tgattatgaa	1380
ctgaataact	cgcttgatgc	caacagttcc	aaatactgga	aagctttacg	aaatcgagca	1440
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tttgcccgcct	attcagggttc	tgaatttgtt	tcaaccactt	tgtataatat	tcgtcgggaa	1560
cgctcgcatcg	aatttgcggc	cgaaggatta	cgccataaat	atctgaaacg	ctggcgtgca	1620
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ccttaccgga	tcaatacaaa	caacattgca	tacaatggct	ataattggaa	ccaaaataaa	1860
tattttaaate	caattgcttt	tgaccacttc	cgtctgacga	cagcagaaga	aggatcaacc	1920
gactatacaa	cctctacgat	ttatcaaaat	ccaggatgga	agatagaaac	gagcagcttc	1980
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<210> 776

<211> 651

<212> DNA

<213> B.fragilis

<400> 776

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attaatgaat	atatgattaa	agccatggaa	gccattggag	cacgttttga	atcgggacaa	180
gtgtttgttc	cgaacctctt	gatgagtgcc	cgtgccatgc	gtggtgccct	cgatatactc	240
aaaccactga	tgcaagggca	ggtcaattcg	tatatcggtc	ggattgtgat	tggtacggta	300
aaaggggatt	tgcatgatat	aggtaaaaaac	ttggtttgctt	cgatgtttga	aggatgtggg	360
tttgaagtca	tcaatctggg	agtggatgta	tcgagtgata	aattcatttc	tgccggcattg	420
gaaaataagg	cagatattat	ttgcatgtcc	gcactgctca	ccactaccat	gaattacatg	480
aagggaagtga	tcgatgccct	tgaaacctcc	gggttgaggg	gaaaagtaaa	agtaatggta	540
ggaggagcac	ctgtcagcga	tgccttttggc	aaatctatcg	gtgccgatgc	ctataaccagt	600
aatgccaatg	cagccgtaat	aatggccaag	aagttgataa	acgcctgttg	a	651

<210> 777

<211> 1914

<212> DNA

<213> B.fragilis

<400> 777

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gcagtgcacg	tactctcgta	cgtcacggcc	gtacattact	tctcggcacc	ccgtctggca	180
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ctaacgttca	acctgggcat	tttgctcgac	cccatctcgg	tgatgatgct	gatcgtaatt	300
tctacagtea	gcctgatgg	acatatctac	tctttcggct	atatgaaagg	cgaacgggga	360
ttccagcgct	actacgcatt	cttatcctta	ttcaccatgt	ctatgctcgg	actggtagtg	420
gcaaccaaca	ttttccagat	gtacttatte	tgggagttgg	taggtgtatc	ttcttacctc	480
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cctctggcac	tcgggctgat	gtttgtcggg	gggtgccggca	agagtgccat	gttcccgtcg	720
catatctggg	taccggatgc	catggaagg	ccgactcccg	tcagtgcact	gattcatgcc	780
gctaccatgg	tagtagccgg	cgtttacctg	gtggcacgca	tgttcccgct	tttcatcgaa	840
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gccagcggtg	cttgccgtgca	gagtgcacac	aagcgtgtac	ttgctttctc	gaccatctca	960
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ggtagccatg	ctacaagcga	tgagatacgg	ggattgcaaa	ggggacgtgt	acagcaatac	1860
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<210> 778

<211> 1320

<212> DNA

<213> B.fragilis

<400> 778

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cgtctgacgg	tgaatggaaa	ccccattatt	tatataggaa	ctaatttttg	gtatggagct	180
attttggggg	cacagggaca	gggaggtaac	cgggagagat	tacttcgtga	actggattat	240
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caatatgcta	agtcggaaaa	agcacaccat	ttgttccggg	atcatattac	tcacgttgta	600
aatcgtgtca	atcgggtatac	tggaaaaaaa	tatagtgaag	atcctgcaat	tatgtcttgg	660
cagataggta	atgaaccccg	ttcgttcggt	gaggacaata	aaaagagttt	tgcagcctgg	720
attgccgatt	gcgctgctct	tattaaatct	atggattcta	accatctggg	ttctattgga	780
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agagacagtg	tgaagtttac	ttcgaatact	tccactgttc	agcgggatcg	gtattacaga	1080
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tatatgggag	atcccgggca	ggaggaacaa	gggctgaatt	cggtttatgc	aacagattcg	1260
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<210> 779

<211> 1191

<212> DNA

<213> B.fragilis

<400> 779

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atccacggac	aggaggaatt	aataccccgg	gccgataaa	gggctattct	gaatgcgcgt	180
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aaagatgcga	atgaacgcaa	gaccatgaat	acccatctgc	atatactcga	accttacacc	600
aacctgtacc	gggtctggaa	agatgcacgg	ctggaacgtc	agctctacaa	cctgatagga	660

ctttttacag	agaagatact	ggataaggac	acatcccatt	tacaactctt	tttcgataac	720
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accgtagtgc	gatactataa	cctgttccga	tatttcgggtg	atcgcggggc	tttgcaacat	1020
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ttctggagcc	ttcgtgccga	cggtagcctg	aaccgggatg	atgataaggc	cggcttctgg	1140
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<210> 780

<211> 1809

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (1138)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 780

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ggagtatact	actoctacca	tctgcattat	caggaacagt	tccagatgtt	tctctttaca	180
tccgactatt	ttgtcgaaca	agtatcccat	cccgggggaa	tggcggacta	tctgggaggc	240
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gtgattctgg	taccgttatt	ggtagctcgt	ttgcccagag	agatgacttg	gagatactac	840
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<210> 781

<211> 777

<212> DNA

<213> B.fragilis

<400> 781

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<210> 782

<211> 1197

<212> DNA

<213> B.fragilis

<400> 782

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<210> 783

<211> 1134

<212> DNA

<213> B.fragilis

<400> 783

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<210> 784

<211> 1197

<212> DNA

<213> B.fragilis

<400> 784

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<210> 785

<211> 423

<212> DNA

<213> B.fragilis

<400> 785

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<210> 786

<211> 483

<212> DNA

<213> B.fragilis

<400> 786

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<210> 787

<211> 3228

<212> DNA

<213> B.fragilis

<400> 787

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<210> 788

<211> 1281

<212> DNA

<213> B.fragilis

<400> 788

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<210> 789

<211> 1218

<212> DNA

<213> B.fragilis

<400> 789

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<210> 790

<211> 2706

<212> DNA

<213> B.fragilis

<400> 790

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<210> 791
 <211> 716
 <212> DNA
 <213> B.fragilis

<220>
 <221> unsure
 <222> (695), (706), (707)
 <223> Identity of nucleotide sequences at the above locations are unknown.

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 gaatggtttg ccaggccaa gttaggaatc tttatccatt ggggaatcta tgccgtgaac 180
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 <211> 840
 <212> DNA
 <213> B.fragilis

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<210> 793
 <211> 2511
 <212> DNA
 <213> B.fragilis

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<211> 1878

<212> DNA

<213> B.fragilis

<400> 794

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<210> 797

<211> 1596

<212> DNA

<213> B.fragilis

<400> 797

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<210> 798

<211> 1611

<212> DNA

<213> B.fragilis

<400> 798

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<210> 799

<211> 1011

<212> DNA

<213> B.fragilis

<400> 799

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<210> 800

<211> 1458

<212> DNA

<213> B.fragilis

<400> 800

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<210> 801

<211> 381

<212> DNA

<213> B.fragilis

<400> 801

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<210> 802

<211> 198

<212> DNA

<213> B.fragilis

<400> 802

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<210> 803

<211> 1557

<212> DNA

<213> B.fragilis

<400> 803

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<210> 804

<211> 756

<212> DNA

<213> B.fragilis

<400> 804

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<210> 805

<211> 345

<212> DNA

<213> B.fragilis

<400> 805

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<210> 806

<211> 519

<212> DNA

<213> B.fragilis

<400> 806

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519

<210> 807

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<212> DNA

<213> B.fragilis

<400> 807

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<211> 558

<212> DNA

<213> B.fragilis

<400> 808

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<211> 3216

<212> DNA

<213> B.fragilis

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<211> 2085

<212> DNA

<213> B.fragilis

<400> 810

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<211> 1464
 <212> DNA
 <213> B.fragilis

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 <211> 387
 <212> DNA
 <213> B.fragilis

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 <211> 318
 <212> DNA
 <213> B.fragilis

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<210> 814

<213> B.fragilis

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<211> 1266

<212> DNA

<213> B.fragilis

<400> 815

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<211> 1155

<212> DNA

<213> B.fragilis

<400> 816

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<211> 2061

<212> DNA

<213> B.fragilis

<400> 817

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<210> 818

<211> 1539

<212> DNA

<213> *B.fragilis*

<400> 818

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<210> 819

<211> 2463

<212> DNA

<213> *B.fragilis*

<400> 819

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<210> 820

<211> 1662

<212> DNA

<213> B.fragilis

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<211> 216

<212> DNA

<213> B.fragilis

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<210> 822
 <211> 534
 <212> DNA
 <213> B.fragilis

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 <211> 246
 <212> DNA
 <213> B.fragilis

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<210> 824
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 <213> B.fragilis

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333

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<210> 825

<211> 189

<212> DNA

<213> B.fragilis

<400> 825

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<210> 826

<211> 3333

<212> DNA

<213> B.fragilis

<400> 826

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<210> 827

<211> 1206

<212> DNA

<213> B.fragilis

<400> 827

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<210> 828

<211> 1050

<212> DNA

<213> B.fragilis

<400> 828

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<210> 829

<211> 1629

<212> DNA

<213> B.fragilis

<400> 829

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<210> 830

<211> 1626

<212> DNA

<213> B.fragilis

<400> 830

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<210> 831

<211> 501

<212> DNA

<213> B.fragilis

<400> 831

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<210> 832

<211> 924

<212> DNA

<213> B.fragilis

<400> 832

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<210> 833

<211> 1623

<212> DNA

<213> B.fragilis

<400> 833

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<210> 834

<211> 1338

<212> DNA

<213> B.fragilis

<400> 834

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<210> 835

<211> 501

<212> DNA

<213> B.fragilis

<400> 835

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<210> 836

<211> 1191

<212> DNA

<213> B.fragilis

<400> 836

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<210> 837

<211> 2022

<212> DNA

<213> B.fragilis

<400> 837

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<210> 838

<211> 891

<212> DNA

<213> B.fragilis

<400> 838

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ggaagtactg	atgatacatt	taactttata	gaatcaatta	aggaaaacga	taagattgat	180
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<210> 839

<211> 1293

<212> DNA

<213> B.fragilis

<400> 839

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cggatatacc	gctataactt	tttctacgac	aactgtgcta	cccgccacg	ggacaagggtg	540
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caaaatttcg	acttagcagt	attacctttg	gcactctgtt	tgctgatacg	ttctgcaagc	1260
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<210> 840

<211> 402

<212> DNA

<213> B.fragilis

<400> 840

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tatcctttaa	agtttcatca	gaagcgcaag	gccacttctg	actatccccg	atgtaactgc	360
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<210> 841

<211> 795

<212> DNA

<213> B.fragilis

<400> 841

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gggttgattg	aagaggggtga	caaagtgcct	gttggccttt	caggaggaaa	agattccctg	180
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795

<210> 842

<211> 189

<212> DNA

<213> B.fragilis

<400> 842

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agatatattc	acccggagga	aggttcgaaa	aacgaattct	attatctaca	gacggagcac	120
tccaatccgt	atgatcgagt	ttccaactgt	aagctatata	ctgcttttca	gtatagcgaa	180
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<210> 843

<211> 1167

<212> DNA

<213> B.fragilis

<400> 843

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<210> 844

<211> 360

<212> DNA

<213> B.fragilis

<400> 844

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<210> 845

<211> 1296

<212> DNA

<213> B.fragilis

<400> 845

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<210> 846

<211> 1446

<212> DNA

<213> B.fragilis

<400> 846

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<210> 847

<211> 609

<212> DNA

<213> B.fragilis

<400> 847

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<210> 848

<211> 1074

<212> DNA

<213> B.fragilis

<400> 848

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<210> 849

<211> 1068

<212> DNA

<213> B.fragilis

<400> 849

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<210> 850

<211> 492

<212> DNA

<213> B.fragilis

<400> 850

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<210> 851

<211> 960

<212> DNA

<213> B.fragilis

<400> 851

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<210> 852

<211> 771

<212> DNA

<213> B.fragilis

<400> 852

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gactctaate	agtccctgga	ttccttgagg	gctgtttgta	ataagtatga	tgctcgga	180
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<210> 853

<211> 672

<212> DNA

<213> B.fragilis

<400> 853

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<210> 854

<211> 1044

<212> DNA

<213> B.fragilis

<400> 854

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<210> 855

<211> 1029

<212> DNA

<213> B.fragilis

<400> 855

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<210> 856

<211> 1089

<212> DNA

<213> B.fragilis

<400> 856

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<210> 857

<211> 1401

<212> DNA

<213> B.fragilis

<400> 857

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<210> 858

<211> 648

<212> DNA

<213> B.fragilis

<400> 858

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<210> 859

<211> 1569

<212> DNA

<213> B.fragilis

<400> 859

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aatctgaaat	cgagccatgg	acacgacatg	gccatcgta	atggtatctg	ccgtatcgga	720
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tcacatgccca	tcggctttat	ccgtgagcat	aatgacgaac	ctttctttat	gtatttggct	840
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ggaccgttgc	gtggtaataa	gtacagtgct	tttgaagggg	gaactcgtat	tcctgccatt	1140
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gactggtttg	cctcttttggc	ttcatttggt	ggagccgggc	tgccgaaggg	agcggcacc	1260
gatagcttta	actacctcga	tacttggttg	ggcaaaaacc	agtccgaccg	atcctgggtg	1320

atagagcagg	cttccaatca	tacattatca	gtccgcacca	aggactggaa	gtacattgaa	1380
cccaatgacg	gaccggccat	gattacctgg	ggaccgaaga	tagaaaccgg	aaatctgagt	1440
acaccgcagt	tatatcacgt	ggtagacgat	gtggcagaac	agaagaatgt	agcttctctc	1500
catccggaac	tggtttttga	actccagaat	atattaagac	atgtccggat	gaaaaacctg	1560
aagccctaa						1569

<210> 860

<211> 252

<212> DNA

<213> B.fragilis

<400> 860

gttcctgagc	aacaaaaagt	tgcccaggat	tttgccatgt	cagaattttc	acttatctta	60
gtgttgcaaa	aagaaaacaa	gcaaaactct	aatatgacat	ggcaaaaata	caaattaaat	120
ctgagaaact	cacacctttt	ggaggaattt	tttcaatcat	ggagaaattt	gactccatgc	180
tttcaccogt	tatcgactca	acactgggtc	agagatgcag	cagtatcttc	ggatatcagt	240
tcagcgagat	ag					252

<210> 861

<211> 375

<212> DNA

<213> B.fragilis

<400> 861

gcctccatta	atgatgttca	tcattgggtac	aggcaatata	tacgtattcg	tacctccgat	60
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acccagaata	gagttggcac	ccaatttggc	ttttgtcttt	gttccatcca	atgccaacat	180
ggcatgatca	atgcctatct	ggtcgagggc	cgacataccg	atcagatgcg	gagcaatgac	240
tttattgacg	ttctctactg	ctttctgtac	acccttgccg	ccataacgat	gtttatcacc	300
gtcgcggagt	tcaagcgctt	cgtgttcacc	ggtcgatgca	cccgatggaa	cggatgcacg	360
tcccataatg	cctga					375

<210> 862

<211> 552

<212> DNA

<213> B.fragilis

<400> 862

cgaacgatta	atgaaacctg	tacgatgaaa	aaattaataa	aactgggtact	cttcctgatg	60
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atgaccggac	gcccgatggg	ctacgccaaa	atgtatatca	tcaatccgga	aaccaaggct	180
gtactgaatg	acaccctcga	ttcattgagt	gtgacagcat	tcggaactga	ttcaataatc	240
atcaataacc	agaaaaaggt	acatgatatc	gctctccac	tacgctatac	aagtgactcg	300
actattcttg	tgtttcatta	cacccggttg	ttaagagaca	caatgggtgat	cctgcaaacc	360
aatactcctt	actttcagtc	gatggattgc	ggatacagta	tgaaacaaaa	tatcatcagt	420
attcatccga	ttgattatac	ggaaaccaat	aaaaagaaat	atcatagcat	agactctcta	480
tatatcaaat	caaatgcagc	taacattaat	ggaacagaaa	atctcaaaat	attctaccgc	540
tacaatcggt	ag					552

<210> 863

<211> 246

<212> DNA

<213> B.fragilis

<400> 863

gctacagata	aaaaaataga	caacattgct	atcaatccaa	aatcagctgg	agaaactaat	60
ctagctataa	caatgggtcaa	tataaagcgt	aatgcttgcc	ccgacatttt	ctcaacagca	120
ttccacatta	aactatttta	tgctgccaat	tttaaatttt	taatcatcat	atacaatcat	180
catctccaag	ttattaacaa	tataaaaagca	ttgatcattc	aaaaatacaa	tcaatatatta	240

gtatag

246

<210> 864

<211> 966

<212> DNA

<213> B.fragilis

<400> 864

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atctttgtaa	atgatggtag	taccgaccgt	tcttgggaaa	ttatcgaaga	gcttcagaaa	180
cagtcgtcca	ctgtgaaagg	gatcaaattc	cgacgaaact	acggaaaatc	cccggtctcg	240
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gtttcaggct	ataaacagaa	aagatacgac	ccgctgtcga	aaactctacc	taccaaacta	420
tttaatgcca	cggcacgtaa	agtttcaggg	attcataatc	tgcacgactt	taattgcgga	480
ttgaaagctt	atcgcaaagc	tgttgtaaaa	aacatcgaa	tatacggaga	gatgcatcgc	540
tacatcccg	atctggctaa	gaatgccgga	ttccagaaaa	taggcgaaaa	ggtggtgcac	600
catcaagcac	gtaaattcgg	aaaaactaaa	tttgaggat	ggaatcgctt	ctttaacgga	660
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gccagtaaat	tatatagtat	gaatcacggt	atgccttate	ggctggtaac	agattctccc	840
tatttctatc	tgtcgttgac	tgccatgatt	attggaacac	aactcttttt	ggcaggattt	900
cttgggcaac	tgatttcacg	caacgccccg	gaacgcaata	attatcagat	agaaaaata	960
atataa						966

<210> 865

<211> 798

<212> DNA

<213> B.fragilis

<400> 865

agtgattgca	aaaccatata	ctctggagaa	gctgaaagaa	acgatcgaaa	cttattttata	60
ggaggaggga	atagtcggtc	tttcaatgca	acaatttatc	atatagtatg	ttctgtagta	120
aataatgcta	taaagataaa	ttggattatg	aagaaagtag	tactaatcgg	ggccagcggc	180
ttcgtcgggt	cggctattct	gaatgaagct	ttgaaccgtg	gattccatgt	gacggcggta	240
gttcgtcatc	ctgaaaagat	caagatagag	aatgaaaaatc	tggaaagtga	gagagctgat	300
gtttcttcat	tggatgaagt	atgtaagggt	tgtaaagggtg	ctgatgccgt	gatcagtgct	360
ttcaaccggt	ggtggaataa	tcccgatata	tacaaggaaa	ccattgaggt	ttatctgacg	420
attatcgatg	gtgtaaaaaa	ggctggaggt	aatcgttttt	tgatgggtgg	tgggtgccggt	480
tactgtttta	ttgctcccg	catccgactg	gtcgattcgg	gagaagttcc	cgaaaagata	540
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gttgactggg	ttttcttctc	gccggcggca	gatatggctc	ctggagtacg	tacaggcaga	660
tatcgccctg	ggaaagatga	gatgattgtg	gatatggtag	gtaacagtca	tatatctgtg	720
gaagattatg	cggctgccat	gattgatgag	cttgagaagc	cggagcatca	tcaggagcgt	780
ttcaccatag	ggtactga					798

<210> 866

<211> 876

<212> DNA

<213> B.fragilis

<400> 866

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tatgatgtcg	attttgaagc	cgcacagcaa	acgcaggcac	caaccggaac	gctcgtagcc	120
cgctaccggc	cgatcccttc	gttgagtgat	ccaaaatact	attcacactt	caccctctca	180
aagttccgca	atggaacctt	ccaactcctc	aactacgacg	aaggtagcgt	agatatgggt	240
ggaggagcca	cctggctcgaa	cttgctgaag	aatggtgcac	gcctggacac	aggatactat	300
atgatggtaa	ccggtactcg	catggcaagc	ggagctgtat	tggctaattgt	gactttcttc	360

accattgaag	agggaaagac	aacaactgtc	gatctgggtca	tgcgcgaaag	caaagaccag	420
gtacaagtaa	ttggtaattt	taattccgaa	tcgacttatc	tgcctatagg	aacctccgaa	480
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atccagaaac	aaattgccga	atcgatgaag	ttgccaaaaca	gcaccatcct	gccccatgttt	780
attatcgggtg	atacattcaa	ccgggtagtc	ttcgtgtcac	aagggttatac	catcggattg	840
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<210> 867

<211> 717

<212> DNA

<213> B.fragilis

<400> 867

ataaagttaa	attatagtgt	tgcggaatta	aggataacaa	acgaatcata	tatgaagcca	60
acaatcaaaa	aagtacaacc	cgtcaaagtc	gtagctccgt	tccttaacag	tcagtccgaa	120
agtccgggtcc	cactggatgc	acttaccgac	caagagaaag	tttccgattt	gtacttcctt	180
aagggaaaccg	tacatcaaat	agctaaacct	tacctaaagta	ttaataattg	cacttttcaa	240
caacaaatat	tcagcgaatg	tcagtttaaa	tcagctcaac	tgacagacgt	acgttttgaa	300
aattgcgatt	tatccaacgt	ttcgtttgcc	ggaactactt	tctaccgggt	agaatttata	360
tcttgcaaat	tgctgggaac	cggtttcccg	gaagccaccc	tcaatcatgt	tttaattgat	420
cattgctacg	gacaatacat	caatctctcc	atggtaaaaa	tgcgaaacagc	ccgtttcagc	480
cattgcaatt	tccgaaacgg	cagcctgaat	gacagcaaac	tgatgccggc	agcttttgat	540
acttgcgaa	tggttagaagc	cgacttttgc	cacacttcac	tcaaagggtat	cgacctgaga	600
aactctagaa	tagcagggtat	tcaactcaat	atagccgatc	tgaaaggagc	catagtcagt	660
tcgtttacaag	caatagatct	gttacctcta	ctaggggtca	aaatagaaga	cgattga	717

<210> 868

<211> 462

<212> DNA

<213> B.fragilis

<400> 868

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caaaaagcaa	tcaacaaata	tacctgtgga	tgcgaaacaga	ccatcgtcac	agatatccat	120
attcaaccga	atcagaattc	cggtgaaactc	tttatctatg	acgatgaaga	tgaagaacta	180
tccagtgtaa	ccatcgatga	atggacaacc	tacgaagggg	acgactttta	cgaagatgct	240
gaaagaattt	tccgtaccgt	gctttgccgc	atgaaagaga	acgggagcct	cgataagtta	300
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cttctgcttg	tagatgacga	cacactgttg	gtgaacgatg	aactattgaa	gggactggac	420
aaagaattgg	acgacttcct	gaaagacctg	ttggagaaat	aa		462

<210> 869

<211> 1236

<212> DNA

<213> B.fragilis

<400> 869

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gggtttctgc	tcatttat	aggctggaaa	ggggactcgc	agccaatggg	gatgattccg	180
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agcatttttc	ttgctttatg	tgctgaattg	ggtacattct	tgacagtgcc	tattgcttcc	480
ggtctggggac	tgtctttaaa	agaaagtgct	tcagtggcaa	tggtaggcgg	agctgatggt	540

ccgatgggttt	tgttcacatc	gcttgctttg	gccaaacact	tgtttgtacc	tattacggtg	600
gtggcttatc	tttatctggg	attgacttac	gggggatata	cttatttggg	gaaattgctg	660
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tgtgtaccca	ctacggcaaa	agtggctcaa	aagttggtaa	gtaaagataa	tccgaattct	1140
tttattttgg	gtgatgcatt	aggagccaac	atttcaggag	taatcacttc	ggccatcatt	1200
acaggcattt	atataacgat	tataccttat	ttataa			1236

<210> 870

<211> 1533

<212> DNA

<213> B.fragilis

<400> 870

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ctctttttcaa	aagctgaagt	cagcagaaac	tggatgccgg	aaagctatca	ctacaaaaat	180
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ggtaaatgcag	gagtctggaa	aacagactcc	tgctttgcta	catttgccga	tttcaaccga	300
ggctctggcca	aaggaatcga	caatcgtaaa	ataagtaata	tcgtccgtgt	agccaataac	360
gatatctggg	gtgccggatt	atattctatc	tatctcctgg	accatgacag	ttggaaagaa	420
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gtcatattga	cacgctctta	tctttatacg	gggtgtttctc	cttatgacga	attccggaaa	540
acagaattga	aaacaccgga	aaactattcc	ccaaagacct	ctttgttccg	gaccatctgg	600
ctgctgcata	goggagagtt	attcgggtacc	cccggcaaac	tggcagtcga	ttttctggga	660
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gttcacggac	gaccactcgg	cggcagtcct	gtcaacggat	tactgacga	tttagttacc	1260
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atttcgggcc	ttctgctaac	gttaatcctt	atttcgggat	atatacgata	taaaagacac	1500
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<210> 871

<211> 1929

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (1889)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 871

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acggggggtga	ggccttactt	aacaacaaat	tgtatgaaaa	ccctaaccgg	cttttctaate	180
attccgatgt	tgtcggttgc	gttcttttca	tgcagtga	cccatttct	gaaagatgtg	240
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gagttgtttg	cagtgtttaa	tgaaaagctc	accattccc	aacaagaggc	tttaattgttc	360
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aacctgccc	aagtgactcc	ggaacaacgt	actgaaaatg	atcggcgcat	ggcacaggaa	1380
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aaaaaagaga	tcacaatcat	taacgaatta	aactcacaac	gtataccaat	gtcaccattg	1860
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ggcccgtag						1929

<210> 872

<211> 1296

<212> DNA

<213> B.fragilis

<400> 872

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gacaaacttc	gttttgaaat	ggaccggaaa	ggaggggtat	catcacgtat	cctttcgcta	180
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gttatctatg	gtatatattg	ggcacagatt	atcggcgaca	atttgctggc	cggatggatc	300
accaatcatt	ttgtaatgg	attggtagac	acgtgatct	ccacactgat	catcttggtg	360
acaggagagt	ttctgcccc	gacgttttt	aagatcaatc	ccaatctggc	cctgaatgtc	420
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1296

<210> 873

<211> 1500

<212> DNA

<213> B.fragilis

<400> 873

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agcctatcgg	cacaaacttt	ggaacaagca	agaggcatgt	atggcagagg	gcaatacgt	180
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ctatggtacg	gtgtgtgttg	cctcaaaaca	ggtaatgctg	cggaggccct	aaaatacctg	300
gagacggcag	taaagaaacg	cattccgagc	ggacaactat	atctggctca	gacttataat	360
gatttatacc	gctttcaaga	tgcagtagat	tgtacgaag	aatacattgc	agacttgtct	420
aaacgcaaaa	aaccgacaga	agaagccgag	cagcttttag	aaaaggctaa	aggaaacctt	480
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gaacaaagta	aatgggcacc	ggctatccgc	gatcttgaga	agagggtact	tcagatgtca	1440
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<210> 874

<211> 552

<212> DNA

<213> B.fragilis

<400> 874

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caggaggtag	atacctttct	tccgtgtaca	aaccgtgtca	tagagcgtga	aggaaaacgc	180
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caggatcagg	tgatcctgac	aggagagtcc	attcccaaag	gtactcgtgt	agtagttgcc	420
aagggcgatt	tacaaggctt	gcggggagaa	ttgggtccgct	acaataataa	atatcatatt	480
ttagtacgta	tcgatatgtt	cggtagcgtc	atgggttaca	ttccggctag	ctacgtccgg	540
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<210> 875

<211> 1497

<212> DNA

<213> B.fragilis

<400> 875

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agcgccatta	cctccgtttg	cgaaggaaga	gggattcttc	tggtagatga	cgaaaaccga	120

gaaaatgaag	gagacctgat	cttctctgcc	caaagtatga	cagaaacaga	catggccata	180
atgatacggc	attgtagtgg	cattgtttgt	ctgtgcatca	cggaggagaa	agcccgacaa	240
ctgaacttac	cgttaatggg	ggagcaaaac	accagtaaat	atggtaccgc	attcaccatt	300
tcgatcgaag	cagcagaggg	agtgaccacc	ggagtatcag	cagccgaccg	catacagact	360
atccggacgg	ccattgcccc	caatgccact	cccgaatctc	ttcatcatcc	cggacatata	420
ttcccattga	tagcccgttc	cggcggaatc	aaagaacgga	gcggtcacac	cgaaggcagc	480
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gatgacggaa	ctatggcgcg	cttacccgaa	atcatagaat	tcgggctaga	acacaaatat	600
ccggtagtg	caatcaatga	tttaaaagaa	tatcagacag	ccccgactt	ccttcccaag	660
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cccggaatga	aaatgctggg	ctatcaagcg	gtcattgcca	taaaatactg	gtcaggagtt	1440
gatgtcgatc	cggatataat	gctggaaaaa	ttaaaagaag	tagtaaaacc	tgcttag	1497

<210> 876

<211> 327

<212> DNA

<213> B.fragilis

<400> 876

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gcttgtgatt	tagageceta	tccactgaca	gacttgtccg	aagagacttt	ttggaatagc	120
gaatcgaatg	cggaattggc	attgacttct	ctgtatagag	gaagcctgac	agacggcgta	180
gagtataacc	cttcggattg	gtggtcctat	cacggaatga	ttatgatgga	gcattcttcg	240
gataacgctt	ttgaccgtcg	gggagagaac	aatcctttct	ttaagatttc	gagtggaaac	300
cctgactgca	gacaatgctt	ttatttaa				327

<210> 877

<211> 921

<212> DNA

<213> B.fragilis

<400> 877

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tcctccgaat	taattatcaa	cgaagacggt	tcggtattcc	atttgcattg	aaagccggaa	120
tggttggcag	acaaagtaat	attggtaggt	gatcccgga	gggtggcact	cgtagcttct	180
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atcgaaaagt	ttgaatataa	aggttacaaa	ataaccaact	tcgaaatgga	gagttccgcc	780
cttgccggcc	tcagcaagct	gatgggacac	aaagccatga	ccgtttgtat	ggttatagct	840
aaccgcttga	tcaaagaagc	gaacacaggc	tataagaata	ccatcgatac	attaattaaa	900
actgttctcg	atcgaatctg	a				921

<210> 878
 <211> 1161
 <212> DNA
 <213> B.fragilis

<400> 878
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 gtaataattaa atcgttattc ggcaattgaaa cctaattggg aatatgatgc tcaattttatt 180
 gatgatagag ttagtgtaat agaactttgt aatttgaagg gaatacccaa atgtatgtca 240
 aagttcttat taattttatac aataataatt gaattctgga aacttatatt cttgaataag 300
 aaaaaagaaa tagatgttct ccatgtggct tcaggacatt ttatagatat tttctattat 360
 gttataattg cacgttgtat aggtgctaag gttgtttatc attattgtga atatagatct 420
 tccttttaaat caagaaatgt ataccatcgg attaatggta aattgatcaa ttgctatgct 480
 ccgaagtttt gggacgggtgc tatttgtatt agtcattttt tgggtatctaa gacaaaagaa 540
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 aaaatatgtg aatatacagc gtgtcatggc gtagtggtga caactcggta tggggaaata 960
 ccttattact ttgaggataa aataaatgca ttgattgcag atgattttta cgtggcatca 1020
 atagccgaac agttagactg gctatatgac aatatggatc agacagcacg aattaaaaag 1080
 aactcttatt tattggggcg tagagttttc aatttaattt cttataaaga ttctgtgaca 1140
 gaatttttaa aagagttgta g 1161

<210> 879
 <211> 210
 <212> DNA
 <213> B.fragilis

<400> 879
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 atgacgaagg taagcccat catggcaaaa gtggataaca ataagctaaa cataacacag 120
 tatgatttta gattgaaaaa taaaatgcaa tgtataccga ccgccggaaa atacaagacg 180
 cacctcccg gcatctatcg gaatggataa 210

<210> 880
 <211> 903
 <212> DNA
 <213> B.fragilis

<400> 880
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 gctgtccgaa gcacacacca tttcctgacc gaagcagaca tacaatttta taagccgctg 120
 atccgacatg aatatcttgc cgcagtccga ttgtacatca ttgcggaaga ttcaggaact 180
 attgcagcct tcatgggatt aagtaatgat tgcatagaaa tgttgtttgt ccgtccgaat 240
 gcccatggac atggctacgg tagtcggctg gttgaatttg ccattcggaa aaaacgaatc 300
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 tttgagacta ccggtcgcga tgcattggat gcaacaggta agtcattccc cattttacac 420
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gaacaaacag tatctgttgg tgacatagaa atgactaatt tcttgatgta taaacgaatt 900
taa 903

<210> 881
<211> 192
<212> DNA
<213> B.fragilis

<400> 881
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catgatatct attgggaaaa tcagtgtaca gaccatctca tgacagatga attgccaaga 120
gaggaggggg aacctttact gctatctgtg gcagatgtta tggaaatttt agttcggaaa 180
attttgaaat aa 192

<210> 882
<211> 1305
<212> DNA
<213> B.fragilis

<400> 882
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ggtaacccta cagtagaagt agacgtagta ttggaatcag gcattatggg acgtgcatcc 120
gttccatcgg gtgcatcgac cgggtgaacac gaagcgcttg aactccgca cggtgataaa 180
catcgttatg gcggcaagggt tgtacagaaa gcagtagaga acgtcaataa agtcattgct 240
ccgcatctga tcggtatgtc ggccctcgac caaataggca ttgatcatgc catgttggca 300
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agtcgttcgg accgtatggc aaaatacaat cagctgcttc gtattgaaga agagttggga 1260
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<210> 883
<211> 543
<212> DNA
<213> B.fragilis

<400> 883
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gagattcaga aagaagtgat tcgcgtggcg aacgaaatta atcgtgattt ggcaggtaag 120
aaccctgtgt tcctcagtggt gttgaatggc tcgtttatgt ttactgccga cttgctgaaa 180
cacattacga tcccttgcca gatctctttt gtgaagctgg cttcttatca gggagtatca 240
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aaggtggact tgaatattga atatgtggca atgaatattc ccaatgattt cattgtagga 480
tatggtctcg attatgatgg ttccggccgt aactatccgg atatttatac agttgtagac 540
taa 543

<210> 884
 <211> 477
 <212> DNA
 <213> B.fragilis

<400> 884
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 gtaaaagtgt gcgatacagg tatcacgatt acccgactgg ctcaaattgg caatgctgaa 360
 atcaatggca atatcataga ggtcaagtca atggacggat tactgaatga aaaaactccg 420
 attgttgtca atcggatcac tgatggaata atctttgtcg aaaaattaaa atcctaa 477

<210> 885
 <211> 528
 <212> DNA
 <213> B.fragilis

<400> 885
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 gtaaagacta tctctattgc cgactttcct attaatcggt actatgttta tgcaccgtta 180
 ggactaagt tcaacgagga cctgaaagac attttccttc gtcagaccgc tctgaaactg 240
 gtgaataaca atgccgacct cgagattgat ggagagatta ccggatataa ccagtataac 300
 caggctgttt cggccgacgg atactcttct gaaaccaagc tgaccatcac agtgaatgtt 360
 cgttttgtga acaatacgaa tcatgaacag gacttcgagc aacagttctc ggctttccgt 420
 gtttatgatt cgagggagtt gctaacagcc gttcaggacg gactgattgc ggagatgact 480
 aaagagatta cagatcaaat atttaacgca acggtagcaa actggtaa 528

<210> 886
 <211> 1068
 <212> DNA
 <213> B.fragilis

<400> 886
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 tatgcccaga ccgaagttac agcgggagtt acccggggaa aagattacgg tgtaacctat 120
 gcacttccta aaacagcaat caatattgaa gtcaaagtca ataaagtac atatactccg 180
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 cccgccacga cacagaaaaa gaagataaat ccacgtgatt ttctgaccga agagattctg 480
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 gaaagtaaaa atgccctgg acgcggacag gcagacaaca tgcccaaaga tggggagcaa 600
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 ggtaccttga ataaagacga aaagatatct aacatccgcc tcaactccga taaggaaatg 720
 gacaacgaag tagctttccg cttttcgaag aagctgggca tagttgccaa taacgatctt 780
 gcaggagagc cggttttatat cacgctgaag aatctgaaaa ccgtcaacgt accggaagac 840
 gatggcaaaa agaaggtgga cggcattgcc tataatgtgc ccggcaaagc acaagtaaca 900
 ctaacggagg ggaaaaagca atggtttaac ggagaacttc ctgtcacaca attcgttacc 960
 atcgaatatc tggctccggc gcttttcaat aagaaatcga ctgttcagggt tactttcaac 1020
 ccggatacag gaggcttgat caaggtagat agagaagaag gagaataa 1068

<210> 887
 <211> 3054

<212> DNA

<213> B.fragilis

<400> 887

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<210> 888

<211> 1251

<212> DNA

<213> B.fragilis

<400> 888

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<210> 889

<211> 1410

<212> DNA

<213> B.fragilis

<400> 889

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<210> 890

<211> 813

<212> DNA

<213> B.fragilis

<400> 890

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<210> 891

<211> 1263

<212> DNA

<213> B.fragilis

<400> 891

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<210> 892

<211> 1191

<212> DNA

<213> B.fragilis

<400> 892

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<210> 893

<211> 183

<212> DNA

<213> B.fragilis

<400> 893

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<210> 894

<211> 1575

<212> DNA

<213> B.fragilis

<400> 894

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 <211> 549
 <212> DNA
 <213> B.fragilis

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<210> 896
 <211> 408
 <212> DNA
 <213> B.fragilis

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<210> 897
 <211> 1266
 <212> DNA
 <213> B.fragilis

<400> 897
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<211> 2697

<212> DNA

<213> B.fragilis

<400> 898

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<211> 783

<212> DNA

<213> B.fragilis

<400> 899

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cgatattcca	aggcacttga	aattattaaa	aaattaagtt	tgaaatatcc	aaaaaaaaat	720
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<210> 900

<211> 252

<212> DNA

<213> B.fragilis

<400> 900

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atcatttcag	gagttattct	cttttggatc	aaaattatta	ttagctggag	ttttacatac	240
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<210> 901

<211> 936

<212> DNA

<213> B.fragilis

<400> 901

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<210> 902

<211> 435

<212> DNA

<213> B.fragilis

<400> 902

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<210> 903

<211> 912

<212> DNA

<213> B.fragilis

<400> 903

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<211> 192

<212> DNA

<213> B.fragilis

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atagagaatc	attcgggtgg	tattggtaac	ccggaaagat	tgaaatctat	agtcatccat	180
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<210> 905

<211> 240

<212> DNA

<213> B.fragilis

<400> 905

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gatttttcaag	agttcttcga	aggagcttac	tttattatat	ttaagcttcc	caccgtttgt	180
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<210> 906

<211> 1128

<212> DNA

<213> B.fragilis

<400> 906

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<210> 907

<211> 519

<212> DNA

<213> B.fragilis

<400> 907

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ccggaagaca	caagaacgat	gtttcttcgg	aaagaagaac	agatgttaca	gcatgataaa	480
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<210> 908

<211> 372

<212> DNA

<213> B.fragilis

<400> 908

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<212> DNA

<213> B.fragilis

<400> 909

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<212> DNA
<213> B.fragilis
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<211> 738

<212> DNA

<213> B.fragilis

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<211> 747

<212> DNA

<213> B.fragilis

<400> 915

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<211> 204

<212> DNA

<213> B.fragilis

<400> 916

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<210> 917

<211> 1158

<212> DNA

<213> B.fragilis

<400> 917

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<210> 918

<211> 1422

<212> DNA

<213> B.fragilis

<400> 918

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<211> 2868

<212> DNA

<213> B.fragilis

<400> 919

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<211> 249

<212> DNA

<213> B.fragilis

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<211> 1521

<212> DNA

<213> B.fragilis

<400> 921

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<210> 922

<211> 2154

<212> DNA

<213> B.fragilis

<400> 922

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<210> 923

<211> 1284

<212> DNA

<213> B.fragilis

<400> 923

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 <211> 657
 <212> DNA
 <213> B.fragilis

<400> 924
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<210> 925
 <211> 1458
 <212> DNA
 <213> B.fragilis

<400> 925
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<210> 926
 <211> 579
 <212> DNA
 <213> B.fragilis

<400> 926

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<210> 927

<211> 474

<212> DNA

<213> B.fragilis

<400> 927

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<210> 928

<211> 1965

<212> DNA

<213> B.fragilis

<400> 928

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<210> 929

<211> 633

<212> DNA

<213> B.fragilis

<400> 929

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<210> 930

<211> 3885

<212> DNA

<213> B.fragilis

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<211> 1050

<212> DNA

<213> B.fragilis

<400> 931

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 <212> DNA
 <213> B.fragilis

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cgtgggggtg	tccggagaaaa gagcaaggaa agcgatgatg catcctgcga taccgctgc 180
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 <212> DNA
 <213> B.fragilis

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 <212> DNA
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<210> 936
 <211> 192
 <212> DNA
 <213> B.fragilis

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 <213> B.fragilis

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<210> 938
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 <212> DNA
 <213> B.fragilis

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<210> 939
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 <212> DNA
 <213> B.fragilis

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<211> 396

<212> DNA

<213> B.fragilis

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<210> 941

<211> 204

<212> DNA

<213> B.fragilis

<400> 941

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<210> 942

<211> 891

<212> DNA

<213> B.fragilis

<400> 942

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<211> 993

<212> DNA

<213> B.fragilis

<400> 943

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<211> 1296

<212> DNA

<213> B.fragilis

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<211> 252
 <212> DNA
 <213> B.fragilis

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<210> 946
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 <212> DNA
 <213> B.fragilis

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 gtggtaaaat tgcacttata tatcacctgg aagaaacaga accctacaat acataaaaagg 480
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<210> 947
 <211> 279
 <212> DNA
 <213> B.fragilis

<400> 947
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 tttttattca gcccatctcc ttccgaccgt aaaaaagagt ttctacacat tttcaaaata 180
 caaaatgaca ggattgtaag tgatcatgaa aaaacaagtt gtgataccta ttatgtgcgt 240
 tttctcttac catccgggat tctgtaccag tttttttga 279

<210> 948
 <211> 2136
 <212> DNA
 <213> B.fragilis

<400> 948
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 ggagtttatg ctgagcaaac ccgcatcaat ctcatgtga aacaagttcc cctaaagcaa 180
 gtgcttaaat cgatcgaatc gaagagtga tacactttct tctacaatga tgccgaaatt 240
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 aaaattcttc cggactgcaa atgtgtagtg gagaatagaa agattatttt ggttcccggg 360
 gcggagaaac aaaatacccc aaatgataat actgcgaaaa cgaaagagat aaccggtacg 420
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gaactgattt	caagttcact	gcctactatt	aatctggcta	caggtgatat	gaatatgtcc	2040
cagagtataa	cgacctgggc	tctgagaggt	gcttttgccg	gtttgggata	tattttataac	2100
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<210> 949

<211> 1536

<212> DNA

<213> B. fragilis

<400> 949

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ttaggtacct	tggatgtaga	tgctgcagga	gttataaaaag	ttgatgatat	tcctcaaaaa	180
gtttacataa	caaaaacagg	cgagaatcag	tttaagatgg	aactgaagaa	cttttagtttt	240
caaacaatgg	agttaggaaa	tatctcagtt	gataacatcg	cagttattaa	aaagggtaat	300
agttgtactt	ttagtggtaa	agcgaattta	acttttagcag	ttggagcatg	cgatgttact	360
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gctaagatct	taactttttc	ttttgcaaat	gaatttggtta	cttctcaacc	tgttattgat	540
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cagactgata	aatgttctat	ttatgcgggt	ttatatgaag	aatcttttga	tagcaaagggt	1260
aataatattc	cattgactgg	agattataaa	aataaagaag	tatatatcgg	gtcttcaagc	1320
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tctgttcctt	ttaaacctgt	tggagataat	aaatatgatg	caaataaaaa	gtattatgtt	1440
gctgtgatat	gctcatctag	cttcgaagga	gattactata	aaggtgctcc	gggaagtact	1500
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<210> 950

<211> 804

<212> DNA

<213> B.fragilis

<400> 950

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cttagaggat	tagaatatga	agtaaaagca	ggatttagta	ttggcggcac	ttccccatta	180
ccattgccca	aagaaatacg	ttctatagat	agctacaatc	ctaatatggc	catagccatt	240
gaagggaatg	caaccaagtg	gtttggttct	gataaaaaat	ggggaatgct	attagggctc	300
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aaaaattcct	accttacaat	acccattctt	gcaaagtata	aattaactaa	gcgatggaat	480
ctaacagtag	gtccttattt	ttcatatatg	cttgaaggag	atTTTTctgg	taatgtatat	540
gaaggttatc	tacgtaaaac	agatccaacg	ggacctaaag	tggaaattcac	agatggtaaa	600
gtcgcaactt	acgatttctc	caatgacctt	cgtaaatttc	aatgggggat	gcaactagga	660
ggagaatgga	aagcttttaa	acacttaaat	gtatatgcag	atctctcatg	gggattaaat	720
gacatcttta	aaaaagactt	caaaacaatt	acatttgcta	tgtatccaat	ctatcttaat	780
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<210> 951

<211> 1248

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (8), (16), (29)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 951

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atcagtcaga	tactggataa	gcagcaaccg	gtatatgtgg	gagctcccg	attggttgcc	180
ggtaacttaa	cctgggaaaa	ggtaactact	accaatcttg	ccttggtatg	caatttcttt	240
gataaccggt	taagcataac	aggtgaggtta	tatgtacgtc	gtacaaaaga	tatgttaacc	300
ccgggagtta	cgcttccaag	tgttttgga	accgacgtgc	ccaaacagaa	tgcagccgat	360
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tacgaaaatc	ccaagggatt	gctgggcat	tattatgtag	gaaaagagat	tggtgagata	540
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cagtcatggt	gtacttctta	tccgggtacc	cgctcttgg	caccgggtga	tctgaagttt	660
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gattataaaa	ttataggtaa	tagccgtgct	cgttatacat	ttggtttatc	ggccaatgca	780
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aaaggtaata	tgtatgacca	ttggacggag	gaaaatccgg	atgcgtactt	cccccgatg	960
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ttgttgaata	agataggaat	tgagcgcttg	cgcattttct	tctccggtga	taatttgtgt	1140
gaattttcgg	gtttatacaa	gcattacaaa	gtagatccgg	aaagcttagg	tgacattgtc	1200
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<210> 952

<211> 606

<212> DNA

<213> B.fragilis

<400> 952

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tataacaacag	aagatggtaa	aagagactta	gtagaagaaa	cagcagccga	acatcctttc	120

caattcattt	caggtttggg	cactacgctc	gaagcttttg	aatcacagat	agtaaacctt	180
cataaaggag	acaaatttga	atttactatt	ccttttgccg	aagcttatgg	tgaatatgac	240
gaagaacatg	taatcgatct	tcccaaaaac	atctttgaga	ttgacggaaa	attcgataac	300
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ggtagtgtag	ttgaagtaaa	agccgatacg	gtagtgtgg	atatgaacca	tccgttggcc	420
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attcaggaaa	tgattaaaat	gatgaccggc	gaaggcggat	gcagttgctg	aagctgtggc	540
gacggttgcg	gtgacgactg	cggagacagt	tgtggagaca	gctgcggttg	tggacattgc	600
cattaa						606

<210> 953

<211> 1383

<212> DNA

<213> B.fragilis

<400> 953

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ataatcgctt	taatacagcg	ggaggtgatt	cgggctatcg	gatgtacaga	gccgattgca	180
gttgcatgtg	gtgtagcaaa	agctacagag	actttggggg	ccaaaccgga	gaaaataaag	240
gtattgttga	gtgctaatat	cttgaaaaat	gcaatgggag	taggaatccc	cggtagcgga	300
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ctcgaggtgc	tgaaagacag	tactccggaa	gctgtagaag	agggaaagaa	actgattgat	420
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ccgttggtatg	aaatccgctt	tattcttgag	acggcacggc	ttaataaaaa	agcggcagaa	720
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tcacagggtta	tgaatgaaac	agacagggtg	gtgctcgaca	tcatgacaca	taaagggtgc	1380
ttaa						1383

<210> 954

<211> 1065

<212> DNA

<213> B.fragilis

<400> 954

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acaattaaat	gtatatacaa	aatgaaaaag	atatctatac	tatttatatt	ttccttgatt	180
cttggtttat	ttgtcagtga	agtaagcgcg	gccggccac	gtttgaagca	acgtcccaag	240
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cccaatttca	atcggttgat	gaaagaagga	gcttctacat	tgaataaccg	ttctatcctc	360
ccttcacga	gtgctcctaa	ctgggcctcc	atgtttaccg	gagtaggacc	ggaacttcac	420
ggttacacta	cttgggggaag	caaaacaccg	gaaattcctc	cttttatcac	caaccaatat	480
ggccgttttc	cgggactgta	cggattgttg	cgcgatacac	atcctaaagc	ggaactcggg	540
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catacctata	aatgggaatc	taaagagtat	tatgaaaagt	tagatgaatt	ggatgggtat	780
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acgatggtta	ttgacgtacc	tgccacagaa	gcctggttgt	tgggtgtaga	gcctcacgaa	1020
gcttggttgg	gcaatccggg	aacaactgca	ttttttacta	aataa		1065

<210> 955

<211> 192

<212> DNA

<213> B.fragilis

<400> 955

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acaaggtcta	tcttacgtat	tttatgttct	aaatttaaga	ttaagttggg	tatcgagcga	120
aatcgattta	aaaaaaaaatt	aatctatgat	tcgaatcgag	caaataataat	atatctccat	180
catcatcttt	aa					192

<210> 956

<211> 1680

<212> DNA

<213> B.fragilis

<400> 956

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gatctgaccg	gttttgacaa	tccctggccg	gctgtttctg	atgaattgaa	atctgcacag	120
aacaatgtga	agacgattcc	gacaatcggg	tatcatgccg	gatcggcaac	tttgtcacgc	180
tggagtcttt	ataagcagat	acgacaggcg	aatgagttca	ttgcctatgc	ccacgttatt	240
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aaagtatggc	aaaaaacaga	taagaaaatt	tattttttata	aagggaatgcc	tgacgataat	1140
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gattttctatt	tgttatatgc	agaagctttg	aatcatgtaa	atccgggtga	tgacgcgcatc	1320
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ccgggaatta	tcggttaaccg	ggagttgcag	gaaaaagcga	tccgtcacga	gcgtcgtatc	1440
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gaggggtata	aacaagggtg	tccggttcat	ggtatggata	tgaatgctac	cgatcttgaa	1560
ggtttcatga	aacgtactgc	ttttgaaact	cgtatttttg	aaaaacgtat	gtatctgtat	1620
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<210> 957

<211> 1137

<212> DNA

<213> B.fragilis

<400> 957

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tcacaaacag	cccaaggaca	atcttttact	cccggagaga	tatggcccga	taatcaccag	120
gtacatatca	atgcgcatgg	cggaggcatt	ttatatgaaa	acggaacctt	ttattggttt	180
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atgggtgacc	gctggactcc	acaaaacgct	attgacgggc	gctacatctg	gcttcccatt	1080
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<210> 958

<211> 1359

<212> DNA

<213> B.fragilis

<400> 958

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<210> 959

<211> 582

<212> DNA

<213> B.fragilis

<400> 959

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gcagaagacg	tagtgcagga	tggttttgtt	gctttatgga	ataaacgtac	agatattgaa	180

ttt gatggcg	cgg taaaagc	ctatcttttt	aaggctgtct	ataataaatc	gcttaatatc	240
ctttccagta	agaaatatac	cgaagaagaa	tccgtagaac	aattttccga	tcaaatcgaa	300
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<210> 960

<211> 1131

<212> DNA

<213> B.fragilis

<400> 960

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gcggatggtg	cgggggtatac	tatctccttc	tccaaaagtg	ctccgattac	tatccgtaac	300
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<210> 961

<211> 1137

<212> DNA

<213> B.fragilis

<400> 961

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ggcaaatata	aactaagtat	cgtattctcc	tctagcattg	aaggagatca	ttttcgtggt	1080
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<210> 962
 <211> 1059
 <212> DNA
 <213> B.fragilis

<400> 962
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 aactggctga aacaatcaga aaagaaccgg aatgaatttt ccgaagtcg tgatttatgg 180
 cttttaggca acacgatagc taccgacgat ctggaaacag agatagcgct agagcgattt 240
 aaaaatcgga tacagtcaac agaatccggt ttacgtaaaa acagattcgt tttccggaaa 300
 cacttcgttc cgttcttgcg tgtggcagct gtctttttga tgttatttac tgtatggtct 360
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 ttgactgcca atggaagtaa gggacgattt gttttgccgg atagtacggt tgtatggctt 480
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<210> 963
 <211> 2475
 <212> DNA
 <213> B.fragilis

<400> 963
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<210> 964

<211> 894

<212> DNA

<213> B.fragilis

<400> 964

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<210> 965

<211> 258

<212> DNA

<213> B.fragilis

<400> 965

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<210> 966

<211> 1980

<212> DNA

<213> B.fragilis

<400> 966

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<210> 967

<211> 195

<212> DNA

<213> B.fragilis

<400> 967

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<210> 968

<211> 1725

<212> DNA

<213> B.fragilis

<400> 968

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<210> 969

<211> 1266

<212> DNA

<213> B.fragilis

<400> 969

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<210> 970

<211> 1143

<212> DNA

<213> B.fragilis

<400> 970

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<210> 971

<211> 2991

<212> DNA

<213> B.fragilis

<400> 971

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<210> 972

<211> 297

<212> DNA

<213> B.fragilis

<400> 972

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<210> 973

<211> 1092

<212> DNA

<213> B.fragilis

<400> 973

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<210> 974

<211> 588

<212> DNA

<213> B.fragilis

<400> 974

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<210> 975

<211> 1038

<212> DNA

<213> B.fragilis

<400> 975

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<210> 976

<211> 1173

<212> DNA

<213> B.fragilis

<400> 976

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<210> 977

<211> 543

<212> DNA

<213> B.fragilis

<400> 977

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<210> 978

<211> 3252

<212> DNA

<213> B.fragilis

<400> 978

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<210> 979

<211> 1653

<212> DNA

<213> B. fragilis

<400> 979

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<211> 459
 <212> DNA
 <213> B.fragilis

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<210> 981
 <211> 1461
 <212> DNA
 <213> B.fragilis

<400> 981
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<210> 982
 <211> 1293
 <212> DNA
 <213> B.fragilis

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<212> DNA
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 <212> DNA
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<210> 986
 <211> 1899
 <212> DNA
 <213> B.fragilis

<400> 986
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<210> 987
 <211> 342
 <212> DNA
 <213> B.fragilis

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<210> 988

<211> 1032

<212> DNA

<213> B.fragilis

<400> 988

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ggaaaaaatg	gtgatttgtt	tgttcagaag	gcgcccgtcg	ctactctgga	tgtattagcc	720
gatgcattaa	agtctcttta	ccatagtaac	gcggatgtca	aagtgattgg	taccggtcac	780
ggtgagaaac	tctatgaaac	tcttgttacc	cgtgaagaga	tgtctaaagc	agaggatatg	840
ggtgattatt	atcgatatcc	atgtgatacg	cgtgatttaa	attatgataa	gttttttgtg	900
gaaggaaagt	aggaggtctc	caaaatagaa	gattaccatt	ctcataatac	ccgtcgtctt	960
gatgttgagg	ggatgaaaga	acttctcttg	aaacttgatt	ttattcgcga	agatcttggc	1020
cttgaaaaat	ag					1032

<210> 989

<211> 1245

<212> DNA

<213> B.fragilis

<400> 989

acaaaatcgt	ctggagaaaa	tcctgataat	atcgaaatga	atattttgtt	tctgaccctt	60
aaccgtgttt	cagatctttc	tgaacggggg	atatacacgg	atttgatgcg	ggaattttat	120
tgtcatgggc	atagggctca	tatggttgtt	cccgccgaac	gtcgctttca	tgaatctact	180
tcaataaaaag	agagttgtgg	cgctcaaatg	ttgagggtga	agacattgaa	tatccaaaag	240
agcaatgtgg	tggagaaagg	catcggtaga	ttgttattgg	aaatgcagta	tcaatgtgcc	300
ataaagagat	attggaagga	tatccggttt	gatttgatac	tttattcaac	tcctcccat	360
actttcaata	gggtcatcag	ttcacaaaaag	agacgttgta	aggcgaaaaag	ttatctttta	420
ttgaaagata	tttttctca	aaatgccgtt	gatttgggaa	tgttttcaaa	gagaagctta	480
atztatagac	ttttccgtaa	aaaagagaag	gatttatatc	agatatcgga	ctttataggc	540
tgtatgtctc	ctgccaatgt	ggattatgtg	ttgacacata	atccggaaat	aaaggctgat	600
agagtagaga	tatgccccaa	tagtattaaa	ttgttagaga	agtcattaat	ggcttcaact	660
gtaagaaaaa	acataattgca	gaaattgcat	attccaatta	ataagactct	ttttatatat	720
ggtggcaatt	tggggcgctc	acaaggtttg	attttcttgt	tggacgtgat	agccgcaaat	780
gaggaacgta	atgacagtta	tttcatcatt	gtaggcagtg	gcactgaata	tggcaagata	840
aagtcttggg	ttgaggcgaa	tcacccggat	aattcaatgc	tgctttcttc	acttccaaaag	900
aaagagtatg	atgatttggg	aaaggcttgt	gatgtcgggt	tgattttcct	tgatagacgt	960
tttaccatcc	ctaattaccc	ttcccggtta	ctctcttatt	tagaaaaccg	gatgcccggt	1020
ttattggcta	cagacctgaa	tacggatata	ggacggattg	ctgaacggaa	tggttatggc	1080
ttttggacag	aaaatgggaa	tttgatata	tttatggaaa	tgggtgattc	cttatctgca	1140
gacagagaaa	aaataaaaagt	gatgggcgag	aaagggtatg	aatacttgaa	gtctaattat	1200
acagtagaaa	gaggggtaccg	gatgataatg	aaacattttg	agtag		1245

<210> 990

<211> 183

<212> DNA
<213> B.fragilis

<400> 990
ctgcatctgt tagaactcca acagttacag aacctagttt ggaagcctct cttattatat 60
ttaaattgacc tggatgaatc atatccgcac tcattccaac ataaactttt ttacattttt 120
ccatcttaca tagaatttat tagaaaaaac aaacaggaag tgtagttat aacaatttat 180
taa 183

<210> 991
<211> 489
<212> DNA
<213> B.fragilis

<400> 991
agaatttccc cctcagctc cccccaaagg ggaggaagaa gagcggaagg gggattctgc 60
ttatctcccg ataccgggat acgccttcaa tacaatgacg cacaattact cgggactgat 120
ggacacgcta aagagattga gcattaccga caccggggaa gttaaactcca tactcaggct 180
gtcggactat gggaggaagg gaacgacggt atggaaactg attgccaaca cttgctggag 240
cgacatcgga gccaaaggaa gatacctgat agcggcgcta aacaagacga aaagaaggta 300
gcagagagtg tcagtcacct atttgtagtt gacaaaaaag caaatataca ggcttttgac 360
cagaaaggga ttcagcgaaa caaagaagta aaaagtgtgc ttaacgaact aaaacacagt 420
gttttttaag cacaagattt ctctcgccca aagctttgtt ttaacgctac gttaaagctt 480
gttcttttaa 489

<210> 992
<211> 186
<212> DNA
<213> B.fragilis

<400> 992
gaatgcctac cgaaagatag gaatcttttc tcatttggtg atggagtaaa tattgtttct 60
ttaattgatt cggtaaaaaat gattttttcg cttaatcttg tacttgttct gccttttggc 120
aaaagcttat tagctcttta tgaactcttt tggggggaat gccgatgcgg ataccaaatt 180
ctatga 186

<210> 993
<211> 297
<212> DNA
<213> B.fragilis

<220>
<221> unsure
<222> (56)
<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 993
aaagcagcta cggcaaccgc atcattgccg ctgaatggga tacacacaag aagctntcgt 60
tcctgggtata catttatatt aaaaggaata gataatgtag ggctgctgaa tgaaatcaca 120
caagttatatt cacgccagct taatgtgaat atccggaaac tggatatgga aacggacgat 180
ggcatttttcg aaggaaaggc cgggttgtat gtgcacgatg tggaagatgt aaaagctatt 240
tgcaacaacc tgcgcaagat tccgaatata aagtcgggtg cacgtgtaga aaactaa 297

<210> 994
<211> 1164
<212> DNA
<213> B.fragilis

<400> 994

aattctaaca	ccatgctgaa	atcaaaatat	aaaatctatc	tgttactact	ctgcctgaca	60
ggttgtgttt	cagaatacaa	cgcacaacta	ccttcttccg	atgaagaatt	gctggtagta	120
accggcgaca	ttatcgctaa	tacagaagcc	atattctcat	taagcaaaag	tattccacta	180
tccgaagaca	tgccggaaga	ttatcgaaac	atattatgcca	gaattgctgt	agtaggcagc	240
gacggctatc	gaagtgatth	cggaaacggct	cttgggtgatg	gtaaatacca	ggtcagtatc	300
ggtgaattgc	aggatgatgt	atcctacgga	atagagatag	aatacgacgg	agagatttat	360
acctcgtctc	cttccacacc	gatggatatct	tctgaaatag	acagtgtttc	gtggatacaa	420
ccagaacctg	aacaagcact	ttctatacgg	gtatcgaccc	atgggtgatcc	cggaaaaact	480
caatactaca	tgtggaacta	tccgggaagac	tgggagataa	gagccagcta	cattacaact	540
tgtacttttg	atccggatat	gaaccgcatac	tatgaagaca	gcaattatcc	aactttctat	600
tgttggaata	aggaaatatc	aagaaatata	ttgattggct	ctacggaaaa	gttgaaagaa	660
catctgatca	taaataataa	gctactcgat	gtgccgggtca	atgaagacag	attcactgta	720
ctatacagca	tacaggtaca	gcaacgggca	ttgagtaaag	agggatatga	atattacttg	780
aatgtacagc	aacagaatga	agaaatggga	ggaatcttta	ctccacaacc	ctctgaaatc	840
caaggaaaca	ttagttgtat	cagtcagcct	ggacgaagga	cgatcggtta	tgtaggcgctc	900
tataaaaaaca	tctctgaaaa	gagaatatac	attcatccca	acgaaattaa	acgtcctcct	960
ctatacagtg	gctgtgaaga	agtgtcggat	agcgaaatgg	atgaacaggg	ctatagcaca	1020
tatctgataa	gataccttgt	cggttatcgt	ccagtcggta	caggcactca	cattgaccac	1080
tggggccctac	ggagatgtac	agaatgtgaa	gccaacggag	gaagtaaaaa	caagccttca	1140
ttctggccca	acgatcatca	ataa				1164

<210> 995

<211> 366

<212> DNA

<213> B.fragilis

<400> 995

ttgagaaaca	ctctacaaac	aaaaagaaat	ctctgtcatt	ctaaaatcaa	aagtacaaat	60
agccgtaatc	aaattcacaa	tatatgggga	atttccttgc	ttatcaaaca	aatacttagt	120
atTTTTgttt	caaattcaca	atatattggg	aatatgaaac	aaattggaat	acagattcgc	180
caacgaagaa	aatgtttggg	tataaatcag	caaacacttg	cagatttagc	acaaatcagt	240
atcaatacta	taacaaaaat	tgaatatgga	gaaataaata	ttaatTTTca	aaagctctat	300
gccatatttg	aggtattagg	attagaactt	tctctgaaaa	ttaaaaataa	ggaggggacat	360
ctatga						366

<210> 996

<211> 2046

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (1088), (1885), (2007)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 996

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caggaaattgc	tgaacgatta	tcttgctacc	aagcaccgca	aacgtattga	gattataaac	120
aaggccttca	atttcgccaa	tcaggcacat	aaaggcatca	aacgacgctc	gggggaaccg	180
tatatcatgc	accccatthc	cgtcgcgaag	atcgtatgca	atgaaatagg	ccttggctcg	240
acttccattt	gtgccgcttt	gctgcacgat	gttgtcgagg	acaccgatta	tacagtagaa	300
gatatcgaaa	atatcttcgg	ggccaagatt	gcacagattg	tcgacggact	gacaaaaatc	360
tccggaggta	tttttggtga	cggggcttcg	gcacaagcag	aaaacttcaa	gaaactcctg	420
ctcaccatgt	ctgatgatat	cgggtgatc	ctgatcaaga	ttgccgaccg	cctgcacaac	480
atgcgtacac	tccgttccat	gttgcccaac	aagcaatata	agattgcagg	cgaaaccctt	540
tatatTTTcag	ccctcttgc	caatcgctg	ggactgtata	agatcaagac	ggaactggaa	600
aacctcagtt	tcaaatatga	acatcctgaa	gaatatcagg	agattgaaga	aaagctgaac	660
gcaacagccg	cgaacgcga	taaggatatc	aacgaattca	ccgtcccat	acgcgagcag	720
ttggataaaa	tgggattaaa	atatcgaatc	ctggcacgtg	tgaagtccat	ctactctatc	780

tggacaaga	tgcagacca	gcattgttct	ttcgaagaga	tttatgatct	tctggctgta	840
cggatcat	tcgaaccacg	caacatagat	gaggaactga	acgactgttt	cgatatttat	900
gtttccatct	ccaaaatcta	taaaccgcat	cccgcactgc	tgcgcgactg	ggtgagccac	960
cccaaagcta	acggatacca	ggcactgcat	gtcactttga	tgggcaataa	tggccagtgg	1020
atcgaagtcc	agatacgcag	tgagcggatg	aacgatgtag	ccgaacaggg	atttgccgcc	1080
cactgganat	ataaagaaag	aggaggcagc	gaagacgaaa	gcgaactgga	gaaatggttg	1140
cgtaccatta	aagagatact	cgacgatccg	cagccggatg	ccatcgactt	tctcgataca	1200
atcaaattaa	acttattcgc	ctcggagatc	tttgtcttca	ccccgaaagg	agagctcaaa	1260
accatgccgc	agaactccac	tgccttgat	ttgccttct	cactgcacac	ggatatagga	1320
agccactgta	taggtgccaa	agtgaatcat	aaactggtgc	ctctaagcca	taagctgcaa	1380
agtggtgacc	aagtggaaat	cctgacatcc	aagtcacagc	gtgtacagcc	gcaatgggaa	1440
gtgtttgcc	ctactgcgcg	tgcaagggct	aagattgcgg	ctattctgcg	taaggaacga	1500
aaaaccttcc	agaaagaagg	agaagaattg	ttgaatgaat	tctttaagaa	agaagagatc	1560
cgcccgagg	cagccgtcat	cgagaagtgt	tgcaaactgc	ataacatgaa	gaacgaagaa	1620
gagtttcttg	tagccatcgg	taacaaaacc	atcgttctgg	gagatgccga	caaaaatgaa	1680
ctgaaagaga	aacaaagcag	caactggatg	aagtatctga	ctttctcttt	tggcaataat	1740
aaggataaac	agcaggagga	aaaagaaccg	caggaaaagg	aaaaaatcaa	caccaaacia	1800
attctcaaac	tgacggaaaga	tgccttgcaa	aagaaatata	tcatggccga	atgttgtcat	1860
cccatccccg	gtgacgcagt	actgngatac	atggacgaga	atgaccgcac	catcatccac	1920
aagcgtcaat	gtccggtagc	ggccaaactg	aaaagcagct	acggcaaccg	catcattgcc	1980
actgaatggg	atacacacaa	gaagctntcg	ttcctggtat	acatttatat	taaaaggaat	2040
agataa						2046

<210> 997

<211> 888

<212> DNA

<213> B.fragilis

<400> 997

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gcaattgtgc	tgaaactgat	gtgtaagatt	tacaaggagg	gatactacat	acgatgggat	180
gaagaacaat	gcctgatttt	cgcaaacaaa	gcaggaagag	aggtgcaggc	agaagagggtg	240
caggggatca	tgcgatttct	gttcacccaa	ggaatactgg	acagaaacag	ttatcaggaa	300
aacggaatac	tgacttcgga	aagtatacag	aaagtatgga	tggaaagcgc	aaagcgaagg	360
aaaagagagt	tgtcggagct	cccttacctg	atggtgaaac	cggaaaaaga	aaatggaaaa	420
gccgacactc	ccccggcact	acaagaaatt	cagcaaccag	agctgttcaa	aaaggaaaaa	480
acacctgtta	acccgaaaaa	tgtagtacat	catgtagccg	ttgacgcaaa	aaatgcatgc	540
aattccggac	aaagtaaagt	aaaagaaaaa	aaagcagagg	aaaataaaga	atttcccccc	600
tcagctcccc	ccaaagggga	ggaagaagag	cggaaagggg	attctgctta	tctcccgata	660
ccgggatcac	ccttcaatac	aatgacgcac	aattactcgg	gactgatgga	cacgctaaag	720
agattgagca	ttaccgacac	cggggaagta	aactccatac	tcaggctgtc	ggactatggg	780
aggaagggaa	cgacggtatg	gaaactgatt	gccaacactt	gctggagcga	catcggagcc	840
aaaggaagat	acctgatagc	ggcgctaacc	aagacgaaaa	gaaggtag		888

<210> 998

<211> 366

<212> DNA

<213> B.fragilis

<400> 998

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aagcaaatct	ctgacaatag	agaccttaag	tcaaacagag	gacgaaaaaa	ggagaaaccc	120
atacaaggga	ttgtttttgaa	acactacgaa	tgcttaagc	tactaatcac	actctatcaa	180
gatggggcaa	tgggtataaa	aaaggagaca	tcacaagttg	cattagcacg	atatatagac	240
gacaaaaaac	tattagggaa	tattcgaaat	ggaatattca	ttccattgaa	gttcagcact	300
attctaaagg	aaataaacac	catctggaac	gaaatgctac	gagataaatc	cattggcata	360
aaatag						366

<210> 999
 <211> 360
 <212> DNA
 <213> B.fragilis

<400> 999
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 aaaaacattg tcatagcaga cctgacaaac atagacgaca cgatatgcaa atactttgt 120
 atctgtcagg ggaactctcc cagccagggtc attgccattg tagattccat aaaagaat 180
 acccgcaaag gtgccggcac caaacctctc gccatcgacg gacagcgaaa tgcagaatgg 240
 gtagctatgg acttttcaga tgtattagta catgtattcc taccggaagc cagaaacttt 300
 tataatttgg agcacctgtg ggcagatgcc aagttaacta caattcccga cattgattaa 360

<210> 1000
 <211> 225
 <212> DNA
 <213> B.fragilis

<400> 1000
 aacctctcga ctatgattga attaacttgc tgtccttcta ctttacaaaa gggatttctca 60
 acctattcgc ctgttgcat t gaaagagctg ttcaatagcc aaaaggtaaa ccatatactg 120
 ccatacaatg gcatggacaa taatgaaacg gaacaaaaag aatttcagga taacaacaaa 180
 cacatgtcta tatccggagc tcaacaaaat aagtccagcc aatga 225

<210> 1001
 <211> 1104
 <212> DNA
 <213> B.fragilis

<400> 1001
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 gcaggcattg aacaaccgtc atctgtaaat ccttatctga aacggaagggt aaagaagcgt 120
 caattgtcgg ttagtgagtt tgtggaggga attgtcaagg gagatgtgac gatcttgagt 180
 caggctgtga ctttggtaga aagtgtgcgt cctgaacatc aagctactgc ccaggaagtt 240
 attgaaaaat gtctgcctta ttccggaaat tcaatccgtg taggtatcag tgggtgtaccg 300
 ggagccggta aaagcacctc gattgatgtc tttggattgc acgttctcga aaagggagggt 360
 aagttagctg ttttagccat cgacccgagc agtgaacgca gcaaagggaag tattttgggt 420
 gataaaaccc gtatggagca gctttcagtg catcctaaat catttatacg tcctagccct 480
 tccgcgggtt ctttgggggg agtagccgtg aaaaccgtg aaacaatcat tctgtgtgaa 540
 gcggccggct tcgataagat atttgtagag acggtgggag tgggacagag tgaaacggct 600
 gttcactcga tgggtcgattt ctttctgttg attcagttgg ccggtacggg agacgaactt 660
 caaggtatta aacgcggtat catggaaatg gcagatggta ttgtgattaa taaggctgat 720
 ggtagcaata tcgataaagc caaattggcc gctgctcagt tccgtaatgc tttgcatctt 780
 tttcccgctc ccgattccgg atggacaccg cgtgtactca catattccgg attctacaat 840
 cttggggtaa aggaaatatg ggatatgggt tatgagtata tcgattttgt gaaaggtaat 900
 ggctattttg aatatgccg taacgaacaa agtaaatact ggatgtatga aagcatcaat 960
 gaacagttac gtgacagttt ctatcataat gccaaagatcg aatcgatgtt acaagaaaag 1020
 gagcaacaag tgctcagggg aaatctgacc tcttttggtg ctgccaagag cctactcgat 1080
 acctattttg aagatctgaa ataa 1104

<210> 1002
 <211> 1206
 <212> DNA
 <213> B.fragilis

<400> 1002
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 ggtgttccgg attcttttatt aaaaaacata tgtgcttata ttgcggataa caaggatgca 180

aagcataata	ttataacage	aatgagggg	gcggcagtcg	gtttggctgt	aggtcattat	240
ttggctacaa	gggaaattcc	agttgtgtat	atgcaaaact	caggagaggg	aaatattatc	300
aatcctcttg	cgtcattgac	tgataaagaa	gtctataata	tacctattct	tttactgatt	360
ggatggcggtg	gtgagccagg	agttcatgac	gaaccgcagc	atgttaagca	gggaaaagtg	420
actattcctt	tactggatgt	aatggggatt	aagaatacac	tgatgagtaa	gagtgaagtt	480
gatttcacta	agcaattaga	tgatgcgttg	gtctatatgc	gtgaaactaa	cgaagcattt	540
gctttaataa	tagaaaaaga	tacattcgaa	tcatattcgc	ttaaattaaa	ggaggattct	600
gtattacaac	aattatcaat	gagtcgagaa	aacgctattc	aaatggttgt	agattcaatt	660
ggaaaaaagg	atgtaatagt	ttcaacaaca	ggtatgattt	cgcgagagct	ttttgaatac	720
agaacaaaaa	tgaatgaaag	ccatcagagt	gattttctta	cagttgggtc	tatgggacat	780
gcttcacaaa	tagcattagg	gattgcactg	gaaataccgc	atcgtaaaat	ttattgtttt	840
gatggtgacg	gtgctgtgat	tatgcataatg	ggatcaatgg	caattattgg	agataagggc	900
cctgaaaatt	tgatccatgt	tgtgtttaac	aatggatctc	acgattctgt	aggtgggtcag	960
ccaactgtag	gacttaagat	taatatccct	gcaatagcaa	gagctgtcgg	ttataaagtt	1020
gtatatagtg	ttgattgtga	agaagcttta	aagactgctt	tagaaaaggt	cataaaagaa	1080
gcaggaccta	ttcttctaga	ggttaagggt	aaaaaaggga	atcgaaaaga	tttgggaagg	1140
ccatctatta	ctccaataca	aaataaatta	tcttttatga	cttttttgaa	taatgaaaaa	1200
aaatag						1206

<210> 1003

<211> 1260

<212> DNA

<213> B.fragilis

<400> 1003

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ttagccgac	ttatttgcg	taacattctt	ttaagagtag	ttgccaaact	agtgaaaaag	180
accaaagcaa	cctgggatga	tattgtgttc	gaccgtaaag	ttttgattta	cctcagtcac	240
cttgtccccc	ccatcattat	ttatgtgttg	attcctttgg	caattccgaa	tgtaagtgcc	300
ctcgatttta	tccgtcgtat	ctgcatgatt	tatatcattg	cggtttttct	gcgtttttatc	360
agtgcatctt	tgctggctgt	ttatcatgta	tacagtgcgc	gagaacagtt	tcgtgatcga	420
ccattgaaag	gtttgttgca	aacggcacaa	gtgatactat	ttttcattgg	aggaattggt	480
gttatcagtg	tattgataga	taaactctccg	atggtattgc	tcaccgggct	tggtgcttcg	540
gctgccatcc	tgatgttgg	gtttaagac	agtatcatgg	gatttgtgtc	cggcattcaa	600
ctttctgcaa	ataatatgct	gaaagtaggt	gactggattg	ctatgcccaa	atacggagcc	660
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caagagtcgg	gtggacggcg	tgtgaagcgt	tctatcaata	tcgatatgaa	cagtgtgaaga	840
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gagcagaccg	agcaggtgg	gaaagagtat	aataaagaac	atcacataga	caactctatt	960
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<210> 1004

<211> 840

<212> DNA

<213> B.fragilis

<400> 1004

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<210> 1005

<211> 615

<212> DNA

<213> B.fragilis

<400> 1005

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<210> 1006

<211> 1068

<212> DNA

<213> B.fragilis

<400> 1006

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<210> 1007

<211> 1527

<212> DNA

<213> B.fragilis

<400> 1007

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<210> 1008

<211> 1038

<212> DNA

<213> B.fragilis

<400> 1008

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<210> 1009

<211> 765

<212> DNA

<213> B.fragilis

<400> 1009

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<210> 1010

<211> 360

<212> DNA

<213> B.fragilis

<400> 1010

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<210> 1011

<211> 1002

<212> DNA

<213> B.fragilis

<400> 1011

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gcagggattt	ttgcactaat	tgttcatggc	atccagactc	tgctgggtat	tttattgggt	960
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<210> 1012

<211> 1335

<212> DNA

<213> B.fragilis

<400> 1012

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<210> 1013

<211> 1152

<212> DNA

<213> B.fragilis

<400> 1013

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<210> 1014

<211> 855

<212> DNA

<213> B.fragilis

<400> 1014

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<210> 1015

<211> 945

<212> DNA

<213> B.fragilis

<400> 1015

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gggtttaata	atcttttctaa	tttcaatcgg	atcttcaaga	aaaagaaaga	atgttcgccc	900
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<210> 1016

<211> 324

<212> DNA

<213> B.fragilis

<400> 1016

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acgtgttatt	tggccgggtga	agaagtatgg	ctcaaatttt	atactattga	cacacatttt	180
cgcccatctt	ctttcagcaa	agtgggatac	atagaaatat	caaatactga	acggcctaaa	240
gcacagctta	aactggcact	tgacaatggg	agcgggttcg	gcaaagtaaa	gattcctaca	300
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<210> 1017

<211> 867

<212> DNA

<213> B.fragilis

<400> 1017

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ccggtacgcg	aagccccc	agcacgggca	cgccgccatc	gcgagccggg	cgtttctact	180
cgggccaccg	acagtgtgaa	agtggagaaa	gcagtcgtcc	tcccaccgat	agacagtttg	240
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ctggaaagga	tagaaacacc	cgtcatgcca	tcggtcgtaa	aggcagatag	cctgccaccc	360
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<210> 1018

<211> 1206

<212> DNA

<213> B.fragilis

<400> 1018

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tctggttttg	aaaatttaga	aaaaaaatta	gactatatca	taaatattcc	cgatatcgga	180
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<210> 1019

<211> 1029

<212> DNA

<213> B.fragilis

<400> 1019

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ttatccaata	ggatagttga	cagtcttaag	ttttgggaat	atgatatttt	gttctcttat	180
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gttgtctgga	tgggtgagga	agggaaatgtg	cgacgaaaag	gggtggataa	ggcattgcga	540
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<210> 1020

<211> 375

<212> DNA

<213> B.fragilis

<400> 1020

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gccagagata	ttgcattggc	aaatgttgaa	tctcttgcta	atgctgaagg	cgatggtata	180
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aaagatgatt	ctacgggaga	gtattatttg	gtgtgtaatt	caggaactac	cgaaagcggt	300
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<210> 1021

<211> 981

<212> DNA

<213> B.fragilis

<400> 1021

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<210> 1022

<211> 756

<212> DNA

<213> B.fragilis

<400> 1022

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gagcataatt	ataatgtcct	gaccaaacag	gtagaagatt	tgacggctga	gaatgaatcg	360
gaatttggga	atgatccggt	ttgggttaac	aaggatatga	tgtggattgg	cgggggatac	420
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756

<210> 1023

<211> 903

<212> DNA

<213> B.fragilis

<400> 1023

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taa						903

<210> 1024

<211> 810

<212> DNA

<213> B.fragilis

<400> 1024

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<210> 1025

<211> 1443

<212> DNA

<213> B.fragilis

<400> 1025

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<210> 1026

<211> 951

<212> DNA

<213> B.fragilis

<400> 1026

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<210> 1027

<211> 2778

<212> DNA

<213> B.fragilis

<400> 1027

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agtataacta	ttgactcttt	attggagact	gtagaaaaaa	atacacccca	taggattttc	180
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<210> 1028

<211> 1017

<212> DNA

<213> B.fragilis

<400> 1028

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actccttttg	ctgtatgtta	taagaattca	ataaagtact	cagtggctca	taatgatatg	360
cttcctgatt	atgctgtgat	atttcctcag	tttacttata	ataattcttc	atatctgaca	420
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aatgacttga	ccataatggt	gaatcaggta	aatattcagc	gatttggtaaa	taaccctgtc	960

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<210> 1029

<211> 1257

<212> DNA

<213> B.fragilis

<400> 1029

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aagctgagac	tgttgattat	agtcgggtacc	cgtccggaga	ttatccggtt	ggctgccgta	180
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gatgctgtag	gggatgattt	gggttcgaca	atgggtaata	ttttgaatgc	gagctataaa	360
ctgatgtcac	acttaacgcc	tgatgccggt	ttgggttctcg	gtgataccaa	ttcttgcccta	420
agtgtaatca	gcgctaaacg	cttgcatatt	cctatttttc	atatggaagc	cggtaacctg	480
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<210> 1030

<211> 426

<212> DNA

<213> B.fragilis

<400> 1030

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tgtgagaaaag	ttttttcttt	gaatcgctct	tattatggaa	tttatgttcc	tcaaggtata	300
tggagaaaaa	tgcaaaattt	ctctactaat	gcactggcgt	tagtgttatc	ttctacaaat	360
tatgatccag	atgattatat	tttggaatat	atagattttg	tgcaaagtaa	aaagaattca	420
ttatga						426

<210> 1031

<211> 594

<212> DNA

<213> B.fragilis

<400> 1031

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gctccggggc	gaccgatgat	cttattcgaa	ggtcacatct	tttggcgtga	actcaagaag	180
cggggactag	atccggagag	gtatgtttgcg	ggcaatgaaa	atattcttta	tcctaaatgg	240
gagaagggtc	attattatgg	cgggatgaaa	gagtatgaac	gtctggaaaa	ggcctggcaa	300
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aactatgcga	tgtgogggta	tggcagtggt	gaggaaatgg	tgaaagatat	gtgtgtcgga	420
gaagataaag	aactggaagc	ttttgcgagg	tttgtgaaac	ttgctaagtt	gcagtcctat	480

ctggagcaga aagactgggt cgggtttgcc aagaggtata atggacccgg atatgcccg 540
aatcagtatg ataaaaaact ggaaggggct tatcggaagt ttacgaagga gtag 594

<210> 1032
<211> 501
<212> DNA
<213> B.fragilis

<400> 1032
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tgggagtatg ttgaagaata a 501

<210> 1033
<211> 891
<212> DNA
<213> B.fragilis

<400> 1033
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acatttatcg aagtgatiga gaaaagacaa ggattgaaga ttgcttgttt agaggatata 780
gcttttggac aaagggtgat tactattgat aaattgcgaa aactggcaga aaagatgaag 840
aataatcagt atgggaaata cttggtgaaa attgtagaag gactgaattg a 891

<210> 1034
<211> 798
<212> DNA
<213> B.fragilis

<400> 1034
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tattatttcc tgagccgtcc ccgtcgcttt ggcaagagtc tgctgatatc tactcttgaa 180
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gaaagcctgg atcgaatatt gaacgatacg ttggctaaat gggaaatggt gtacgggact 360
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cagtcggggc agcgggtggt gattttgatt gatgaatatg ataaaccgat gttgcaggct 480
atcggtaatg aggagtggg agagaagtat cgtgatacac tgaaagggtt ttattctgtg 540
ctgaaaacga tggacgggta tatccgcttt gcccttttga cgggagttac caagtttgggt 600
aaggtaagtg tgtttagtga cctgaataat ctgaacgata tctctatgga cgaaccttat 660
gtggagtgtg gtggaattac agaaaaggaa atccatcatt atctggaacc ggaaattcgt 720

cagttggcga aatatcaaaa gatgtcgtac gaagatgctt gccgtcttca ccacagggct 780
ggaaggatcc tcgaatag 798

<210> 1035

<211> 888

<212> DNA

<213> B.fragilis

<400> 1035

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atggaaaata	aaagacctct	gactctcgtc	tccaatgacg	acggcatcat	ggcaaaagg	180
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gcccctcggt	ccggcagtg	atgtgcatta	acggtgacac	agccggtgca	ctatcagtta	300
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ggttgtctca	atgggattcc	ttctatcggt	ttctctat	gtgaccacgc	ccccggagct	540
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agaatctg	aacaggccaa	aggacattgg	agcggagaat	ggcaggcttg	ccccgggaga	720
gacgatgcga	atttctattg	gttaaccgga	gaatttatcg	atcatgaacc	ggaaaacgaa	780
aagaatgatc	actgggcact	ggctaattgga	tacgtagcga	ttacacctac	tgtagtggtat	840
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<210> 1036

<211> 549

<212> DNA

<213> B.fragilis

<400> 1036

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cctatgcaat	ataagataag	tataaaagaaa	gggaaaaaag	tccgtgtttt	ggttcctatc	180
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caaccgatg	aactcaactt	gtccaaagga	accaaagtcc	gtattacagg	tggtgacttc	420
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gctatacaag	gtgtcatagc	cgttgccatg	gccactattc	accctgatct	tatagaagta	540
atcaaataa						549

<210> 1037

<211> 2043

<212> DNA

<213> B.fragilis

<400> 1037

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ggaagcagtt	ctgtcagtaa	gaacatctct	tacgatgagt	tccagcagta	cgtagctgac	180
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aataacaaac	aagaaaacgc	cgttcactct	gcagatggag	aagatgtaga	cacaactact	1980
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<210> 1038

<211> 423

<212> DNA

<213> B.fragilis

<400> 1038

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<210> 1039

<211> 597

<212> DNA

<213> B.fragilis

<400> 1039

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cttcttggtc	atcccgtatt	acgtccgtca	gaagtgcggg	gaccactgat	cgctcagtatt	180
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ctctgtggaa	atgtattggt	gggggagggg	agctggattg	gcgccggtac	taccattatt	480
cccgggtgtg	agataggaaa	gtggagtgtg	atcgggtgctg	gttccgtggg	gactaaggat	540
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<210> 1040

<211> 618

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<210> 1043

<211> 5784

<212> DNA

<213> B.fragilis

<400> 1043

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<211> 1089

<212> DNA

<213> B.fragilis

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<211> 846

<212> DNA

<213> B.fragilis

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<212> DNA

<213> B.fragilis

<400> 1046

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<211> 1140

<212> DNA

<213> B.fragilis

<400> 1047

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<211> 819

<212> DNA

<213> B.fragilis

<400> 1048

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<211> 1416

<212> DNA

<213> B.fragilis

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gtagtgatgt	ttgcctccat	cttcggtact	ttgggttccaa	tgacactcga	aaagatgaaa	1320
atagatccgg	ccatagctac	aggaccgttt	attgccatta	cgaacgatat	catcggcatg	1380
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<210> 1050

<211> 1104

<212> DNA

<213> B.fragilis

<400> 1050

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cactttgaac	aggcgtagcg	tgaatattgt	ggtgttagtc	atgggtgttg	ttgtgataat	180
ggtactaatg	ctataagttt	ggcattactt	gctgttggtg	tgaagcctgg	tgatgaggta	240
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cctgtttttg	tagatattga	tcctcttact	tatttaattg	atgtgacaaa	ggtggaaagc	360
catattacgg	aaaagacaaa	atgtattctt	ccagttcatc	tttacggaca	gtgtgtcgat	420
atggatgaac	ttatagcttt	ggcctggaaa	tataaattat	ccattattga	agactgtgcg	480
caagctcaag	gtgcagaata	taaagggtat	aaggcagggt	caatgtctaa	tgcttctaca	540
acctcattct	atcctacgaa	aatattaggt	gcttacgggt	atgggtggaat	gattattacc	600
aatgatgcag	aggtggaagg	gaaattgcgt	cgtttgogat	tttatgggtg	agagaagatg	660
tattatgcta	tcgaacatgg	ttataattct	cgtttggtatg	aagttcaagc	tgccatcctt	720
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catgcttatt	atttgtatgt	agttcgtcat	tctaatacgtg	atgaaatcat	ggcagcatta	900
aaagaaaata	atatatttgt	aaatattagt	tatccatggc	ccattcatac	catgacaggt	960
taccagttcc	ttgggtataa	ggaagggtgac	ttccctgaaa	cagaatctgc	tgcaaaagaa	1020
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atattacaca aaatattaaa atag

1104

<210> 1051

<211> 1140

<212> DNA

<213> B.fragilis

<400> 1051

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atctcttcta	ataaggagac	ccatcatttc	ggacaaatcg	aatggaaacg	tccggtttct	180
gtagaatata	ctattaccaa	tacagggtgat	aaaccttttg	tactgactaa	tgttaccact	240
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acagtttagtg	ctacgtttga	tgctaaagcg	ctagggcatt	tcaataagtc	aatcggcatt	360
tacagcaatg	cacagcctag	tttggtttat	ctgaattttg	acggggagggt	ggttcaggaa	420
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gttgctttga	aaaaaaactgt	actgcaaccg	ggtgaaagta	ctcggtgag	ggtgactgtt	1020
ctgaaaaaga	accttggaag	gaaaaagaga	catttacgta	tcctgatgat	caccaatgat	1080
ccggtgcaac	cgaaagtgga	gatcgatgta	aaagctacga	ataacgaatc	acataattaa	1140

<210> 1052

<211> 1209

<212> DNA

<213> B.fragilis

<400> 1052

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cgtgagcaag	actttataaa	agaggctttt	gatacgaact	gggttgctcc	tttgggacct	180
aacgtggatg	cctttgagca	atctttgggt	gaatatttgc	atgaagaccg	ctatgtagt	240
gctttgagt	ccggaacggc	tgcacttcac	ttgggcttga	ttcttctgga	tgtgaagccc	300
ggtgatgaag	tgatctgcc	aagctttact	tttgctgcct	ctgccaatcc	gatttcttat	360
ctggaggcca	aacctgtttt	tgtggacagt	gagaaggata	cctggaatat	ggatccggta	420
ttgctcgagg	aggctataaa	ggaccgttta	cgcaagacgg	gcaggttgcc	gaaagcgatc	480
attcccgttc	acctttacgg	tatgcctgcc	aagatggacg	agatcatgga	tattgcgggt	540
cgttatggta	tctccgtatt	ggaggatgcc	gcgaggcctt	tgggttcgga	actgaacgga	600
cggaagtgtg	gcacattcgg	tgaactggcc	gctctctctt	tcaatggcaa	caagatgatc	660
acgacttccg	ggggagggtc	tctgatctgt	cgtacggaag	aggaggcccg	acagacaaag	720
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aactatcgga	tgagtaatat	ttgtgcgggt	atcggctcgt	ggcagatgtt	tgtcctcgat	840
gaacatatgt	cccgctcgcc	tgccattcac	tctttgtatg	ttgatttgct	gaaagatgtg	900
gcgggtatta	cggtcacgga	gaacctgat	tcgcggtttg	cttccaactt	ttggcttact	960
tgtattctgg	ttgatccgaa	gcttgccgggt	aagagtcgtg	aggatatccg	tttgaggctg	1020
gactccgaga	acatagagac	gcgtcctctg	tggaaagccga	tgcattctca	gcctgtgttc	1080
acggatgctc	cgttctatgg	gaatggtagc	agtgagagggt	tggtcgatat	cggcttgtgt	1140
ctgccttcgg	gacctacatt	gacagatgag	gatatcagga	gagtgggtga	tacgatcaga	1200
gcgatataa						1209

<210> 1053

<211> 840

<212> DNA

<213> B.fragilis

<400> 1053

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tgggaccgtt	tcaatatagt	ctgggacctt	cgtcgggatg	tcaatatact	atccggaatc	120
aatggagttg	gaaaaaccac	tatcctgaat	cgatcggtcg	ggtatctcga	gcaactgtcg	180
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acagcccgtg	tggcagataa	gaatgtaaag	tccgaactcg	actggcaact	ctatctgttg	360
cagcgccgtt	atctggatta	tcaagtcaat	ataggcaata	agatgattga	gctgttgagc	420
agcaataacg	aggaagaacg	tagcaaagca	gccactcttt	ccattgctaa	acgtcgtttt	480
caagacatgg	ttgacgaact	attcagctat	acccgtaaaa	aaatagaccg	tagacgcaat	540
gatattgctt	tctatcagga	tgggtgaact	ctgtttcctt	ataaactttc	ttccggcgaa	600
aagcagatgt	tagttattct	gcttactgta	cttgtacagg	ataatgcca	ttgcgtattg	660
ttcatggacg	agcccgaagc	ttctttgcat	atcgaatggc	agcaaaagct	gatatcgatg	720
atccgtgaac	tgaatccgaa	tgtgcagatt	atactaacga	cacattctcc	tgcagtgatc	780
atggaaggat	ggctcgatgc	tgtgaccgaa	gtaagtgata	ttgcaaccag	ctataagtag	840

<210> 1054

<211> 303

<212> DNA

<213> B.fragilis

<400> 1054

gtatcacatt	ctcaggaaat	aaaaaagaga	gtatcctttt	ctggacaccc	tcttccctac	60
gcatctgctg	cacatacttt	actattgttt	gatttcccat	attatacccg	tttaggtaca	120
aatacaataa	aagactccca	ctttttatacc	cgatatggta	taaaagtggg	agcaagtcag	180
gaatctatac	ccatttgggt	atattgtttac	tcattctatc	tgattacatc	tatgactttc	240
ctgatatttt	cattagaacc	tactttctcc	tatctattac	atttcttttc	tactccttcg	300
taa						303

<210> 1055

<211> 234

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (92)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1055

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gaatatgtat	gggaaaataa	gttgacatc	gngcgtacgg	catggcagta	tgatccgtat	120
acgcacgaat	gggtagacat	gcctttggta	tcgaaaggca	aaaaacaatc	tgaagaactt	180
ccagagcctg	agtatgggtg	caaacaacaa	tgtaagtgtc	tctcagaaag	gtaa	234

<210> 1056

<211> 1560

<212> DNA

<213> B.fragilis

<400> 1056

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gtgacaaaca	acaatgtaag	tgtctctcag	aaaggtaaat	atggaagtgt	acgcacttca	120
ttgacccatg	tgtataataa	aggacagtat	ccgaaccaga	aactgaataa	gatcacttat	180
tgggtgtcgg	gtgatatgaa	gtggaagaaa	ttctcttttg	acggaggatt	gacttataat	240
aagcgctttt	atcccaatga	catgggagcc	ggatacgggtg	gtagcggatt	cctttataac	300
ctgttgggtg	ggtcgggtgc	cgaatatgat	atacgcgact	ataagaacta	ctggatcaag	360

caggacgaac	agcagaactg	gatggatacc	aagtgggtatg	acaaccctta	tttcatagca	420
aatgaaattg	tccggttcgag	tgattacgat	ttgattaacg	gatatctttc	tgccaactat	480
gattttactc	cctggttgaa	cctgtcgtcg	cgttcgggtc	tggttcata	ctcgcagaag	540
aaagagtggc	ggaatgccgt	cagtgcgcgt	ggtggctggc	ataaacaagg	ttattatggg	600
ctgcaacgtt	taggaggata	cagcttaaac	aatgacctga	ttttgtctgc	cgatcacaaa	660
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aatatcctgg	gcgaaacgca	gaatgggttg	aaaattccgg	ggtattattc	attgaagtca	780
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tgggtcttct	cattgcccgt	ggagacacgt	tcttatttct	atccttctgt	agccggtagt	960
gtgggttctt	cacagtccat	cccaatgccc	gaagtgattg	acttctggaa	agtgaggggg	1020
gcatggacgc	agaccaagag	tgacttgagg	gtatacgata	ccaacaatac	ttacagtgtt	1080
tctaccgatt	tgtggaacgg	tgagagcgcc	gcatattatc	cgacatctat	ccgtgggtga	1140
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aatcgccctga	aactggattt	tacatattat	aataaactct	attacaactt	gacccgcagt	1260
gcaggtatca	gtaactcttc	cggattttacg	tctacattga	tcaatatcga	tgaagaatat	1320
gtggggacggg	gagtagagtt	gacttttatcg	ggcgatatta	tcaggacgag	agacctgaaa	1380
tgggagtcgt	ccttcaactg	gtcgcgtgac	cgttggtatt	ataccaaaat	agaccgggtg	1440
tattctacac	aaaaaccttg	ggtagccgtc	gggaaacgtt	gggactggta	cggtattttac	1500
gattgggagc	gtgattcaca	gggaagtctt	caccacgggg	gtggaaggag	caacgtctga	1560

<210> 1057

<211> 825

<212> DNA

<213> B.fragilis

<400> 1057

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agggctgggc	caaatatccc	gttttcaatc	cggcggaccc	cgttcgggca	tccggtatcg	120
gtcggctatt	ccaacatata	ctccttttgc	agggactttg	tcagcacgcc	ccgtttcctg	180
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gccaacgcgt	cggcactgag	cctgcatata	gagagccgc	aggcctattg	ggacgcggca	300
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gaggaattca	aggatgaagc	catggagaag	ttcgcttcag	gagtgaccgg	cagggagaat	420
gtgggcaaat	acatgcacac	gaccagggtc	tgggatgcgg	acgccaatga	cttcaggggc	480
tggacgataa	ccccatcga	caagaaaata	agggattata	tcgaaagcca	gatcaagatc	540
gccaacaagg	ccgatgccgc	ggccacatcc	gggttcggac	tggatccggg	gctctcaaac	600
ctgatcatgg	ataacaagct	gtcctcaggg	tcggaaaaac	tgtactccat	caaggtgtac	660
aatgccagtg	agacggccat	accggacatg	atcctgtgca	aaccgttgat	gcactacata	720
cggggcaatt	atccgggaag	cagaacacag	gtggggcttt	accggagcgt	agtggaatcc	780
gaacagagtg	tatcacccgc	aaacaggatg	aaagaaaata	tataa		825

<210> 1058

<211> 477

<212> DNA

<213> B.fragilis

<400> 1058

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tctgccatct	atccgactca	ggtcggacag	gggaggagcc	ttgtccggga	acaggggtat	180
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agcgtcgggt	tttccggggc	gggggtgggtc	gccacttcca	acatccccct	ctatatccgc	300
ttcctggata	tgaagaaaca	tggaaactat	ggcatctata	accgccaggt	atgggggaatc	360
ctctggaaca	attcgctcca	gaccataaaa	tacggatatg	gcaaggaggt	ccgcgaccgt	420
atttatgccg	gattacagga	agcttttccaa	agaatggaaa	tacgtacgga	ttcctaa	477

<210> 1059

<211> 456

<212> DNA

<213> B.fragilis

<400> 1059

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aggattccgc	aaataaagaa	ggtggtgctt	gtcaccttcg	accccgacat	gggcgctttg	120
gtccaagggc	ttaaagcgga	cgaactaccg	gcgctgctac	tcatacatccc	aagcgccaaa	180
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gacaagaccg	atccgcagcg	taaggggact	tatcagggtg	taaaggagtt	gcagcccgtc	300
atggagaaga	tgaagcgca	gatgatcgat	gacaaggctg	cgggatgtca	cctgctctcc	360
cgtctggacc	tgtcgagctt	atccaccatt	cccgaagcgg	gattttattc	ggctctttgcc	420
ggatggagcc	tgggatttga	atccgaaacg	ccatga			456

<210> 1060

<211> 402

<212> DNA

<213> B.fragilis

<400> 1060

gaagcaatga	agtattttac	aatcaaggaa	ttaagccaca	gcgatacggc	cgtggcgcg	60
gggattgaca	atacccttac	gggggaggtg	gttcacaacc	tgacagagct	ggtggaaaac	120
gtcctcgacc	cgctccgtga	aaagtacggg	aagcccatcc	gggtaagttc	cggttaccgg	180
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gccgcccata	ttaccgtagg	cagcaaggag	ggaaaccgcc	ggcttttcga	gatcatccgc	300
aaggaactgc	ctttcgacca	gctgatcgac	gagaaggatt	tctcctgggt	gcatgtgtca	360
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<210> 1061

<211> 2847

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (2724)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1061

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gatctgatgg	cagcgggtgg	tgcaatcgtg	gacaggcaac	tcgcgcaagc	gggggagaat	300
tacgtgtcgg	ctgcggacaa	ggccgctcaa	aaagcccgcg	agctgcaaaa	caggcagatg	360
gaaatcggaa	ggctcctgct	tcccctgcaa	gaaaaatgga	gcggtctctt	ccagtctctc	420
aagctcgggt	tttcagatgt	ggcgctccgg	gtattggaac	ataaaaaaag	catcattacg	480
cttatctccg	tggttaccgg	ttttattctg	gtttataaaa	cggttattct	tctgcaaaaa	540
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gccatgcaga	gaggaaacat	cctcagaagc	gctgccgcca	tgaaaatgta	taatgcctcg	660
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gaagccacgg	ccgcagtga	ggactacacg	gacaacctgt	tgtccatggc	caggatacgc	1140
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aaggatatcc	atgccaaaccg	gaatctctgg	gacagtttca	aactggggct	cgccaaaggg	1260

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gcccggaaca	aactcaggca	gctggccgac	atccgggcaa	aatgacgga	aagctccgcc	1860
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ttgaattatg	caaacctgca	tattacgcag	cagcagcgcg	acatgttgct	gttgagcctg	2040
gaggagtcca	attcccggga	aagactcggt	atcctgaagg	aataccggaa	ggatgtggaa	2100
gccctggagc	tacagacggg	ggatgtgaaa	atacaggccg	tcaaactctc	cgggcaaaaag	2160
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accatgcttt	cctctttcaa	aaaagagttc	aaccttttca	atctgcggga	tgaaacggac	2280
cttcagctca	agggtgctgga	agcgtcatac	cgggcccggc	tggaaactgat	ccgcaatgcg	2340
ctcaaaaacg	agcttgtcac	aaaggatcag	gccgcccggc	aggaaaagga	gctggaagaa	2400
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ttggagaagt	acgggctgct	cggattccag	caacgctatg	ccatgcagat	ggcgccctc	2520
aagcgggaga	aggaacaggg	gttgataggt	gccgaagcat	atgcaaaggc	cgaaaagatg	2580
ctcaagatac	agttctggaa	agaggctttc	gattattatt	ccaacctgtt	ttcaggggct	2640
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gccgcggcac	agggaaacgc	gcangaagtc	gaacgcctga	aaacggagaa	agcgcagaag	2760
aagctggaga	tcgagaagaa	atacgccgac	gtgcagtttg	ccgtaaaagc	caccagatca	2820
ttgcccgaca	cggcgtggcc	atcatga				2847

<210> 1062

<211> 951

<212> DNA

<213> B.fragilis

<400> 1062

tatacaaaata	tgaaactgat	atttgataaa	gattcaaaacg	gcacgcaggga	actggtcgac	60
gccttggggc	tgatcgatgt	ccgcacggac	ttctccaaat	ggaagccgta	cataccttta	120
agcatacgtc	gcctgaccgc	catcataggg	caggaggttt	atgacaagggt	tctcgacttc	180
taccaatcgg	caagcgtcga	tccggatggc	aagctcaccc	gcctgttggg	aatggtgcag	240
cagtcgctag	cgctgtttac	ctggctgaaa	atcatcccca	cactggatgc	gcagcatggg	300
aacacaggca	ggcagaagcg	cttgggggag	cacgaaaaag	ggctgacagc	cttacaggag	360
tacaaggatg	aagccaacat	cctgagtcag	gcctacgagt	cggtagatgc	cctgatagca	420
tatctggagc	aggaaaagtt	cgattttctg	atacaaagcc	ccaaaaggaa	ggctgtatcg	480
gaattgctcc	tgaatagcaa	ggaggcattt	gatttttact	atgtaaccgg	cagccaccgg	540
ctgtttctga	ccctggcacc	catcatccgg	gaggtgcaac	agaggcatat	catcccgata	600
atcacgtacg	gccgttatga	aaagctggta	gcggggccagc	agggtggcaga	ggggttccga	660
gacgccgtct	gtcggccgct	ggccctgctg	tccatgagca	aggccgtgga	acgtttgcc	720
gtggagggtcc	tgcccagcgg	tgtggtgcag	gtgcagcttg	caggaagcgt	ccgtgaaaag	780
ctcagggcgg	aagccgaagc	gcgcaagaca	gtggcaaaaa	gcctggaaca	agatggcatg	840
cgggatcttg	ccgcgctgga	ggacctggtc	gcggcgctcg	acgccgcacc	ggatgaaccg	900
gatctgtatg	taccctcgat	cacccttcaa	tcaaaaggca	taacattctg	a	951

<210> 1063

<211> 648

<212> DNA

<213> B.fragilis

<400> 1063

aatacggata	tggcaaggag	gtccgcgacc	gtatttatgc	cggattacag	gaagctttcc	60
aaagaatgga	aatacgtacg	gattcctaaa	gacacattgt	ccttttgtcc	gggagacggc	120

cgcctat	ttgtcct	aaataac	atgggaa	tacaacc	ttatatc	180
tgga	tggtca	ggacggg	cagaagg	tgctga	gcgcaac	240
accaaag	tcaaggc	gaacgtg	ctgaaat	ccatgg	tcttgcc	300
caggga	tccagag	ggagtata	gaactga	cgcaact	ggccaac	360
cgtacc	cggaaa	ggagaag	cgctgct	aaagcgt	gaacaac	420
gacaa	atgccc	ctcaaaa	gccagac	ttcgcag	attggac	480
acggta	cgttaca	ccaagag	gcccgtc	aggcgga	ggcaaag	540
aaggagg	tgga	aaggccc	acccgag	gtgaaag	cattttt	600
ccttacc	atgaaat	cggtag	gtttttt	cgttat		648

<210> 1064

<211> 795

<212> DNA

<213> B.fragilis

<400> 1064

attatgg	tcagaag	cggaaat	ggatttat	ataccggg	ggggcag	60
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agctggc	cccgaag	acgggtg	ggtgtga	tcgtgcc	gggtgcc	180
aacgacct	ccggcg	acaacgc	ctggata	tttacgg	tgaggg	240
atgggta	tacaggg	gcagtgg	gagggccc	gcttctt	ggaggcc	300
gactccg	acaaccg	ttaccgc	tgatact	atgacgt	acaggcg	360
ctggagag	gggattac	cgactata	ctccgtg	tggtgg	ggtgcac	420
caagggt	gggtaaa	catccgt	cggggac	gtatcgg	ggatgga	480
ataatcag	tggaacat	cccttac	aaatgcc	tcgaata	cgatgac	540
caagatt	cacagaac	atatgtg	cgactgg	cttcccc	cccgac	600
ctggggc	tatcccg	tcaatcc	ggacccc	ccggcat	gtatcgg	660
gctattc	catatact	ttttgc	actttgt	cacgccc	ttcctgg	720
ctttccc	gctgga	gcgggc	tcgcccc	gctggc	tataatg	780
acgcgtc	actga					795

<210> 1065

<211> 858

<212> DNA

<213> B.fragilis

<400> 1065

accggat	tatgtacc	cgatcac	tcaatca	ggcataa	tctgact	60
aaagaa	cgtaca	tcaaaag	gagattc	actccct	ggagtt	120
cccaagg	attaccg	cctggag	gtatta	tgaacgc	ggagatt	180
cctttcc	tgcgctg	gctgctt	tgcttct	ggatga	cagcctt	240
ctgtgc	gagaaat	ggaagag	ttggcga	tccccgc	ggacggg	300
ttcgata	cctcgc	gggatg	gtttacg	ccgcctg	aactggc	360
aacctg	ccgcct	ggagtgg	ggcccgg	atatgct	ggggatt	420
ttcggac	ttatcga	catgggg	atggcgg	tgga	ccgggag	480
ggaaatg	aagata	ggaactg	tcttct	gcagact	ttataag	540
cagggcc	aggaaac	cactcct	ttcccgt	gcttcc	atacat	600
tttctcg	tctggg	gatttac	gtcccat	caacca	gaaggac	660
gacttct	tcctgtt	gaaatcc	cggggga	cagggga	taccggg	720
gtggga	cgtacg	ggccgc	ggtgttt	gtgattt	acaggta	780
gacaccc	tctggg	gatgct	atttata	gcaggtt	aatgtta	840
aacaata	agcaat					858

<210> 1066

<211> 507

<212> DNA

<213> B.fragilis

<400> 1066

aaaggcgaat	cgaaaacatt	aaaaatagga	aaaaagacta	tggggcaatt	agacaaaacg	60
gatgttga	tacttcaggt	attacagaaa	gatgcgaaag	tgaacactaa	agagctttct	120
gagaagctcc	atatatcaaa	aacgccgata	tatgaacgca	tcaaacgact	cgaaaatgat	180
gggtatataa	aaggatatgt	cgctttggtg	gataataaaa	aagtcggatt	gcctttgatt	240
gttttctgta	atgtctctct	ggcagttcac	gacgacgaac	atataaagcg	ctttcaagag	300
gagatcaagg	agatcgatga	aattatggag	tgtatttcta	cggcggtat	ttatgatttt	360
ttcattaagg	tggctcttgaa	agatctggat	gcctataacc	gattcgtttt	tgagaaactg	420
actaaagttc	acggtatagt	taagatgcag	agttcgtttg	ttcttagtga	gattaaacat	480
acgacagttt	tgaatataga	ccgatga				507

<210> 1067

<211> 648

<212> DNA

<213> B.fragilis

<400> 1067

cagctcttgt	tggcccgtca	ggaagtggaa	aagagtacgg	taatgaaact	ttgtgcccg	60
ttttatgatc	cgacaaaagg	gcgtatactg	tttggtggag	taccggtacg	agagattgaa	120
cctgaaaaat	tgatgagtcg	tatttcgatg	gtttttcagg	atgtttattt	atttcaggat	180
agcatacgca	acaatattcg	gtttggtaaa	agtgatgcc	cagatgaaga	gattgtagca	240
gcggccaaaa	aggcctgttg	tcacgacttt	atcatgcac	tgccacatgg	ttacgataca	300
atggtgggag	agggaggctg	tacgttatca	ggtggtgaaa	aacaacggct	ttccattgag	360
cgtgccatgc	tgaaagacgc	acagatcggt	ctgctggacg	aggcaactgc	ttcgcttgat	420
cccagaaacg	aagtagagat	acagaaggct	atcgatacgt	tgattaaagg	acgaacgggt	480
attgttatcg	cccatcgctc	caagacaata	atgggggccc	accacatcgt	tgtcttatcc	540
gatggaaaag	tgggaagaaca	aggtacgcat	tcggaattga	tgtgccggga	tggtttatat	600
cggaagctct	ggaacattca	agaaagtaca	ttgggatgga	cattatag		648

<210> 1068

<211> 423

<212> DNA

<213> B.fragilis

<400> 1068

attatatacc	caaagggaat	taatatcatg	atacagacaa	tacaagtaca	aggaacagaa	60
aaacgcttat	accaacttat	tgctccattg	gtgatgaatc	cggatgtttt	aagtgcaaat	120
aataattatc	cttttaaaac	gacagaacaa	tacgtgtggt	tcattgctat	cgataaaaaa	180
tcggttggtg	gttttatgcc	ggtggagcat	agaaggagcg	gatgcgtaat	caacaactat	240
tatgtcagcg	gtgataaccg	tgaacactc	tcattattaa	tctccagtgt	tttggagca	300
atcggaagag	aagtacgttt	gtttgccgtt	gttatggtca	accatcaggc	tgtatttgag	360
gaacacgggt	ttataatgga	gaaggcatgg	aaacgttatg	taaaaatgca	aaaagatgaa	420
tga						423

<210> 1069

<211> 1827

<212> DNA

<213> B.fragilis

<400> 1069

ataaatcgg	tgatcatggt	aaataagaag	aaagaagggc	tgtcccgtct	gtttgagatt	60
gcaggacaga	aaaaaagtct	gcttctgttg	gcaggcttgt	tatcggctgg	gagcgcggtg	120
tgtatgctca	tacctatttg	ggcgatctac	cggatactct	atgaattgtt	gaaccatagc	180
cgggagctgt	cgtccatcga	tgagaccaat	atgatccgtt	gggggttggt	agcctttggc	240
gggctgatcg	gcggattatt	gttgctgtat	gcttcctga	tgtcatctca	tgtggcagca	300
taccgtattc	tctacggact	gcgtatccgg	ttgacggaac	atatcgggag	attgccgctg	360
ggttatctga	acggaacatc	aacgggagcc	atcaagaaga	cgatggaaca	gaatgtagaa	420
aagatagaga	acttcatagc	ccacacgatt	ccgattttgg	tgaacgttat	ggcaacagta	480
gtggtgatgt	tcctcatatt	cttttcgctc	gatggatggc	tggcaggtgt	ctgtttggca	540
gtgatcgtac	taagtatatt	cttgcaattt	tccaattttca	tgggaaaaaa	ggcacgggaa	600

tttacacgca	tctattacaa	cgcgcaagag	cagatgagtg	cttctgccgt	gcaatatgtg	660
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gccgaaatcg	aagcttacaa	gacctatgca	ttgaaagt	gcgacactta	cgaatcgggt	780
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ttactaatgc	aaaatgactc	cgggagtctt	acgctggcag	ctgtatggct	tttctttatc	900
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cgggaaatca	atgaaggtgt	atcgcgtatt	gatcgtattc	ttgaaaatca	gccggtctcg	1020
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cggatcatcg	tactgaaaga	tgggaaggca	gtacaatgcg	gacggcatga	agaactttcc	1740
tctcaagaag	gggtatataa	aaagatgtgg	aatgcttata	cgagtgcgtt	ccgctggcaa	1800
ttgaatgtga	aacaagaaaa	agaatag				1827

<210> 1070

<211> 558

<212> DNA

<213> B.fragilis

<400> 1070

aaacatat	caatgagt	aaagaaaagt	ccggtatata	atgtaatagc	agttcccgt	60
gaaaaagt	aggccaac	ttacaatccg	aatgtggtg	ctcctccgga	gatgaggctt	120
cttgaact	ctatctgg	agacggcttc	actatgccct	gcgtctgcta	ttatgataag	180
gaaaaggat	tttatatc	tgtcgcacgt	ttccaccgtt	attctgtgct	gaagacttcg	240
aaacgtat	ttcagagaga	aaacgggatg	ttgcctattg	tggtaatcga	aaaggatcct	300
tccaatcgt	tgagttccac	tatccgccat	aatcgtgccc	ggggtacgca	caatatagaa	360
ctgatgtgc	atattgttgc	cgaacttgat	aaggcaggca	tgtccgatca	atggattatg	420
aagaatatcg	gtatggatcg	ggacgagttg	ttcgcttaa	agcaaatatc	gggtttggcc	480
gatctgtttg	ccaatcgtga	cttcagtgtt	cccgaagatg	accagccggg	aaatgtagat	540
aagaaaccta	ctcgttaa					558

<210> 1071

<211> 1014

<212> DNA

<213> B.fragilis

<400> 1071

agaatgagtg	caataagaaa	tattacaata	ggcgtacgg	aaaggcttta	taaacctgta	60
ggctacacta	tgcttgccaa	tttgggtgaac	attgttcctt	tttgcctttc	tatcgaggcg	120
attcgtatta	tattccgtgc	tttcaacgga	ggcgggcaat	cgttgatac	caccgggttg	180
tgggtatata	ttggctgtat	gacaggttat	atagctgtta	tgggtactggc	ggaaagggct	240
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gcagaacatt	tacgcaaact	ttcgttaggt	tttctgggta	aacgggatcc	gggtgattta	360
tcatecatgc	ttattaccga	ttttacaatg	gcggaaacag	gtatctcgca	ttatttgcct	420
caactgatgg	gagcattggt	gatgcctgta	ctggcctttg	tttcgcttct	ttggatcgat	480
tggcgcgatg	cggctgccat	gttcgtggct	cttcgctttg	caatgggcat	tttgtggttg	540
agcacgagcg	tacaggagag	gctgagtggc	aggcagatca	aagcaaaagt	caatgccgga	600
aaccgcctgg	aagagtacct	gcaaggcatc	cgggtgatga	aagcctacaa	tctgctgggt	660
gatcgttttg	ttcggttgcg	tgatgctttt	gccgaattac	gtcgtgcctg	cattcggttg	720
gaggetctat	tgggaccttt	tgttctattg	gctattacac	tcggtgcgtgc	aggattgaca	780
ttgatggtac	tgtgcggaac	atacctgctt	ttaggtggcc	agttgtcgat	tctcacgttt	840

gtcatgttcc	ttgttgtcgg	ttcccgtgta	ttcgacccgc	tgacttccgc	tcttaccaat	900
tttacagagt	tccgtcattt	ttctatttcg	ggaggacgta	ttctttctct	tatgaacgaa	960
cccgaaatga	aagggacaaa	agaagctccc	gaagacggta	atatcatctt	ttga	1014

<210> 1072

<211> 354

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (280), (285)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1072

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cttacaccgg	tcttgcgata	tacagaagga	gaagaacagc	agctatttagc	tccggtagtg	120
atagccggac	cccgtcgcta	tcgggtgctg	aaacgatctt	tagctttcgg	tactgacaat	180
tttgaaatgt	ttcctatgct	tgtcgagaat	cgaaagagcg	gtactcccca	gactgtgaat	240
attcacttcg	gattacccta	tcatgaatgg	atgcgccggg	catanctgat	tatacgtgaa	300
aggtgcccgg	ttgtgcccga	cgtcttgctc	gtcaggatga	ccataccggt	ataa	354

<210> 1073

<211> 471

<212> DNA

<213> B.fragilis

<400> 1073

atacctttgc	aggtacaaaa	gtatatagaa	tatatggaaa	caaagattct	ttcaaatgcc	60
acacacaaat	gtgttttagt	gatcgataac	gctcaaccta	cgggcatagt	agccaatatt	120
gccagtgtct	tatccatgac	gctaggggtg	agagtcagca	acattgtgag	tcatgatgta	180
tatgataaac	aaggtgaaa	gcatttgggc	ataacacaa	tgccgattcc	tatacttggg	240
gcttcacagg	agaagataaa	agagctccgg	aactattttc	actctttaga	aattgaagat	300
ctgggtactg	ttgacttttc	cactattgcc	caacaatcca	gaacttatga	tgaatatgaa	360
cgtgaaatgt	atagtgccaa	tgaagatgat	ctgcactatg	taggtatcgg	tatttgtgca	420
gagaagaaa	ctataaataa	agcaaccggc	agcctgagtc	tgatcagata	a	471

<210> 1074

<211> 183

<212> DNA

<213> B.fragilis

<400> 1074

ttgataaggc	agctatactt	gccgttattg	gcgaacatac	ggatttcgcc	acacgtaaaa	60
aatcggttgc	aggcggttga	tgtaggaact	acctacagga	tgttactgag	ggactattat	120
ccgcctacac	gtagtaatgt	atataccatt	tttaatgtgg	cgagagcttt	caatgtagtc	180
tag						183

<210> 1075

<211> 1305

<212> DNA

<213> B.fragilis

<400> 1075

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cgtatcgtct	tcaatgagtt	cgataatgtc	tatctttcct	tttcgggagg	aaaagatagc	120
ggagtgtctg	tgagcttatg	tattgattat	attcgccgga	ataacctgaa	gataaaactc	180
ggggttttcc	atatggatta	tgagatacaa	tataagatga	cgattgacta	tatagcccg	240
atgttggaag	acaataagga	tattcttgaa	gtataccggg	tttgtgtacc	tttcagggtg	300

gctacctgta	cttccatgta	ccagtccttc	tggcgctccgt	gggaagatag	taaaaaagac	360
ctctgggtgc	gtccgttacc	tgagaacgcc	atgactaaag	aagactttcc	tttttataat	420
acacaaatgt	gggattatga	gttccaaatg	cgttttgcca	gttggcttca	tgagaaaaag	480
gatgccgtgc	gcacctgctg	tctgatcggt	attcgtagcg	aggaaagttt	caatcgttgg	540
cgctgtatth	acctcaatcg	caagtaccag	atgtatcatc	gttatcggtg	gacttcgaag	600
gtaggaaacg	atatctttta	tgcatacct	atatacgact	ggaaaactac	ggatgtatgg	660
actgctaacg	gaaagtttaa	gtgggattac	aataaactat	acgactatta	ctattgggcg	720
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cgtgcccga	acggatatct	ccggaagtta	caggtcagtg	tacaattctg	gcgtaataag	1020
ggagggtgtc	tgagcgacga	aactattcgt	aggctgaatg	aagccaaggt	acctattatt	1080
gtaatggaca	actccaatta	taaaacgacc	aagaagccgg	tccgcatgga	atatcaggat	1140
gatattgata	ttccggagtt	cagggaaatc	cccacctaca	agcgcagtgt	catctgtatt	1200
ctgaaaaatg	atcatgcttg	caagtatatg	ggattctctc	cgacaaaaga	ggaaatgagt	1260
aaacgaaatc	aagtaatcga	acaatataaa	aacatattgc	aatga		1305

<210> 1076

<211> 291

<212> DNA

<213> B.fragilis

<400> 1076

agcggaatca	ataatgtttc	cgccacgatg	ttttcaaatt	catgtttttg	tttcattcta	60
tacttttatg	atgttagtgt	cagagtagcg	ctgaaaaatg	aacggtatcc	aaaatcgttc	120
acaaaaaaag	aagagaacct	tcgtaaagat	tctcttctca	attttaatcc	ggtaaacggc	180
gattttatatt	tttgtcttct	attgctcata	ctctcagcaa	agccctccaa	ccttgaattt	240
caaacaatat	atactcatgc	acgatatact	ccatttcctt	gctatcgata	g	291

<210> 1077

<211> 327

<212> DNA

<213> B.fragilis

<400> 1077

aacatggaaa	aaatagagat	tgtattacgc	cggaacaaa	ataacagaaa	tggcatttat	60
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cttcatccgg	aagtcgaagt	cagaaaaatg	attggagtgc	aacccgatga	aaactatgct	180
atagcccgcg	tcaataaaaa	aattataaaa	aaattagaaa	ggaagtatca	gacatccatg	240
atggatgact	ccataaaaa	actacttccg	ccgttcaacg	aagatgaaaa	tatcttccctg	300
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<210> 1078

<211> 924

<212> DNA

<213> B.fragilis

<400> 1078

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acccatagcc	tggcacgtgt	cctgaaagag	ggaaccacag	gagtggagca	gttttatgcc	180
ggaatgggaa	tgggggcttt	cggattattc	atggtgattg	cgggagtgtt	tgtgaaagg	240
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gttatgggtga	tgatactcta	tctgttctgt	actcggaacg	gatgcaactt	cttgaactgg	480
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ctgatgtttt	gttatgatga	acggttcttt	ggcgatcacc	atccggtgac	actgttggtg	660
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gtgtttgatc	gtattcattt	gttccccggt	ctgtgggaaa	atccgggtgg	acataagcag	840
gaattgcttc	ttatagcggc	ttctatcatt	tttacagggt	ggtggcttgg	atataataac	900
ctattagt	ttaaagaataa	atga				924

<210> 1079

<211> 954

<212> DNA

<213> B.fragilis

<400> 1079

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gccgacgatg	acattggatt	tgggatctat	acggatattg	cagatcttcc	tatgaccggt	180
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gtagtttttg	atgttccatt	ccaaatcgta	ccgaatgtgg	tcattaccct	gatgccgtgg	300
caactcgttt	ttatcaaaga	gattagttag	gatttcagga	tcactttttt	caaaatttcc	360
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atcatgcaac	tgttaagggt	ttacttctgg	gatgtctata	ctgtgtatat	caatgatcct	600
caggctgaga	agagtctgaa	gtttacacgt	aaagacgaat	atgtctatca	atttgtacgt	660
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atttctccca	aaaggctcac	aaatcttata	cggagtatac	gtggtcaatc	agcgctgaa	780
tggattgttt	attataccat	tcttgagatc	aagtcattgt	tacgggagtc	atccctggac	840
attaagtcga	ttgccgccag	ggttaatttt	cccgatcaaa	cgacattgag	taggtatttt	900
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<210> 1080

<211> 645

<212> DNA

<213> B.fragilis

<400> 1080

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atgcgcgaaa	tagccgatgc	tgtagatgta	ggcgtaggaa	atctctataa	ctattttgag	180
aataaagatg	agttgttttt	tgtgatactt	cgtcctgtat	cggatgcttt	ggagcgaatg	240
ctgcaggaac	atcatggagc	caaaggagca	gatattatgc	ttatatgttc	cgaagagtat	300
ctcaagtctg	ctgtcgatga	atataatcc	ttgataaaca	agcatggtga	gctgatgaag	360
attctattgt	tccattcaca	aggctcttca	ttggaaacat	tcaggaaga	ctatacaaac	420
cgttcgacgg	agatgggtta	aacatgggtt	gccgaaatga	aagagaagca	tccggaaatc	480
aatgtgggtg	tatcggattt	tatgatccat	ctgcaagcag	tctggatgtt	cacccttttt	540
gaagaaatgt	tgaagcatgc	tatcgatagc	aaggaaatgg	agtatatcgt	gcatgagtat	600
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<210> 1081

<211> 867

<212> DNA

<213> B.fragilis

<400> 1081

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aagatagata	accatcacca	ctcgtgtatc	ttatttcttt	taaaagggga	aatactgaca	180
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aacgatacta	atcaaagcaa	aagcatgaca	gaaacagaat	ttatactact	gttcttcgac	300

aatcaagtca	atcttcacag	taaaatgtcg	attgaattgt	ctgccattca	tcttgagtct	360
gaaaagagtt	gtttttattc	cttatctatc	tgtcctccgc	tacgacatgt	gttggacagt	420
atttgcttct	atctcaaaca	gaaagttcag	tgtagtcata	tgcatagaact	gaaacagaaa	480
gagatattca	tggatttcgg	tacattctac	aatcgaacag	atatggccca	cttcctgatg	540
cccatcacag	ggcgagatcc	gaatttcaaa	agtttcgtat	tggaaaacta	cctgcagata	600
cgaacatca	aacagtttgc	acaattatat	cattgttccg	aacgttcttt	caatcgtaaa	660
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attaaagggc	aattagccaa	tcgtaatat	ccgatcagtg	aaatagccag	aacctttcat	780
tttgcttcac	cttcacattt	cactacttac	tgtaaaaaaa	gacttggaat	cactccgagc	840
gaattcagag	aaaaaattgc	aaaataa				867

<210> 1082

<211> 603

<212> DNA

<213> B.fragilis

<400> 1082

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ccgttgaagc	agcgtagcga	gacacataca	gcctatctga	atcttgagggt	ggacaaatat	180
gtaatgtcgc	gcaattataa	gaataatgcc	aacgtgcttg	ctgatgtcga	ccgattgtc	240
aatgagatac	aaaacgattc	caacctgacc	gtaacggaat	ttcgggtgac	aggctatgca	300
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gctatacttg	ccgttattgg	cgaacatacg	gatttcgccca	cacgtaaaaa	atcggttgca	540
ggcgttgaat	gtaggaacta	cctacaggat	gttactgagg	gactattatc	cgctacacg	600
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<210> 1083

<211> 594

<212> DNA

<213> B.fragilis

<400> 1083

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tgggtatacg	ataagtatcg	ttgtgtgaat	tgcagtccta	aaataaagag	tgggcataaa	540
aactatgtcg	gtcctaccaa	agcggctggt	tcattggtct	actttattcg	ctaa	594

<210> 1084

<211> 360

<212> DNA

<213> B.fragilis

<400> 1084

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gtagcattgg	taatgggatt	aggtagttct	gtagcatttg	cacaggaagt	tgaaaactct	120
acggcagtag	aaacgcaggc	acaagctcca	caagatgagt	ttacgaaaat	tgatgccccaa	180
aaacttccgg	atgcagttat	gaatgccttg	gctaaatctt	atgaagggtgc	ctcaatcaaa	240
gaagtttatt	cggtgacaa	agagaccggg	aagatttata	aggtgattct	tacaacccaaa	300
gattctcagg	aagttaccgt	acttctggac	gaaaaggggc	aagagataaa	agaggcataa	360

<210> 1085
 <211> 828
 <212> DNA
 <213> B.fragilis

<400> 1085
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 gctgagcaac tggttgagaa catcgaatat gattattcca ggttcgatgg ggccaagttg 180
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 cgtgtcggaa atgacggaaa ggctgtattt tatgagttgg atctaccgga ggttattgct 360
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 atgaaatttt tccgttcccg ttggggattt tttttcgggc agatattggg caggatgacg 780
 aagttgtgct acaagttcag ttccatgctc gggataaaaa taggataa 828

<210> 1086
 <211> 186
 <212> DNA
 <213> B.fragilis

<400> 1086
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 cggcacagtc cggatgtgaa gtttgcattt cacttcattc atataaatta caataaccata 180
 ctataa 186

<210> 1087
 <211> 717
 <212> DNA
 <213> B.fragilis

<400> 1087
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 aatcgtttcg gtacacaacc tgaactggat ccggtgacgg gagaaatcgt gaccgcctct 180
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 ttcttttatc ttgtcaagca attacgcatt gcctcgtggg gagcgaatat acgtatggct 540
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<210> 1088
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 <212> DNA
 <213> B.fragilis

<400> 1088
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<210> 1089

<211> 1455

<212> DNA

<213> B.fragilis

<400> 1089

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<210> 1090

<211> 3270

<213> B.fragilis

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 <212> DNA
 <213> B.fragilis

<400> 1091

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 <212> DNA
 <213> B.fragilis

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<210> 1093

<211> 1632

<212> DNA

<213> B.fragilis

<400> 1093

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<210> 1094

<211> 216

<212> DNA

<213> B.fragilis

<400> 1094

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<211> 1332

<212> DNA

<213> B.fragilis

<400> 1095

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 <212> DNA
 <213> B.fragilis

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<211> 990

<212> DNA

<213> B.fragilis

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<210> 1099

<211> 747

<212> DNA

<213> B.fragilis

<400> 1099

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gtgggagacg	tcaagttaga	gcagtgtctg	gatccggcaa	agttcgcgga	atggatagat	720
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<210> 1100

<211> 429

<212> DNA

<213> B.fragilis

<400> 1100

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<210> 1101

<211> 222

<212> DNA

<213> B.fragilis

<400> 1101

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tacaagaata	tgtttgacta	ccgtcaaaaat	gacagtttcc	ccacttatca	taaaccttgt	180
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<210> 1102

<211> 1146

<212> DNA

<213> B.fragilis

<400> 1102

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<211> 765

<212> DNA

<213> B.fragilis

<400> 1103

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<210> 1104

<211> 843

<212> DNA

<213> B.fragilis

<400> 1104

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 <212> DNA
 <213> B.fragilis

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 gtcgaagctt tggcaagtgg agaagagcct tcacagattc attgttattg gcgaggtctc 180
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<210> 1107
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 <212> DNA
 <213> B.fragilis

<400> 1107
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 ggagaagtga aaacagggtgc ttatgttgat ttgcaactga ttgcacgtga agtgatccaa 240
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<210> 1108

<211> 1320

<212> DNA

<213> B.fragilis

<400> 1108

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<210> 1109

<211> 897

<212> DNA

<213> B.fragilis

<400> 1109

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<210> 1110

<211> 183

<212> DNA

<213> B.fragilis

<400> 1110

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<210> 1111

<211> 270

<212> DNA

<213> B.fragilis

<400> 1111

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<210> 1112

<211> 2031

<212> DNA

<213> B.fragilis

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<210> 1113
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 <213> B.fragilis

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 aagatcgat ttaatgacat cagccgggag ctggttgata aaggcttggc cgcatacaaa 180
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<210> 1114
 <211> 807
 <212> DNA
 <213> B.fragilis

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<210> 1115
 <211> 246
 <212> DNA
 <213> B.fragilis

<400> 1115
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 ttaatctgtc atctgaatca ccagcccttc gacgatttgc gcatactgta tgccgtactg 180
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<210> 1116
 <211> 258
 <212> DNA
 <213> B.fragilis

<400> 1116
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 aatgtagagg cgtagctgg ttctgagatt aatgatgagg attgtgtcag tgcattctaat 180
 cgttattgct ctgttttgat agtgacccca aatgggaatt atctagaaac ttattttgac 240
 caaaaaacaa agtactga 258

<210> 1117

<211> 1584
 <212> DNA
 <213> B.fragilis

<400> 1117
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 <212> DNA
 <213> B.fragilis

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<210> 1119
 <211> 2079
 <212> DNA
 <213> B.fragilis

<400> 1119
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<210> 1120

<211> 240

<212> DNA

<213> B.fragilis

<400> 1120

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<210> 1121

<211> 204

<212> DNA

<213> B.fragilis

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<210> 1122

<211> 1065

<212> DNA

<213> B.fragilis

<400> 1122

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aggattaata aagacgaagt aattgctaga ggtgcatttc cttttgaaat gattgattca 180

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<211> 1074

<212> DNA

<213> B.fragilis

<400> 1123

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<210> 1124

<211> 852

<212> DNA

<213> B.fragilis

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<210> 1127
 <211> 606
 <212> DNA
 <213> B.fragilis

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g g a g c t c t t g	a c t c a c a g a a	t c a t a t t a t a	c c t a a t g t g g	c a g a g c t t c c	t t t c g a t g c g	660
g g t g a g g t g t	c c g g t t t a g a	g a a g g g t a t c	g t t t t c g g a g	g t a t a t t g a a	g g c a a a t a g t	720
a a a c a a t c c a	a a t t t g t g c t	t t c a a t a c g t	g c t t c t g a t a	t t t t c g a a a t	t t a t c g t g t t	780
t c t g a c g a t g	g a a t a a a t c g	t g t c t a t g t g	a g t c c t t t t a	a g c a t a t t c c	g a a a a c c t g g	840
a a g a a g g g a g	g c g g t t a t g c	a a t t g a t t a t	a a c c a a a g t a	t t g g a g g a a t	a a a a a t a t a	900
g c a g t c t c g g	a t g a c t t g a t	t t g t t t t t c a	c t c t t t t t a c	a a a a t t a c a a	t g a g g c t g c a	960
a a a c a g a c t	t t g c g t c t a a	t g a a c t g t t c	t g t t t t g a t t	g g g a t g g g a a	t a a a g t g a a a	1020
a a a t a t g t g t	t a c c t t t t t c c	t a t a g g t a a t	t t c t g t a t t g	a t g g a a c t c a	t a t c t a t g g a	1080
g t t c g g a a c t	t t g a a g a t a a	a a t t a t c a t t	t a t c g t t t t a	a c a t g t a a		1128

<210> 1129

<211> 3297

<212> DNA

<213> B.fragilis

<400> 1129

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a c c a c g c t t a	c c g g c a a t g c	c a c a t c a c c g	c t a t g g a t g c	g c g a t g t a c a	g a t t t c g c c g	120
g a c g g a a c a g	a a a t a g c g t t	t t g c t a c a a a	g g a g a c a t t t	a t a a g g t a t c	t g c g g g a g g a	180
g g a a c a g c c a	t c c a g c t c a c	a a c a c a g c c t	t c g t a t g a a t	g t a c c c c c a t	t t g g t c a c c c	240
g a c a g t a a a c	a a a t a g c t t t	t g c c a g t g a t	c g t a a t g g c a	a c t t t g a t a t	t t t t g t a a t g	300
c c t g c g a c a g	g a g g t a c a g c	a c a a a g a c t g	a c t a c c c a t t	c t t c a t c c g a	a c t g c c t t c g	360
g c t t t t a c a c	c g g a t g g a a a	a t a c a t t c t c	t t t t c a g c a t	c c a t c c a g g a	t c c g t c a c a a	420
a g t g c t t t g t	t c c c g a c a a c	a g c c a t g a c a	g a a c t a t a c a	a g g t t c c c g t	g a a c g g a g g a	480
c g t a c g g a g c	a g g t a c t g g g	t a c t c c g g c c	g a a g c c a t t t	g t t a t g c g c c	a t c a g g a g a g	540
t t c t t t c t c t	a t c a g g a t c g	t a a a g g t t t t	g a a g a t g a a t	g g c g g a a a c a	c c a c a c t t c g	600
t c c a t c a c c c	g c g a c a t t t g	g c t g t a c g a c	a c t a a a a c a g	g a a a a c a t a c	c a a c c t g a c c	660
a a t c a t g c c g	g a g a a g a c c g	c a a t c c c g t a	c t t t c a c c g g	a c g g a a a a a g	c g t a t a t c t t	720
t t a a g c g a a c	g g a a a g g t c	a t t t a a t g t t	t a t a g t t t t c	c a t t g g a c a a	c g c a c a a g a c	780
c t g a a a g c a g	t a a c a t c g t t	c a a a a c a c a c	c c g g t a c g t t	t c c t g t c a a t	g a g t c a c g g c	840
g g a a c g c t a t	g c t a t g c a t a	c g a c g g a g a a	a t a t a t a c c c	a a a a g g a t a a	t g c c a c t c c a	900
c a g a a a a t a a	a c a t a g a t a t	t g t c c g t g a t	g a t c a g g a c a	a a a t a g c a g a	c c t g a c t t t t	960
a c a a a c g g g g	c a a c a t c a g g	g a c t g t a t c a	c c g g a t g g g a	a g c a a a t t g c	a t t t a t c g t a	1020
c g g g g a g a a g	t a t t t g t a a c	c t c a a c t g a t	t a t g c a a c t a	c a a a g c a a a t	c a c c c a t a c a	1080
c c c g c a c g c g	a a g c c g g g t t	a a c a t t t g c t	c c g g a c a a t c	g t a c a c t g g c	t t a c g c a a g t	1140
g a g c g t a a c g	g c a a c t g g c a	a c t t t t t c t t	g c t a a a a t a g	c c c g t a a g g a	a g a a g c t a a t	1200
t t c c c c a a t g	c c a c c a t c a t	c g a a g a a g a g	g t g c t g t t a c	c a t c c g c a a c	c g t g g a a c g g	1260
g c c t a t c c g c	a g t t c t c a c c	g g a c g g t a a a	g a g c t g g c a t	t t a t a g a g g a	g c g t a a c c g t	1320
t t g a t g g t a a	t c a a t t t g g a	t a c g a a a a a a	g t t c g t c a g a	t c a c c g a t g g	t t c c a c c t g g	1380
t t c a g c a c a g	a t g g a a a c t g	c g a c t a t c a a	t g g t c a c c t g	a c g g c a a a t g	g t t c a c c c t c	1440
g a a t t t a t c g	g c a a c c g g c a	c g a t c c t t a c	t c g g a t a t a g	g a t t g g t a a g	t g c a a a g g g t	1500
g a c a g t c c g a	t t a c c a a c c t	g a c c a a c a g c	g g t t a c a t g a	g c g g a t c t c c	c c g t t g g g t a	1560
c t g g a c g g c a	a t g c c a t t t t	g t t c a c a a c c	g a a c g a t a t g	g t a t g c g t g c	a c a t g c t t c c	1620
t g g g g t t c a c	a g a a t g a t g c	c a t g c t g g t a	t t t c t c a a t c	a a g a t g c t t t	c g a c a a g t t c	1680
c g c c t g a g c a	a a g a a g a t t a	t g a a t t g c a a	a a a g a a c t g g	a a a a g g a a c a	a c a g a a a g a c	1740
a a a g a a a a a g	c c t c a a t t g a	c c c g a a a a a a	g a t a a g a a g a	a g g a t c c c c a	a a c a g a t a c t	1800
g a g a a g a a a g	a t g a g a t c a a	a a a t a t c c t a	g t a g a a c t g a	a t g g c c t t g a	g g a t c g c a t c	1860
a t a c g c c t c a	c t c c c a a c t c	t t c g a a c c t g	g g c a g t a c t a	t t a t c t c a a a	a g a c g g c g a a	1920
a c t c t c t a c t	a t c t g t c a g c	a t t c g a g g g c	g g a t t t g a t c	t a t g g a a a a t	g g a t c t c c g t	1980
a a a a a g a g a	c c a a a c t g c t	t c a t a a a a t g	a a t g c c g g a t	g g g c t t c t a t	g g a t a t g g a c	2040
a a a g a t g g a a	a a t c c c t g t t	t g t c c t g g g a	g g t a a t g c c a	t g c a a a a g a t	g g a c c t c a g c	2100

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cccgtcatag	gctatcgact	tccggatggg	agctatctgg	aaaacacaca	gttgggaaccg	3180
gatattaaag	tagccaactc	accggaaaca	atcgtcaaag	gggaagatac	acaattgaaa	3240
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<210> 1130

<211> 1773

<212> DNA

<213> B.fragilis

<400> 1130

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attgaaatga	atgaaagttt	cgcgagtcag	tttcaaaccg	ccaccattat	tccaatgttc	180
ttatggcaac	cgtcatggtc	ttatcctatt	gagggcctgg	caatagggtt	acttatctcc	240
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tacaccaaaa	taaaagaaat	tacagacaag	acacctacag	aatacatgca	ttattttcaa	1620
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tttctaggct	tttgtaatgc	caaatatattc	ggaaaacgat	ttaagaaatt	ctataaagtt	1740
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<210> 1131

<211> 1131
 <212> DNA
 <213> B.fragilis

<400> 1131
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 gttccaacag aagaattatt ttctaaaata tctgtcattc cattggaaac caatgatagt 180
 tcctttcttg taaggcctgt gaaagttatt ataaaagata acagatatta tattgtcgat 240
 gaaggggttc cggctgtgtt ttcttttgat gaagaagggc atcttttgca taaaataggt 300
 aaaaaggggac aagggtcccg agagtatcgt gaaatatacg atgccgttat taaagaaaaa 360
 gaaaatacag tgtatatgct gtctccattt ggctctcttt atgtgtattc tctggatgga 420
 aaattcataa aagaaataaa actgccaaact aggtcgaatt atcaattgat agaggagctg 480
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 gttatttcta aagagtcctt caataatgtg aaagaatttt ggcatgtccc tcccgttctc 600
 actactctga attctaaacc tttttataat tatgaacata aagtataatt ttcgatcct 660
 tatcaaaatg aagtatatga agtaaggaca gatagcttac gggttgcata ccgttgggat 720
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 aatgaagact ttccaaacta tgaaaaagtg cttccttcgg aggaatataa gaagctggaa 1080
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<210> 1132
 <211> 1068
 <212> DNA
 <213> B.fragilis

<400> 1132
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 tcgcttaaga gtgataagga agtttagttta aacaaggaaac tattagctcc ctatctgatg 180
 tgttcttatg attccactct gtgtctaata gattggactg ccaatccgat ggtgcatggt 240
 tataacatga atacagggaag agagatgggt gcttttggga ataaaggcat gggaccggat 300
 gattttctat ctatatccca aatgtatgta gatatgggca agcgttcttt ggtactgtat 360
 gatcagtctt tgcaaaactat aagttctttt caaattgata gtttagctca aggcagtctt 420
 tcaaagatag atttgttttc agctcctaag ttaggaatga atagggtata tgcttattcg 480
 gattccatat ttacggaag tgggactttt gaaagtggct tgatagcgaa atgcaatcag 540
 aaagagattt taaatcaata tctccctttt ccacacacag agcaagcggg aaatcgggat 600
 gtaaactatt tgttgtttca gggggatctt attatgaagc cggataaaaa acgttttgct 660
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 gtgtcttctg ttaatgtctc taccgattct cctaaaggat ttcttcgttg ggtagccact 840
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 gaaatttatg tttttgattg ggaaggacgt gctgtaaaga aagtgatact ggatagatgg 960
 ggtgtatgca tctcgttgga tagtaatgat gaacgactct gcctgatgac aaaggaaacg 1020
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<210> 1133
 <211> 1080
 <212> DNA
 <213> B.fragilis

<400> 1133
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 atatcgcgag aactggttgt tttaaatgat acgtttttat tttcgtatcc tttgcaaata 180

gaatgtatag	actcaatgct	actggtattg	gataatgtta	ataataatTT	cttccatcta	240
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attggttttg	aggacatata	tgtaaccaat	aatagtatat	atacattatt	acatagtata	900
gggagtgaag	ctttaccttc	ggaaattact	gtatttgatt	gggcgggaat	tccaataact	960
aaaattaaaa	caggggtgctc	cctctcta	attgccgtcg	atgggaagga	taacacaatc	1020
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<210> 1134

<211> 246

<212> DNA

<213> B.fragilis

<400> 1134

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gtagaggcgc	ttgccggcag	tgaacacgtt	accaatttag	gttgcttggtg	tgacggatct	180
gtagattgtc	ctattaacca	tatcaaagta	gaacatgtgg	ttcaaggatt	tagtcttggg	240
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<210> 1135

<211> 252

<212> DNA

<213> B.fragilis

<400> 1135

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caaaactgtg	aggcgcttgc	cggtagtgaa	cacgttacca	atttaggttg	cttggggtgac	180
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<210> 1136

<211> 1230

<212> DNA

<213> B.fragilis

<400> 1136

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cagaggaaca	tggaaagcaat	gtatgccgaa	accgagtatc	ttctgaagga	agttttgaat	180
gaggaactac	acagaaagca	gcaagaattg	aatctatttt	atatctccaa	agtaacaatc	240
gatactattc	cttttaaagat	tcgtgttaca	acaagtaagg	gagtcaagac	ttttactggt	300
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<210> 1137

<211> 1131

<212> DNA

<213> B.fragilis

<400> 1137

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<210> 1138

<211> 198

<212> DNA

<213> B.fragilis

<400> 1138

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gtaaaaaaag	taaatgctac	atttactcat	tccaattatt	ttttcgctat	cttcgtgcgc	180
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<210> 1139

<211> 465

<212> DNA

<213> B.fragilis

<400> 1139

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465

<210> 1140

<211> 936

<212> DNA

<213> B.fragilis

<400> 1140

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<210> 1141

<211> 234

<212> DNA

<213> B.fragilis

<400> 1141

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cgatacattt	tgaacatcac	tttcggcaga	cacccctcgc	gctctacggg	catacctgac	180
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<210> 1142

<211> 333

<212> DNA

<213> B.fragilis

<400> 1142

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aatggaattg	tagatgaagc	tgttctggaa	aagctgaaac	tcaatatacg	ttctctgatc	180
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aacaatatga	aagcattcgg	gttgacagca	ctcatcaagc	tctatctcac	ttggttgcca	300
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<210> 1143

<211> 453

<212> DNA

<213> B.fragilis

<400> 1143

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gatccgattt	caaagtcggg	aggaattgag	caagatatct	cacctcccca	tattccaccg	180
cctccgttgc	cgagtcagat	atttcttcat	gtcggtgaaa	tttccgaaac	tccatatccc	240

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caagtggata	tgaaatggta	caatccgctc	aatccggggcc	agcctccatt	aggaagacaa	420
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<210> 1144

<211> 450

<212> DNA

<213> B.fragilis

<400> 1144

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<210> 1145

<211> 2241

<212> DNA

<213> B.fragilis

<400> 1145

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<210> 1146

<211> 3072

<212> DNA

<213> B.fragilis

<400> 1146

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1146
 3072
 DNA
 B.fragilis

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<210> 1147

<211> 3075

<212> DNA

<213> B.fragilis

<400> 1147

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<210> 1148

<211> 777

<212> DNA

<213> B.fragilis

<400> 1148

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<210> 1149

<211> 339

<212> DNA

<213> B.fragilis

<400> 1149

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<210> 1150

<211> 378

<212> DNA

<213> B.fragilis

<400> 1150

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<210> 1151

<211> 1230

<212> DNA

<213> B.fragilis

<400> 1151

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<210> 1152

<211> 2946

<212> DNA

<213> B.fragilis

<400> 1152

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<211> 342

<212> DNA

<213> B.fragilis

<400> 1153

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<210> 1154

<211> 1179

<212> DNA

<213> B.fragilis

<400> 1154

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<210> 1155
 <211> 591
 <212> DNA
 <213> B.fragilis

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<210> 1156
 <211> 1383
 <212> DNA
 <213> B.fragilis

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<210> 1157
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 <212> DNA
 <213> B.fragilis

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<210> 1158

<211> 486

<212> DNA

<213> B.fragilis

<400> 1158

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<210> 1159

<211> 792

<212> DNA

<213> B.fragilis

<400> 1159

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<210> 1160

<211> 2070

<212> DNA

<213> B.fragilis

<400> 1160

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<210> 1161

<211> 615

<212> DNA

<213> B.fragilis

<400> 1161

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<210> 1162

<211> 198

<212> DNA

<213> B.fragilis

<400> 1162

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gggcaaccga	ataagaagaa	gaataagagg	atggcagaca	ttgtggcagt	taatgttaaa	180
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<210> 1163
 <211> 1929
 <212> DNA
 <213> B.fragilis

<400> 1163

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<210> 1164
 <211> 677
 <212> DNA
 <213> B.fragilis

<400> 1164

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<210> 1165
 <211> 408
 <212> DNA
 <213> B.fragilis

<400> 1165
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<210> 1166
 <211> 792
 <212> DNA
 <213> B.fragilis

<400> 1166
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 ttggaacttc accggaaaga aatccgcata cccgatttat cactcctgac agaatggaac 780
 gagaaacgat aa 792

<210> 1167
 <211> 1254
 <212> DNA
 <213> B.fragilis

<400> 1167
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 aagtatgacg cagtatcgga acgttgggga cggagcgacc tgcttccgat gtgggtggcc 180
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<210> 1168

<211> 2589

<212> DNA

<213> B.fragilis

<400> 1168

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<210> 1169

<211> 1107

<212> DNA

<213> B.fragilis

<400> 1169

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gataagaagc	ggctgaccgg	taggaagtgt	tcaggaaaaa	tttattttatc	cgataatata	1020
gataatgtat	tgacaactat	atcattgctg	tattctactg	attacaggaa	agaagaacgg	1080
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<210> 1170

<211> 942

<212> DNA

<213> B.fragilis

<400> 1170

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cgagacggaa	cgaagggtat	gggaggctgt	acgtactgta	ataaccaaac	attcaatccc	180
gagtattgta	aaacggagaa	atccgtcacc	cggcaacttg	aggaaggaaa	gcaattcttt	240
gcccataaat	atccggatat	gaaatatctg	gcttattttc	aggcttatac	caataacctat	300
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<210> 1171

<211> 879

<212> DNA

<213> B.fragilis

<400> 1171

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gaagtactga	ttccccgattt	ccaaggacgc	aaagagctta	ttgaccaagt	gataaaagcc	480
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accacaaaac	acttcccggg	tgcagcatac	attactccgg	aacagtttgc	tgtttataaa	780
gaaacaggac	tgaagaaagg	gttcgaacaa	gtggaaagcg	caccattagt	acgctcctcg	840
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<210> 1172

<211> 450

<212> DNA

<213> B.fragilis

<400> 1172

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ttaccgtcgg	aggacggcaa	gatgccggac	tggaaatttt	cttttagtct	gaaacgtata	180
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tgcgatatcg	acaacgagat	tcatgaggaa	atcagtattt	gtgttacgga	agaacccatt	300
caaaaggtaa	tggaaaagg	tttgaaagga	tcgggacttg	tttatcagag	actcgacagg	360
caaattgttg	tttatcgttt	gctgggacac	aatgcctgta	gagtagattc	tgtgagagtg	420
atgactaata	tggaacagaa	tgatcgatag				450

<210> 1173

<211> 1095

<212> DNA

<213> B.fragilis

<400> 1173

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agtctgcttt	tcgcagactg	ccgggtgggg	aaagcggaac	ctgtggcgga	ccctatggaa	180
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ttctattcgg	atacaacctt	ggtccgtctt	atagaagatg	tggaggccaa	ataccggaa	420
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tcgatggtag	gtacctggat	cggtagcaaa	atcatcactt	cgtatatgaa	acatcataag	1020
aaaacaactt	tacggcaatt	gcttgaaatg	agcgactatg	aacgtatgtt	cacggaatcg	1080
cgttttaatc	cgtaa					1095

<210> 1174

<211> 258

<212> DNA

<213> B.fragilis

<400> 1174

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ttccattgct	ttctcaacct	ttttagcagc	cttttgcgca	ccttctttta	cgtctttggc	180

tgcatctttg	gctgtatctt	tgactttctc	aatgcacatc	ttgggtgcttt	ctttcacgtc	240
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<210> 1175

<211> 2712

<212> DNA

<213> B.fragilis

<400> 1175

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gcagatacgt	atgaaaaaca	cgaagttgcc	agtattcagc	agcaaaaggt	aaaagcgaac	180
ggtactgtag	tagatcagac	cggcgaacct	ctaactggcg	tttctgtaaa	agtaaaagac	240
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tatggctcac	agaaaaaggt	taatgtcacc	gggtgccgtag	gcatgggtcaa	ttccgaagta	480
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cagaaatggg	cagcaggtga	catcatgtat	gccgatctcg	acaatagcgg	ctcagtgga	2700
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<210> 1176

<211> 732

<212> DNA

<213> B.fragilis

<400> 1176

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accttgtttg	gtatttttgt	ttcctggcaa	atgttactga	ttcttttagg	aatttacttg	180
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gtagtgtttc	gggtgtactac	ctgtctgggc	gggtgtcagg	acaaacgttt	tggcgggggt	660
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ataaaaagtt	ga					732

<210> 1177

<211> 825

<212> DNA

<213> B.fragilis

<400> 1177

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atcgtttgcg	atgatgtctg	tactgccgaa	ctgaaagtgt	gtacttatcg	ttattttcaag	780
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<210> 1178

<211> 963

<212> DNA

<213> B.fragilis

<400> 1178

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taa 963

<210> 1179
<211> 474
<212> DNA
<213> B.fragilis

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atcagtactt cggtagtgtt ttccggattt agtcgtttga tttcacgaat tgtttgtgcc 180
caatgggctg cacccaaatac aggcagatca tcgcggtcta cagatgtgat aactgcgtgt 240
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atcatgaacg tagctgtccc ttttccccag cattcgcca tgttggggca acgcccactg 420
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<210> 1180
<211> 1110
<212> DNA
<213> B.fragilis

<220>
<221> unsure
<222> (1097)
<223> Identity of nucleotide sequences at the above locations are unknown.

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taccatactg ctgcctacga atttgagact gcagaagaga tgggaagctgc tttctgtggg 180
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<210> 1181
<211> 201
<212> DNA
<213> B.fragilis

<400> 1181
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<210> 1182
 <211> 1125
 <212> DNA
 <213> B.fragilis

<400> 1182
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<210> 1183
 <211> 2022
 <212> DNA
 <213> B.fragilis

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gcacacgaac	ttttcggaga	tacattatta	aaagtcggta	aagagacaga	agcagccatc	1980
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<210> 1184

<211> 624

<212> DNA

<213> B.fragilis

<400> 1184

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<210> 1185

<211> 435

<212> DNA

<213> B.fragilis

<400> 1185

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<210> 1186

<211> 2238

<212> DNA

<213> B.fragilis

<400> 1186

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tcgggcaagt	tcagccccga	aaacattttat	ggtgtggttc	ccatgcctga	cggcgaacac	180
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<210> 1187

<211> 846

<212> DNA

<213> B.fragilis

<400> 1187

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cttccggctg	caatagacgg	gattttatct	gtcggattgc	tttgctcctc	ggcctatctg	180
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ctttaa						846

<210> 1188

<211> 1209

<212> DNA

<213> B.fragilis

<400> 1188

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tcttatctga	ttgatgatga	aatgggtggca	ctgatcgata	cagtggatat	ttgctatttc	180

gaagtatatc	ttcgaaaaat	cagaaatatac	ataggcgacc	gtcctatcaa	ctatttgatt	240
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gacatttgta	togttggcaa	taaacagact	ttcggtatga	togaagggtt	ttatggtgtg	360
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gagaaaagta	aatttgaatt	ggtcgggtgat	cctgtagaaa	tgaaacaggc	catgaaggag	1140
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<210> 1189

<211> 879

<212> DNA

<213> B.fragilis

<400> 1189

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<210> 1190

<211> 615

<212> DNA

<213> B.fragilis

<400> 1190

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<210> 1191
 <211> 738
 <212> DNA
 <213> B.fragilis

<400> 1191
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<210> 1192
 <211> 1374
 <212> DNA
 <213> B.fragilis

<400> 1192
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<210> 1193
 <211> 1533
 <212> DNA
 <213> B.fragilis

<400> 1193
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<210> 1194

<211> 798

<212> DNA

<213> B.fragilis

<400> 1194

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<210> 1195

<211> 843

<212> DNA

<213> B.fragilis

<400> 1195

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aatatcagct	atatctatta	tggaggaaca	gctgagacat	tgggcatagc	ccgaaaagga	300
gacaatcaaa	atcttgaatc	aatctgggaa	aaagaagtct	ttaaatatat	ccatccggat	360
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cacaaaaaac	gtgcagatta	ctttcttatg	agtaaaactcc	gtatgcgtga	tccttccggg	480

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cgggaactgt	ttataagcaa	aaataccgtc	agccgacacc	gacaaaatat	attggaaaag	780
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<210> 1196

<211> 588

<212> DNA

<213> B.fragilis

<400> 1196

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gtcaacgatt	ttttcagtgc	cgtacaggat	ttcgtatcg	gtctgccggg	aatggctctg	540
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<210> 1197

<211> 264

<212> DNA

<213> B.fragilis

<400> 1197

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aaaattagtc	aatcattaag	aggtagaagc	aagtcagctt	cgcataatcca	agcaatatca	180
caaggcatga	ctaattactg	gaagactata	ccagtcaaaa	cagatgataa	cccaagtgat	240
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<210> 1198

<211> 639

<212> DNA

<213> B.fragilis

<400> 1198

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aagactatta	gagaacgtgt	tgcaagtgg	taccagaatt	tccgtagcaa	tggtggtaag	480
gtagggcgaa	aagtggata	tacgaaaagc	gatgaggtta	tgaggggaaga	gtatgcagaa	540
gaattaagat	tactgaaaag	agggtactca	ctgcgaaata	cctcaaaact	gacgggaaca	600
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<210> 1199

<211> 1344

<212> DNA

<213> B.fragilis

<400> 1199

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<210> 1200

<211> 198

<212> DNA

<213> B.fragilis

<400> 1200

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aataaattta	aaacggcatg	taaccaaata	cgcagcgcga	tgaacaggac	tgaacacctac	180
aactccacca	cacaatag					198

<210> 1201

<211> 192

<212> DNA

<213> B.fragilis

<400> 1201

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gaaaagcaag	cagcagtggg	cggtttgaac	gctaccttga	agaaactctt	ggatgcttat	180
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<210> 1202

<211> 1260

<212> DNA

<213> B.fragilis

<400> 1202

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aagaatttcg	atatgtctcaa	tcctatttcg	ggcggttctt	acacatacga	ttgtggatgg	300

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aaagctgaat	tgtattggga	aaacaagact	acccgataac	tgatgttgca	tcaactctcc	1200
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<210> 1203

<211> 1296

<212> DNA

<213> B.fragilis

<400> 1203

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gaggaatacg	atggtgactt	tgaccatcag	ttccttgaaa	cggagaagta	tgatgcaaaa	480
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<210> 1204

<211> 498

<212> DNA

<213> B.fragilis

<400> 1204

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ctttatcata agaattaa 498

<210> 1205
<211> 198
<212> DNA
<213> B.fragilis

<400> 1205
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agcgtatggc aaagatag 198

<210> 1206
<211> 195
<212> DNA
<213> B.fragilis

<400> 1206
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<210> 1207
<211> 201
<212> DNA
<213> B.fragilis

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<210> 1208
<211> 579
<212> DNA
<213> B.fragilis

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<210> 1209
<211> 708
<212> DNA
<213> B.fragilis

<400> 1209

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<210> 1210

<211> 204

<212> DNA

<213> B.fragilis

<400> 1210

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gtggttctca	cgcatatagc	gtggaccggtt	cttgttacat	ctgcatcaaa	ggtttcctat	180
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<210> 1211

<211> 723

<212> DNA

<213> B.fragilis

<400> 1211

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caggatgaag	aaaccaatca	ggttttcttg	gactttatgg	taaggcaatt	aaagaaatcc	660
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<210> 1212

<211> 276

<212> DNA

<213> B.fragilis

<400> 1212

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cggctctacc	acaatggatg	cgaagtaga	cgatactcaa	tatcagtttt	tgcttctcag	180
gaactgaatc	cgcagaagtc	acgtgtattg	ctgattctcg	gactgaccaa	aaccaatgac	240
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<210> 1213

<211> 1380

<212> DNA

<213> B.fragilis

<400> 1213

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<210> 1214

<211> 984

<212> DNA

<213> B.fragilis

<400> 1214

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aagaacaggg	aaatatctct	cccgttgggc	acttacaaca	tgatatactg	gggtaccccg	360
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aacatgtata	cagccgctcc	ggtcaaccaa	acaaaaacag	tatctttccc	gcttgtaactg	720
tcggcgagacg	gtacacagat	gagcaatgcc	acggctcatg	tttttccatc	atccgccaaa	780
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<210> 1215

<211> 252

<212> DNA

<213> B.fragilis

<400> 1215

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ctgagaaact	cacacctttt	ggaggaattt	tttcaatcat	ggagaaattt	gactccatgc	180
tttcaccogt	tatcgactca	acactgggtc	agagatgcag	cagtatcttc	ggatatcagt	240
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<210> 1216

<211> 675

<212> DNA

<213> B.fragilis

<400> 1216

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caatgggaga	taaaaaataa	tgtattgtcc	atgtccgtta	ctccgcaaag	tgattactgg	180
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aagtttgaat	acttccaggt	gaagcatctg	ccggaccagc	gcagagtgga	atggctgaag	660
aagaatgcag	aataa					675

<210> 1217

<211> 690

<212> DNA

<213> B.fragilis

<400> 1217

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gtatttcctg	cgttttttga	agaagggggc	ttgtatccat	gccaccccaa	gagggaaactt	180
ccacttaaga	gggatggtgc	caaccgaaa	ctgaaaggca	gaaccattaa	tttgcagaat	240
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ggacgtttta	tgttttaattg	gaaagtgcag	gccccgcaag	tgaggagagct	ctttattcag	360
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cccgtaggaa	actatctgta	cgaggcctat	cagaacaaac	taaacgagaa	gcaacaggcc	660
gaggcacgga	aaacgctcgg	catcggttag				690

<210> 1218

<211> 372

<212> DNA

<213> B.fragilis

<400> 1218

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gccggtgccg	gagtcacctt	tgttcattca	cataaacaga	atgaagaaat	ttacggcatc	180
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ggttttattt	gtattcaggt	gaaagcaggc	tccttggaag	gttataccat	gactgatgga	360
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<210> 1219

<211> 945

<212> DNA

<213> B.fragilis

<400> 1219

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<210> 1220

<211> 231

<212> DNA

<213> B.fragilis

<400> 1220

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cagcattact	attttggctc	actctctgca	atttatacga	aattcagtc	ttaaagacttg	120
ggtatcgcat	tggggacatt	aagaaattat	ggattgaaag	aagaaaagcc	gtaccagaac	180
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<210> 1221

<211> 276

<212> DNA

<213> B.fragilis

<400> 1221

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aatgaacagc	aactttttat	taaaatagga	gataaaataa	aggaaataag	gcttgaaaaa	120
ggaataagcc	aacaagactt	ggcagctaaa	tgcaactttg	agaaagctaa	tatgtcacgg	180
attgaagcag	ggcgaccaa	tctaacaata	aaaaacgcat	ataaaataag	tcttgcttta	240
ggagttagac	taaaagacct	attggatgta	gaatag			276

<210> 1222

<211> 183

<212> DNA

<213> B.fragilis

<400> 1222

acagatctaa	ataaaaagac	cttggggcgt	agggagtttc	tcacgggatg	ttgtctttat	60
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gtcttgtcat	tctgcattct	tattttatgt	agagactata	tcgtatttat	gctgaaaaaa	180
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<210> 1223

<211> 462

<212> DNA

<213> B.fragilis

<400> 1223

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ttagatgcga	atggcaatca	ggtatattat	gaagatggca	aaatgcaagg	caaacccaag	180
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accatcaact	ttcttgatta	cttccaagcc	tacatagaca	gctatacaaa	gaaagattgc	420
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<210> 1224

<211> 192

<212> DNA

<213> B.fragilis

<400> 1224

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gatatagaag	acttcattat	ttcattgaat	tatcaaagca	agttacagtt	aacaatctat	120
cccacaacat	atcttgccca	gtcagaacgt	gaagttcaat	tacaaaccaa	ctccaataac	180
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<210> 1225

<211> 2547

<212> DNA

<213> B.fragilis

<400> 1225

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 <212> DNA
 <213> B.fragilis

<400> 1226						
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tacatccggg	cgctggcccg	ctacgtacgt	acctttcgac	gaatcggcta	taagcgaact	180
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<210> 1227
 <211> 1194
 <212> DNA
 <213> B.fragilis

<400> 1227						
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189

<210> 1229

<211> 537

<212> DNA

<213> B.fragilis

<400> 1229

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<212> DNA

<213> B.fragilis

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<210> 1231

<211> 237

<212> DNA

<213> B.fragilis

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<210> 1232

<211> 279

<212> DNA

<213> B.fragilis

<400> 1232

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 <212> DNA
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<210> 1234
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 <212> DNA
 <213> B.fragilis

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<210> 1235
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 <212> DNA
 <213> B.fragilis

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<210> 1236

<211> 972

<212> DNA

<213> B.fragilis

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<211> 1179

<212> DNA

<213> B.fragilis

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<212> DNA
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<213> B.fragilis

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<212> DNA
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<210> 1245

<211> 855

<212> DNA

<213> B.fragilis

<400> 1245

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cctaaattta	tcacaaagga	tatgatagta	cagtttgtgg	actacctgca	atcccgtagt	180
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<210> 1246

<211> 2427

<212> DNA

<213> B.fragilis

<400> 1246

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<210> 1247

<211> 501

<212> DNA

<213> B.fragilis

<400> 1247

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atatcacaaa	aggcggactt	gtcggaggtat	gaatatgcct	caattatcaa	caacgacact	180
tatcatattc	cggtccaact	gatggaatat	gaaatacaac	tatttgatgc	catagagagt	240
tcccgctctta	aacttgtcaa	tgatatacgt	attgacgaac	tttctccgaa	tcaacaatca	300
aagtttgctta	tggtaaaata	tggagtagat	attttagaag	aagaatctgt	cgtaactgt	360
aatttcatag	attatctcac	tggtagcccg	atagcttcat	gccgtggcgc	atatacaacc	420
ttaggattca	gcgtatcagc	agacattaga	ggtgctataa	aacgtgttgc	taaacaaata	480
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<210> 1248

<211> 2151

<212> DNA

<213> B.fragilis

<400> 1248

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gatcgcagat	ccgtttctcc	cgatcggccc	ggctggtttg	ccaatgacga	tggcgaagga	300
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cccggcgcca	ttaccggtat	atggctcacg	acctttggca	gcatacatat	aatcttgcgc	420
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aacggtaaac	agctggactg	ttacagccag	gaagtcgagg	ccacaggtgc	cataaacctc	2040
ggaatgcaca	agcccataga	tggttaagttt	atcctaagga	tagaattgac	cggacagaat	2100
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<210> 1249

<211> 279

<212> DNA

<213> B.fragilis

<400> 1249

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aaaattttca	atgccgacct	atcagccact	ccgcaactgg	caatacagag	ggatatattt	180
atattccaaa	cactgatagg	ctgtcgagtg	agcgacctat	accgcatgac	gcagagccga	240
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<210> 1250

<211> 1443

<212> DNA

<213> B.fragilis

<400> 1250

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acgatcctta	aaccggaaaa	tatgattcat	ccggtgaaac	tcgatattaa	gcccaatcat	1440
tga						1443

<210> 1251

<211> 1068

<212> DNA

<213> B.fragilis

<400> 1251

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cccaatatag	cctgcacccc	gtgggagcta	aactcttttg	aaccatcgga	ataccttggg	180
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<210> 1252

<211> 906

<212> DNA

<213> B.fragilis

<400> 1252

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<210> 1253

<211> 1764
 <212> DNA
 <213> B.fragilis

<400> 1253
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<210> 1254
 <211> 666
 <212> DNA
 <213> B.fragilis

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<210> 1255
 <211> 1206
 <212> DNA
 <213> B.fragilis

<400> 1255

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<210> 1256

<211> 2421

<212> DNA

<213> B.fragilis

<400> 1256

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<211> 1572

<212> DNA

<213> B.fragilis

<400> 1257

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<211> 1020

<212> DNA

<213> B.fragilis

<400> 1258

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<210> 1259

<211> 264

<212> DNA

<213> B.fragilis

<400> 1259

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<210> 1260

<211> 621

<212> DNA

<213> B.fragilis

<400> 1260

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<210> 1261

<211> 192

<212> DNA

<213> B.fragilis

<400> 1261

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<210> 1262

<211> 594

<212> DNA

<213> B.fragilis

<400> 1262

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<210> 1263

<211> 2439

<212> DNA

<213> B.fragilis

<400> 1263

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 <211> 306
 <212> DNA
 <213> B.fragilis

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<210> 1265
 <211> 1767
 <212> DNA
 <213> B.fragilis

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<210> 1266
 <211> 675
 <212> DNA
 <213> B.fragilis

<400> 1266
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<210> 1267

<211> 519

<212> DNA

<213> B.fragilis

<400> 1267

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<210> 1268

<211> 1140

<212> DNA

<213> B.fragilis

<400> 1268

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attgattttt	tactaatttc	cagcatattt	tccaatctgt	cactcaaaat	cttttttatt	180
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<210> 1269

<211> 468

<212> DNA

<213> B.fragilis

<400> 1269

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gaggatttca	aagcggcgaa	tatcagcaag	gcgagagtga	acttccgtcc	ggggcctgtg	360
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<210> 1270

<211> 315

<212> DNA

<213> B.fragilis

<400> 1270

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tacaccaaag	ccgaacttgc	acagctttac	tgccccgggac	tcgaccccg	gtcgcacctg	180
cagaaactct	accgctggat	gcgtaaaaac	accgacctga	cacaggcact	gtccgaagtc	240
aattacaaca	aataccgcca	cagcttcctt	aaacgggaag	tccggtgat	cgtgtattac	300
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<210> 1271

<211> 639

<212> DNA

<213> B.fragilis

<400> 1271

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ggtattctgt	acatcatcgt	ggctctctgt	ctgctattcg	caccgggaag	cagttacatt	180
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<210> 1272

<211> 1449

<212> DNA

<213> B.fragilis

<400> 1272

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caattggctg	atattgccga	tctatatgcc	tccgaacgta	agtttaagga	agcccaggag	180
gtcataacat	acggactcgg	actccatccg	ggacacaccg	accttatgg	cgaacaggct	240
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<210> 1273

<211> 762

<212> DNA

<213> B.fragilis

<400> 1273

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gaagaactgg	gagaagccta	cgagaatgca	gggaaaaga	ttatggagct	gattcagaaa	180
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gcattgcccc	ccatcataac	ggtgactgaa	gacgccatgc	gcaactgtcc	ccgtgccatg	660
cgcgaagcca	gcctggcact	cggagcttcg	cagtggcaga	ccatttataa	agtagtgatt	720
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<210> 1274

<211> 1275

<212> DNA

<213> B.fragilis

<400> 1274

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gtcagagcac	atatagtcga	agtgcctttt	gaggatctcg	atggcttcca	ccaatgcctg	360
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1275

<210> 1275

<211> 189

<212> DNA

<213> B.fragilis

<400> 1275

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gaaaaccctg	tgaaactctg	tgtactctgt	ggtgagccac	cccatagtaa	tattctaaaa	180
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<210> 1276

<211> 462

<212> DNA

<213> B.fragilis

<400> 1276

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tgcccccgcg	caggaacgcc	agttcgtcag	catctcccgg	cagcaggaga	tcaaagccgg	180
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cgtcatgggg	ctgctccagt	tccggataga	aggacggggc	gatgtggaaa	agctgacctc	420
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<210> 1277

<211> 789

<212> DNA

<213> B.fragilis

<400> 1277

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<210> 1278

<211> 450

<212> DNA

<213> B.fragilis

<400> 1278

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<210> 1279
 <211> 1413
 <212> DNA
 <213> B.fragilis

<400> 1279						
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<210> 1280
 <211> 597
 <212> DNA
 <213> B.fragilis

<400> 1280						
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<210> 1281
 <211> 651
 <212> DNA
 <213> B.fragilis

<400> 1281

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<210> 1282

<211> 492

<212> DNA

<213> B.fragilis

<400> 1282

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<210> 1283

<211> 858

<212> DNA

<213> B.fragilis

<400> 1283

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<210> 1284

<211> 444

<212> DNA

<213> B.fragilis

<400> 1284

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<210> 1285

<211> 2046

<212> DNA

<213> B.fragilis

<400> 1285

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<210> 1286

<211> 1200

<212> DNA

<213> B.fragilis

<400> 1286

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<210> 1287

<211> 1863

<212> DNA

<213> B.fragilis

<400> 1287

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<210> 1288

<211> 969

<212> DNA

<213> B.fragilis

<400> 1288

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<210> 1289

<211> 276

<212> DNA

<213> B.fragilis

<400> 1289

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<210> 1290

<211> 630

<212> DNA

<213> B.fragilis

<400> 1290

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<210> 1291

<211> 864

<212> DNA

<213> B.fragilis

<400> 1291

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<210> 1292

<211> 1071

<212> DNA

<213> B.fragilis

<400> 1292

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<210> 1293

<211> 1227

<212> DNA

<213> B.fragilis

<400> 1293

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<210> 1294

<211> 345

<212> DNA

<213> B.fragilis

<400> 1294

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<210> 1295

<211> 2820

<212> DNA

<213> B.fragilis

<400> 1295

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<210> 1296

<211> 1701

<212> DNA

<213> B.fragilis

<400> 1296

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<210> 1297

<211> 1926

<212> DNA

<213> B.fragilis

<400> 1297

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<210> 1298

<211> 1479

<212> DNA

<213> B.fragilis

<400> 1298

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<210> 1299

<211> 669

<212> DNA

<213> B.fragilis

<400> 1299

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<210> 1300

<211> 999

<212> DNA

<213> B.fragilis

<400> 1300

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tcacgtacca	atatttctta	tggtaaagag	ggacgactga	aaatcttggt	ttccagtccg	360
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gaagggctgg	atgtatcatt	gatcggttca	ggtgatattg	ttgcggaaaa	tataacttgc	480
aacgggtgatt	tttctgccct	gttgcaagg	tcgggtgaca	ttgacgtgaa	ggggcagctt	540
cgtgctaaaa	gtgtgaatct	gaatttgcaa	ggctccgggtg	atttgaaagt	agcagggtgt	600
accggaagcg	aaatcagtg	gatgcttcag	ggatcgggtg	acttgaaagt	cggaagtact	660
aatatcacat	cgactgtaac	ggcaaagttg	agtggctcgg	gtgatatgga	tgtattggat	720
attcgtgcc	atagcgtatc	cggacagttg	gatggctcag	gagacatgac	tttgtcgggt	780
tctgcttgta	atgccacgtt	ggttttgaac	aggctcgggag	aactcagtg	gcgaaaactg	840
gatgctgaaa	atgtaacggc	tcatgtcaat	ggatcagggg	aaatctcctg	tacagccacg	900
aagacacttg	aaaccaatat	ccaaggtagt	ggagaaattt	cttataaagg	aaatccgagt	960
atacggtcga	caggtaaaga	tcatctgaac	agactctaa			999

<210> 1301

<211> 1509

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (12), (13), (14)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1301

ttgacggtct	tnnnatggag	cggtctccttc	cagccccgtg	gtgaagacta	tgaacagtca	60
ccctattatc	tcaacctcaa	cggtaaatgg	aaattccatt	gggtgaaaaa	tcctgatctc	120
cgtccgaaaag	actttttataa	accctcattc	tataccggag	gctgggcaga	tatcaacggt	180
ccgggaaact	gggagcgcca	gggatacgga	actgccatct	acgtaaatga	gacttatgaa	240
tttgatgaca	aaatgttcaa	ctttaagaag	aatccccctc	ttgtgcctta	taaggagaac	300
gaagtaggat	cttatcgccg	tacttttact	gtgcttgccg	gatggaaggg	ccgccgggta	360
gtactctgct	gcgaaggtgt	aatttctttt	tattatgtgt	gggtgaacgg	acattttctc	420
ggttacaacc	aaggttccaa	gacagctgcc	gaatgggata	tcaccgatca	gttggagaag	480
ggtgagaata	cgattgcctc	cgaagtatat	cgctggagtt	caggttccta	tctggagtgt	540
caggatatgt	ggcgtctgag	tggatttgag	cgtgatgtgt	atctgtatag	tactcccaaa	600
cagtatatag	ccgattataa	ggtaaacgca	actcttgaaa	aggaacgtta	taaagatggt	660
attttcggac	tcgacgttac	ggtcggaggg	cctgcagacg	gtgtggcatc	cgtatcttat	720
acactgaacg	atccactcgg	acgtcctgta	ctgtcgggtg	agatgcctgt	caagtcgcgc	780
ggactgagta	acttcatcac	attcggagaa	cagcgcctga	aggatgtgaa	acgttggaat	840
gccgagcatc	ccaatctcta	caccctcgtg	ttggagttga	aaaatgcagg	aggacaggtg	900
accgaagtca	ccggttggtga	agtcggtttc	cgtacttcgg	agatcaaaga	cgggcggttc	960
tgcatacaacg	gtgtgcctgt	attgggtcaaa	ggaaccaatc	gtcatgaaca	ttcgcagttg	1020
gggcgtaaccg	tcagcaaaga	gctcatggag	caagatatac	gtctgatgaa	actgtataat	1080
atcaatactg	tgcgcaactc	acattatccc	actgatccgt	attggtatcg	gctgtgcgat	1140
cgttacggac	tttatatgat	cgatgaagcg	aatatcgagt	cacacgggat	gggatatgga	1200
cccgcttcgc	ttgccaaaga	cagcacttgg	ctgacagcac	acatggatcg	tacacatcgc	1260
atgtatgaac	gttcgaaaaa	tcactcctgcc	atcgttatct	ggtcattggg	caacgaagcc	1320
cggaaaacgga	atcaatttcg	agcgtacctc	gaattggctg	aaatcggtag	agaaaagccg	1380
tcccgctccag	tacgaacgtg	ccgagcagaa	ttacaatacc	gatatactatt	gtcgaatgta	1440
tcgcagtgtc	gacgaaatca	aggcctatct	ggcccagaaa	gatatactacc	gtccgttcat	1500
tctttgtga						1509

<210> 1302

<211> 354

<212> DNA

<213> B.fragilis

<400> 1302

cgaggaagaa	tgaacaact	gatacccgca	cttttcgccg	taggcgcagt	aatggccctc	60
atagggggccg	ctgtctttat	caccggatgg	gtctatgcac	cttatatata	taccatcggg	120
gcagggtttg	tcgcatggc	tcagggtgaat	actccgcttc	gggctaaaag	caagacgctc	180
cgccgactgc	gtatccagca	gatcttcggt	gcattagcac	tgatattgac	aggagctttt	240
atgttcacca	cacgtggcaa	tgaatggatt	gcctgcctta	ctatcgagc	catactggaa	300
ttatacacgg	cattccgtat	tccgcaggaa	gaagaaaaag	aactttccaa	atag	354

<210> 1303

<211> 1068

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (231)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1303

gccttcagga	cctgggtggc	atttatacga	atgaagcggg	agagcgtatt	gtttcaggca	60
gcccgcaaac	accacttaaa	cttacttttt	ccattgtttc	gggcaaatac	cagtgcaagt	120
tatccggtaa	gcagggtttat	atcgaggcct	atcacagtc	tttctaaagg	atttgcaaaa	180
ggtttctttt	gcattaaaaa	agaaaccgtg	gataagattc	agcaattttt	nttcgataag	240
tggggcattg	aggaaaggag	ataccaccag	ctcctttcca	ttctgttgcc	cggtctgaaa	300
aacggcaacc	tagcgtcggt	ggaacaatat	ctggggggcca	agcatataga	ggcctatgcc	360
gccgtccctc	atgtagccga	ccgatgggaa	ctggatgacg	cctccctccc	tcaaggagcg	420
gtagtgggtgc	ttacctgtga	aggcgtgctg	tatagctggg	agacctaccg	gctggagaga	480

tatatttccg	ccgcgatagc	caacgaccgc	atatcggttg	tcgttctgtt	tgtgaacggg	540
cccggaggta	tgattacgcg	tgtggatgtc	ctggaaaagc	ttatacggca	gtccccaaa	600
cccatagtgg	cctatatcac	gggcgtatgc	gcttcggcgc	atttctgggt	cgtttccgca	660
tgcgcacgca	gattcgtctc	ctcgcgccatg	gatgaaatcg	gctcctgcgg	ggtggtctac	720
actttccaga	gcttcaagga	gtattacgcg	caaatgggga	ttgagatcga	ggacatttac	780
cccgcacgtg	cggacctgaa	gaaccgcgcc	tatcgcgaca	aggaagaaaa	gcaggatgac	840
accttaatta	aagagaacct	gtcgttttac	caccatcttt	ttgcacagac	catcgcccga	900
aatctgggag	tgaagtatga	cgcgcaggat	ccctgtttca	gagggcagac	tttctttgcc	960
gatacggcac	tggccaaggg	gtatgtggat	gcctacggaa	gcctggagga	tgccatcctg	1020
tgggtatccg	cccagaaaac	cgtaaagcgg	gctaacaaga	tgatttaa		1068

<210> 1304
 <211> 474
 <212> DNA
 <213> B.fragilis

<400> 1304						
cggaaaaatg	cggagtattt	gaaaatcaat	aagttatata	atatgaaaac	aataaaaaaga	60
ccctataccc	ccgtttgtga	tctggagttg	gttccggttg	agtgtatcag	tgattttgca	120
gtcactctgc	cgcgcgcttt	tattgccgtg	cgggatgggt	cttatcgcat	tctgtttatt	180
ccgggatcat	tactctccgg	agtcgaatcc	gagcaggcgg	attcaggaaac	tatatattat	240
aatgtagggc	atacgttcga	ggttgccctt	acaggaccgg	acagccagga	gttgttatct	300
gccatgagcc	ttcaggacct	ggtggccatt	tatacgaatc	aagcgggaga	gcgtattgtt	360
tcaggcagcc	cgcaaacacc	acttaaactt	actttttcca	ttgtttcggg	caaataccag	420
tgcaagttat	ccggttaagca	ggttttatatc	gaggcctatc	acagtccttt	ctaa	474

<210> 1305
 <211> 825
 <212> DNA
 <213> B.fragilis

<220>
 <221> unsure
 <222> (752)
 <223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1305						
caagatgatt	taatactcac	tataaaagta	aatttgttta	tgaaaaatta	tttcgcatca	60
ttcattccgg	ccgtaaaggc	cattctgggt	atcgaggcct	ggagtaagga	cgccgacaag	120
aaagacgcgt	tactggaaga	gcaaaagcag	aaacttaagg	cattgaattt	caatgacacc	180
tttatcaatg	gtttttgtga	ggccctgaag	gatggattcc	cggaggattc	ttcccgcaag	240
gacggggagt	cgggcacgaa	aggcagtggg	cctgacccca	atacctcaa	cgcagtaata	300
caaggattac	tggctgatat	gactgccaa	ctggttacgg	cccaggagga	aatcgctgtg	360
cttaacaaag	agaaagggga	actttcacag	gaggtatccg	ccaaacaaac	agaaatcacc	420
ggtttgcaga	ccaagattca	gaccctttcc	ggccttgccg	agcaagacgg	ggggaaaggc	480
ttccagcatg	cacgtctgga	accggacgct	aaagacattg	tcatgaattg	ggatgacgaa	540
aaacaactgg	gcggcctctc	gggggagatg	ttcgcaatgg	gaccgcctta	taaccagcgc	600
ctgcgcgcaa	agatgcttta	ccgcaagggg	ttgaccctgc	aggtgcccac	tgccagttcg	660
atcgattact	cccgcctgaa	agaagacctg	ggagccttct	accgcattcc	ctggcaggag	720
cgtttacagt	ctttcctgac	cctgcttctc	tncatcgaga	gtattttccc	cgctgaattc	780
gggatatcag	gacctgggcg	tgcttacaaa	catttggggt	ggtga		825

<210> 1306
 <211> 507
 <212> DNA
 <213> B.fragilis

<400> 1306						
aaaaaacatc	aacttatgat	aaccacgaaa	ataacagtag	agccgcacct	ggctcaatat	60

tgctacgcc	aatattcttc	cgatccggaa	ggcagcatgc	cogtccgctt	tgccgaccat	120
ctggatgtat	accatctggg	ttataacctg	ctggaaaaaac	gcccgggttaa	ctgtccccgg	180
gataatggca	atcttgagat	cgtcttgccg	gaccgcagggc	aggggtgacgt	ccccggtggc	240
aatccccgg	agcgtttcaa	ctatctgggc	cagcgcagcc	aggggtatcat	caataagaag	300
ctaaagctga	tgatgcgcgc	cgagctccat	gactttattg	acgagaacaa	gcaccggttc	360
ggtatcgacc	agcttcagtc	agtcactgc	tttatgaaga	agtactgcat	tgacagctta	420
agcgaggatg	ctcttctgaa	agactaccaa	cgttggcggtg	accgggtaag	acgttccagc	480
cttaagcggc	cctacaagaa	aaagtag				507

<210> 1307

<211> 618

<212> DNA

<213> B.fragilis

<400> 1307

aaaaagatgg	aagtagaact	agtaaaaacc	accctgcatg	cggttctgag	cccgtctcag	60
ttacagaaac	cctgtgtccg	aaagaaggag	ctgacgcctc	tccagatctc	gttaaaaaact	120
ggatcgacgg	cctctcaatt	ggtggatgaa	tggggcgggg	caattgccca	actgaacatg	180
ggcgcgccac	tttacgatgt	cgccgcaaac	ggagaaatcc	ctacattggc	tgatgtgggt	240
gtggtcttcg	gtaattcgac	atccgttcgg	attatcacia	gccatctgga	atccgttctg	300
aagtacgccc	gcgttgaatt	gagccgcgag	cagatggcgg	aaaccgcgct	ggcgatactt	360
tcaggatact	ggttctctgaa	cctggccgag	ctctgcattt	tctttaccgg	ccttaagaac	420
ggaagttgtg	ggcagcttgt	ctggggaaaag	agcctaaaca	atcaggcggt	catggtcgcc	480
ctatcggatt	tctgcaagga	acgccgtgaa	gtgatcatte	gcaaagagac	agagcggatg	540
ggcccggggc	tgtggaaaaa	ggcttttcca	gaacggagga	ttttgcgcgc	ggtatttgtg	600
tgggcggtaca	gggtatag					618

<210> 1308

<211> 882

<212> DNA

<213> B.fragilis

<400> 1308

aagtcgccga	gaaatcttcc	aaggctttgc	gtccggcttc	gaactccata	cctaatttgc	60
ctgctgtgta	atatctatcg	agataaaggg	tattacatcg	agtgggatga	agatttgcct	120
tttgtggtgg	ctgacaccat	tgggtaccac	gagggcgag	tagaggaagt	agtaaagaaa	180
gccgtgcaag	tgggattctt	cgacaagtca	ttgttcgacc	aatacaggat	ccttacctca	240
aacggtattc	aaaaccgctt	caaaagcgcc	gtttccagac	gtgaaggatt	tgagtatatt	300
cccgaatatc	tggtttctgt	atgcaataac	cccattcaat	cgaatttctg	tatacagaaa	360
ccctctctca	ccgagtttct	gtatgcagaa	accagcccca	accgagtttc	tgcatgcaaa	420
agtacacaaa	gtaaagtaaa	ggaaagaata	tctccccctc	ctcacgcgcg	tgaaggaggc	480
atttccggaa	tcagactttt	ttcagacaag	tctttaaccg	agtgttacgg	ggagctgaaa	540
gcgaatatcc	cctggatgga	gcaattctgc	atgaacatcc	gtctggatta	tccggatttt	600
accccggagc	tgttttatgg	ctttctggac	aggttcttcc	gtaaactcca	gaatgaaggg	660
gaaatagtca	agtcacccaa	ggacgccatg	tgcgattttg	caaactgggt	gaatattgaa	720
cttgaaaaaa	taaaaaaaga	tggaaagtaga	actagtaaaa	accaccctgc	atgcggttct	780
gagcccgctc	cagttacaga	aaccctgtgt	ccgaaagaag	gagctgacgc	ctctccagat	840
ctcgtaaaaa	actggatcga	cggcctctca	attggtggat	ga		882

<210> 1309

<211> 807

<212> DNA

<213> B.fragilis

<400> 1309

aaaaacaata	taccaatgat	agtagcatgg	ttttcttgcg	gtgtaacatc	cgcagtcgct	60
tgtaagattg	cacttagtct	atacgatgac	gtgcagctct	attatattga	aactggctcc	120
gggcatccgg	acaacgctcg	ttttctatct	gattgtgaaa	gatggtagca	tcagcctatt	180
cacattatcc	gaagcgacaa	atacacttgc	gtagctgatg	tcctacggaa	aggtttttatc	240

aatggtgctgc	atggtgctgc	ttgcactctt	gaacttaaaa	agaaagtccg	gtacaagttg	300
gaaaaggaac	ttggttcttg	ggacggtcaa	gtttggggat	togattatga	accaaagag	360
attaaccgag	ctatccgatt	aaagcagcag	taccagaca	caaagccact	gttcccgtt	420
attgaaaagc	agattacgaa	gccggatgcc	atggggatag	tttgaaaagc	agggattgaa	480
atccctgcta	tgtacaagat	gggtacaaat	aacaacaact	gcatcggttg	cgtgaaaggt	540
ggtatgggat	actggaataa	aatccggaag	gatttcccgg	aagtgtttgc	tcaaattggcg	600
cagattgagc	gtgatgttgg	agctacctgt	ctgaaagata	aagatgggag	tatcttcttg	660
gatgaactac	cgacatggcg	gggcgatcca	gtggaagaga	ttataccgga	ttgctcgctt	720
atctgccaaa	ttgaatttca	agagatcatc	gacaggcagg	taaaacgagt	tttgaaagga	780
gaaattagta	ttaacgatgt	agcttga				807

<210> 1310

<211> 189

<212> DNA

<213> B.fragilis

<400> 1310

accatgaaag	tgcgtcatcta	ttggcagaag	aaatccaccg	tccaccatcg	ccgccggatc	60
cgtgacagat	tcaggcttcc	cgatgggatg	accattaacg	gtgaaactcc	cgccgatgtg	120
aggccggagg	atatgaagga	actacagacc	ctggaagaaa	tgggttatat	taaattaaga	180
aacaagtaa						189

<210> 1311

<211> 348

<212> DNA

<213> B.fragilis

<400> 1311

agtgatcatt	cgcaaagaga	cagagcggat	gggcccgggg	ctgtggaaaa	aggcttttcc	60
agaacggagg	atthttgccgc	cggtattgtg	ttgggcgtac	agggatatag	cgtgaaacgt	120
gaacgggcca	aggccgactt	taatgctttt	ttggagttht	tcccctgtct	gccatcagga	180
tatgaccgca	tagccttatg	gaaggcctgg	ggcggatgac	cggatgccat	caacttactc	240
ttcggcaaca	atcctcccgg	agtggaaagc	gcggcggaat	ctgtcggcag	atacctgtgt	300
gattacaatg	tctatcaggc	ccgtgtaaag	gccaaagcct	ccttgtaa		348

<210> 1312

<211> 192

<212> DNA

<213> B.fragilis

<400> 1312

gaaacgagtt	cacatttcaa	cactttttca	ggagattcga	ccgtacgtcc	acatccccag	60
aacaataaca	cccaaaccgg	acaaaataac	aacaagcctt	tcagtctctt	cctgtctaata	120
aaattaaaag	aagcgctcat	aatcaacatt	ctgttctttt	accatcacat	tccaccacc	180
gagtctctgt	aa					192

<210> 1313

<211> 243

<212> DNA

<213> B.fragilis

<400> 1313

ataaaacaat	caattaaagt	atthttatcac	caagcaacca	cttattttaa	taaaatcaca	60
gactgtaata	acagctttcc	agcttatttt	ccttgatat	ctccattatt	tcacataacct	120
ttgtctaaaa	ttaaggtatt	aaaacatccg	gatgttatat	atcaaaacac	ccggatgttt	180
tatatcagaa	catccggatg	ttatctatta	aaacatccgg	atgttttcag	acataactta	240
tag						243

<210> 1314

<211> 195
 <212> DNA
 <213> B.fragilis

<400> 1314
 cagttttttac cctgttttaaa gcttaatttt cccccgtcac tgtctaaaaa atgccgtaaa 60
 cttgcatcat cgaaaaacaa cgaatattca caatttataaa agcaacgtta tgaaaagtgt 120
 aagcttcaga aaagatttaa ttggagttca ggaagagcta cttcgctttg catacaaact 180
 aacaaccgac cgtga 195

<210> 1315
 <211> 1467
 <212> DNA
 <213> B.fragilis

<400> 1315
 gtctataata cgaaagggaa taaaatagga ttttatatgg caacaacaga ttttatcgcc 60
 gctattgaac tgggttcac gaagatagcc ggtatagccg gaaagaagaa tagtgaatga 120
 agtatacagg tattagctta tgccaggag gattcgtctt ctttcacccg gaaaggagt 180
 atctataatc tggataaaac ggcacaaagc ctgacttcaa tcatcaataa actggagggg 240
 gctctcaata actcaattgc caagatctat gtgggtatcg gcggacaatc gctccgtacg 300
 gtgcgcaatg tggtaagtcg tgatcttgaa gaagaaacca ttatttctca ggaactggtc 360
 gactcaatct gtgatgagaa cctcgagata ccatgatcg atatggatat actggacgtt 420
 gctccacaag aatacaaaat aggaacaat cttcaagccg accctgtcgg tgtagccgga 480
 agccacattg aagggcgttt tctgaatatt gtagcacgtg cttcgctcaa gaaaaatctg 540
 gaacgctgct tcgaacaggc taaaatagaa atagcagacc tattgatctc acctctggtt 600
 actgccgatg cagtactgac ggaaagtga agacgctccg gctgcgcaact gatcgacttt 660
 ggtgccgaca catctaccat ttccatttat aagaataata tctctccgctt cctcactgtg 720
 ctgccgttag gaggaacagc tattaccat gacctcgtct ctcttcagat ggaagaagaa 780
 gaggcggaac gcctgaaaat cagatatggc aatgctttct acgaagagga agaaggcgaa 840
 gaacctgcta cttgccaat ggaagacgga aatagaacga tagagttagg taaactgaat 900
 aatatcatcg aggcaagctac cgaagagatt atcgcgaaac tatggaatca gattcaactt 960
 tcgggatatg acgacaaact tctggccgga ctcatcatca cggagggggc cgccaacctg 1020
 aaagacctgg acgaggttct acgtaaacgg agtaaaatag agaaggtgag aaacgcacgt 1080
 ttctgacgca ataccatcca tgcagacgaa gacgttgtga agaaagacgg tacacaaaac 1140
 accttattcg gactgcttat tgcgggcaac gaaaactgtt gtttattgga aacaccgct 1200
 ccacagccgc atatacaacc tcagcccaag cccgaaccgg tgaacatggt tgaagaagac 1260
 gaaagtctga aggaacagga agccgctgcc cgcgctgcca agaagaagaa agaagaagaa 1320
 gagaaaaagc ggaaagaaga agaaaagcaa cgcaagctgg aagagaagaa aagaaggga 1380
 gaagagagaa gaaataaacc taactggttt aaatcgactt tcgacaagct ctctaataa 1440
 attttttctg acgaagatat gaaataa 1467

<210> 1316
 <211> 1470
 <212> DNA
 <213> B.fragilis

<400> 1316
 aaacattgca cacctggctt taccggattc tgctgtcgtt attgcaaaaag aagttataaa 60
 attagcgcaa caatcatgaa tatagaaacg attcaatctg tatattttgt cggggcaggg 120
 ggtatcgga tgaagtgcct cgtccgctat tttctttcta aaggaaaagt agtggcaggg 180
 tatgaccgta ctccagtgat actgactcaa catcttatag aagaaggagc acagatccat 240
 tacgaagaga atatcgatct cataccggag gcttgcaaaag acaaagctac cacattggta 300
 gtcctgacct ctgccgtacc tcaggaacat gccgaattaa cttacttccg tgataatgga 360
 ttcgaaatag agaaacgtgc acaagtactg ggcaccatta cccgttccag caaaggactt 420
 tgtgtagccg gcacacatgg taaaaccact acctcaacga tgacagccca cttgtttcat 480
 caatcacatg taggttgtac tgcttttctg ggaggtattt ccaaaaatta cggaacgaat 540
 ctactactct cttcaaccag cccttatagc gtgattgaag cagacgaatt tgaccgttca 600
 ttccattggt tgtctcctta tatgtctgtc attaccgcaa ccgatccgga tcatctggat 660

atztatggca	ccgaacaggc	ttatctggaa	agctttgaac	actacaccac	actgattcag	720
cccggaggag	cactgattat	ccgcaaaggc	atttccctac	agccgaaagt	gaaagaagga	780
gtgaagatgt	atacttactc	acgtgacgag	ggagactttc	atgctgagaa	cattcgcatc	840
ggaaacggag	aaatcttcat	tgacttcgta	gggcctgaca	ttcgtatcga	caacattcag	900
ctaggagtac	cggtaaagtat	aaatatagag	aatgggtgctg	ctgcgatggc	acttgcccac	960
cttaacggag	tcacacctga	agagatcaaa	cagggaatgg	ccagtttccg	gggtgtggac	1020
cgccgggttcg	actttaaaat	caagaataac	cggattgtat	tcctgagtga	ctacgcacat	1080
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<210> 1317

<211> 765

<212> DNA

<213> B.fragilis

<400> 1317

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ggcaatcata	ttatctatct	gggtaaaactg	gaacattttg	aggataaact	gaaacgcttg	660
aagacctttt	acgaaaaagg	gctcaaccag	gtgggatgga	ataaatattc	gcgtatcagc	720
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<210> 1318

<211> 2010

<212> DNA

<213> B.fragilis

<400> 1318

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<210> 1319

<211> 1308

<212> DNA

<213> B.fragilis

<400> 1319

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acttataaaa	gtggcgacca	ctggggaccc	atcacacaa	attccatcat	cctgatggta	180
ggtgcggctc	tagtggctct	gatgcacaac	atcccttata	agtggtttca	ggtgtttccg	240
gttttctct	accctatttc	ggtagtattg	ctggctttcg	taactttgat	gggagtcac	300
acaggtgacc	gtgtgaacgg	agccgcccgc	tggatgagtt	ttatgggggt	acagttccag	360
ccttcagaac	tggccaagat	ggcagtaatc	atcgcggttt	ctttcattct	atccaaaag	420
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<210> 1320

<211> 408

<212> DNA

<213> B.fragilis

<400> 1320

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aaagacaagg	gaaacgatta	tacggaaata	gaagaactgg	tacgggagaa	atgctcggca	180
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cctgtagccg	aagtacagac	cggcatgaag	gatgccgtag	aagcagctta	caagctggcg	300
aaaaagggag	aaacagtatt	gttgagtcca	tgttgcgctt	cctttgacct	tttcaagagc	360
tatgaagacc	gtggcgaaaca	gtttaagaag	tatgtaagag	aattataa		408

<210> 1321
 <211> 201
 <212> DNA
 <213> B.fragilis

<400> 1321
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 atttttaatt cttctttttt cactcttcat tcttctctaa ctcagatatt ttcactatat 180
 ttgctctgtt attataatta g 201

<210> 1322
 <211> 546
 <212> DNA
 <213> B.fragilis

<400> 1322
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 gaagacatta aaaacgcaat gaaagcgaaa gataaagtag ctctcgaaac tctcagaaat 180
 gtaaaaaagt tcttttttga agctaaaaca gctccgggag ctaatgacac ccttacagat 240
 gcagatgcac tgaaaatcgt gcaaaaactg gtaaaacaag gtaaggatgc cgcagaaata 300
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 gaaacttatc tgcttaagca gatgagtgcc gaagaattgg aagccgact gaaagaaatt 420
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 aaaaaactgg caggattggc cgaaggacgc gcgatctcag cttaaagtaa agagttattg 540
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<210> 1323
 <211> 204
 <212> DNA
 <213> B.fragilis

<400> 1323
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 gcccggaagg ggaaaaaact gggttttgtt ctgaagcctt ctgaaagggg cggagaagac 120
 aaggcgggtca tagtcccgtc gaaactccga acggttttcc tgacgctctt cgtgaaactc 180
 ttccatgccg aaacgcttag ctga 204

<210> 1324
 <211> 1032
 <212> DNA
 <213> B.fragilis

<400> 1324
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 aaagaagaag aaacaacata tcacgtaccg gtactgctaa aagaaagtgt agatgccatg 180
 aacatatctc ccgacgggac ttacgtagat gtcacctttg gcggtggcgg acattccgcg 240
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caggactttt	ttggcaatth	acagacacct	ttccgcctgg	taaacaataa	agtgatcgta	960
cccgcagagg	atgagataac	acgcaatccc	cggtcgcgca	gtgccaagtt	gagaatagcc	1020
gagaagaagt	aa					1032

<210> 1325

<211> 543

<212> DNA

<213> B.fragilis

<400> 1325

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gatttcatat	tcctgctgat	agattttacc	gttgcggaat	acctgggtag	tcattgtgtgt	180
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agagttgtcg	acaatttcat	ataccaagtg	atgaagtccc	tttacgtgta	tgtcaccaat	480
gtacatcgca	gggctgtttc	taactgcttc	aagtccttcc	aatacttgga	tactatctgc	540
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<210> 1326

<211> 1329

<212> DNA

<213> B.fragilis

<400> 1326

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cggaaggca	tacacgacgt	aacattcggt	ctctgcaata	ccgacaacca	agcattggct	180
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acatttttaa						1329

<210> 1327

<211> 516

<212> DNA

<213> B.fragilis

<400> 1327

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tcgggcaatg	aaacttatgt	agtacgtaat	attgtgttaa	gcgtggaagg	aggtgaagag	480
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<210> 1328

<211> 987

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (928), (942)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1328

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gaagtagtaa	ttaccgaccc	gatcgctntc	aatatggaac	angaacaagt	ggcctgacc	960
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<210> 1329

<211> 1359

<212> DNA

<213> B.fragilis

<400> 1329

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<210> 1330

<211> 186

<212> DNA

<213> B.fragilis

<400> 1330

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<210> 1331

<211> 627

<212> DNA

<213> B.fragilis

<400> 1331

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gtgaatatgg	atttacctta	tttttttggg	ttgactcctc	aagaagaacg	gattcaatgt	540
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<210> 1332

<211> 423

<212> DNA

<213> B.fragilis

<400> 1332

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<210> 1333

<211> 342

<212> DNA

<213> B.fragilis

<400> 1333

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<210> 1334

<211> 2643

<212> DNA

<213> B.fragilis

<400> 1334

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<210> 1335
 <211> 654
 <212> DNA
 <213> B.fragilis

<400> 1335
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 aatgaattat tgcataaaaa agttttgttc ttgtttaatt atcatgactg cggtaactgt 360
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<210> 1336
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 <212> DNA
 <213> B.fragilis

<400> 1336
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<210> 1337
 <211> 1461
 <212> DNA
 <213> B.fragilis

<400> 1337
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<210> 1338

<211> 249

<212> DNA

<213> B.fragilis

<400> 1338

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gagccgggat	gcagcgtaaa	gtttacgaag	cccgatcagt	tgttccacga	atcaaaaatc	180
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<210> 1339

<211> 1788

<212> DNA

<213> B.fragilis

<400> 1339

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<210> 1340

<211> 1170

<212> DNA

<213> B.fragilis

<400> 1340

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<210> 1341

<211> 621

<212> DNA

<213> B.fragilis

<400> 1341

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aaaacatcaa	aggtggtcaa	gactacaccg	gtagaaccgg	cttatctgtc	atctaaactg	180
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<210> 1342

<211> 453

<212> DNA

<213> B.fragilis

<400> 1342

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gcgcgccacg	aacaagctgt	atggaaagaa	gttgagggtac	tggacgaaac	ggaacgcggc	420
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<210> 1343

<211> 2172

<212> DNA

<213> B.fragilis

<400> 1343

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<210> 1344

<211> 357

<212> DNA

<213> B.fragilis

<400> 1344

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gtactgatta	tgggtgctcat	cattttctac	attcataatc	gctacgcaag	ccagcaacag	180
caaatcgaaa	tagataagtt	gaaaaaagaa	ctgatcgaca	taaaatatga	tgcactgaca	240
cgaagtctcg	aattgatgga	aaaaagccgt	cagtcgcgga	tagaggatta	tatatcgacc	300
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<210> 1345

<211> 597

<212> DNA

<213> B.fragilis

<400> 1345

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ggattcaa	accgtgaaat	agctgagaaa	ctggacttgc	cgctcgggac	agtaaagagc	540
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<210> 1346

<211> 507

<212> DNA

<213> B.fragilis

<400> 1346

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gcgttacctc	caccacctcc	tacaccaatc	actttgatga	ttttcgggtga	atctgtaggg	420
aaatcgaa	gtactatctc	gtccatatta	tattgtatta	tgaattatca	ctttatttca	480
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<210> 1347

<211> 369

<212> DNA

<213> B.fragilis

<400> 1347

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aagttgcgtt	tggctgcgat	agacgcaatg	gcaatgattg	aagcagaaac	acctggagat	180
actgaacttt	cgctttcagg	atcatgtaag	attactttta	cttggttatga	tagctggacg	240
ggagcggcgg	atggtagtat	tacttgctgg	ggagctgaat	attgcaaacg	aggaattaaa	300
aaggaaggta	tagttattat	tacagagact	cgggtgggtg	aatgtgatgg	taaaagaaca	360
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<210> 1348

<211> 1245

<212> DNA

<213> B.fragilis

<400> 1348

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tcgttgtcta	atgatttgaa	ggacaggctg	attttgaaac	ctcaatccat	attgattgat	180
ccggacaaaag	tgaaagactt	tattgatttg	acccctttgt	tgagagattc	ggttgagatt	240
attcctttgg	agactaaaga	tgagtgtttg	ttatccgaaa	ttgaacggat	tgaattctat	300
aaagatcgta	tatttgtact	tgatagaact	cgcaaaggag	tttacctgtt	tgatcaatcc	360
gggcgatttta	tcggttaagat	tggttgtcaa	ggaagtggtc	cgggagaatt	tacctctgtt	420
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<210> 1349

<211> 798

<212> DNA

<213> B.fragilis

<400> 1349

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<210> 1350

<211> 516

<212> DNA

<213> B.fragilis

<400> 1350

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ttcctgaaca	atgtgcggaa	aaccgatttt	gtcagcctgc	aacttaaata	cggacgcaag	420
tctacaaagt	cacaaaacgg	ttccgacaag	gagacaaccc	atgttatccc	ccaccagcaa	480
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<210> 1351
 <211> 1059
 <212> DNA
 <213> B.fragilis

<400> 1351
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 gaatctcctg aaaaagtgtt gaaatgtgaa ctctgttctt acataaagag ttatcctgat 180
 tcttcatttt tctctcaggt gggtacaatg caatatcagg atggtaagat ttatttggtg 240
 gatgaggctc ggagagatgt ggctgttatg gatttgaggat tttctgattt tagtttgatc 300
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<210> 1352
 <211> 483
 <212> DNA
 <213> B.fragilis

<400> 1352
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 cgcaaagacg tatttcaaga ctgcctggtg ctctatccgg aagaggtctg gaatgaagaa 180
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 aagatagaaa tctgggagaa agaacgtgog gagaaactct ttatggaacc cgaagcattc 420
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 tga 483

<210> 1353
 <211> 2127
 <212> DNA
 <213> B.fragilis

<400> 1353
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<210> 1354

<211> 1131

<212> DNA

<213> B.fragilis

<400> 1354

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attattcaca	aagaattgct	aatcccgaat	ctctgcggta	tatttctggg	tgaaaaccgt	1080
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<210> 1355

<211> 270

<212> DNA

<213> B.fragilis

<400> 1355

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acaagaagac	ttcgtaacag	atattatggg	aaaaccatga	gaaatgctgt	tagaaaactt	120

cgttcaacta	ctgacaaagc	agaagcaact	gctatgtatc	cgggcatcgt	taagatggta	180
gacaagttag	ctaagacaaa	cgttattcat	aagaataaag	ctaacaatct	gaaatctaag	240
ttggccattt	acatcaacaa	gcttgcttaa				270

<210> 1356
 <211> 861
 <212> DNA
 <213> B.fragilis

<400> 1356	
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ccaaagtittg tegtctocta tctgaagaga attgtacatc aggaagaatt aaatgttttt	180
ctgcgcgatt cgaaagataa agtgggagtc gattttctgg gggcttgtct tgagttcttg	240
gatgcaaagt tggagggtgaa aggtctggaa aatattccga aagacggttt atatacgttc	300
gtgtccaatc atccgctggg aggacaggac ggtgtttctc tcggatatat ttggggacgt	360
catttcgatg ggaagggtgaa gtatctgggtg aatgatttgc tgatgaacct tcatggcttg	420
gcaccattgt gcattcctat taataaaaaca ggcaaacagg caaaagattt tcctaagatg	480
gtagaagccg gattcaagtc ggacgatcaa ctgataatgt ttcccgtctg actttgttcc	540
cggcggcaga acggagtgat tcgcgatcct gactggaaga aaacatttat cgtaaaaagt	600
gttcagtttc agcgtgatgt gattcctgtc cattttgaag ggcgttaact tgattttctt	660
tataatttgg ctaattttatg caaggcactg gggattaagt ttaattattgc tatgctttac	720
ctggcggacg agatgctgaa aaatcgccat aaaacattca cgtcacttt cggaataccc	780
attccgtggc aaacattcga taagtcgaaa actccggcag agtgggcaca atatgtgaaa	840
gatatcgtgt ataaactgta a	861

<210> 1357
 <211> 216
 <212> DNA
 <213> B.fragilis

<400> 1357	
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ctgccgttac gggtaacatt cccaggagtc actctgttgt tatcccgta agctgagctt	120
tctctttggg aactcctct tctcacctca tctctccgtc ccgaattgga acgtatggtt	180
accgatccga aatcggaacg gcgatgcgtg ttataa	216

<210> 1358
 <211> 348
 <212> DNA
 <213> B.fragilis

<400> 1358	
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cggttcaatc aaatgcagtt tcacccttac ctgaaagccg aaaagaaaaa acagcaatgg	120
catttcacag cagccgtaga caaaccttg tttccggcag accaattgtt cggttcactt	180
cccaaaggat tattcagtaa cctggaaggt ataaagacaa gtggcgaact ggcttatcat	240
ttttttctgg atgcaaattt tgccctgttg aacagtctta aaatggaaat cgaacctgaa	300
ggaaaggaat ttccgcatgg aaaactacgg ggtcacaaat ctggttaa	348

<210> 1359
 <211> 846
 <212> DNA
 <213> B.fragilis

<400> 1359	
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ctttctgatt ttgcttttgc gaagaaaggg atttacggca ttttacatgt catcatcctg	180

ctgctttccc	tgtttctggt	catcagcatc	tcgatagata	cgtttaagg	tatccctttt	240
tataaccaat	cggtttatat	gaaagttcag	ctatggattt	gtgtcttatt	tctgttcgat	300
ttcattctcg	agttgtttct	ttcgaaaaat	aagtggcact	atcttagtac	gcatttcata	360
tttttgttgg	tggcgatacc	ttaccagaat	attatatcct	atatgggatg	gactttttca	420
cccgaagtga	cttatatgat	tcgttttggt	cctttgggtc	gaggcggcta	tgcgatggct	480
attgtggtgg	ggtggcttac	ttataataag	gcttcgggac	tggttggttc	ctatctgact	540
atgttgcttg	ctactgttta	cttttcaagc	ctggcttttt	ttgtactcga	acacaaggctc	600
aatcccctgg	tgaccggtta	cggagatgcg	ccttggtggg	cgtttatgga	tgtgactacg	660
gtaggttcca	atattattgc	tgtcacctg	acgggacgtg	tactttcggt	gttgctggcg	720
gcactgggta	tgatgatgtt	cccgatcttt	acggtttatg	tcaccagcct	gattcaaaaa	780
aagaacaaag	agaaagagga	gtattataaa	caattggagg	cagctgacga	aagtaagcca	840
aaataa						846

<210> 1360

<211> 978

<212> DNA

<213> B.fragilis

<400> 1360

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ttgcacccca	aaataaggag	aatgaaccac	gtcaccactt	atatccgcca	ggctttacac	180
gatattttatc	caccgggaga	actcaggagt	ctcacaaaaa	tcatttggtg	tgatctgctg	240
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tgtgatttag	aaagcattgt	cgaacgattg	aagaaaaacg	agccgatcca	atatattcag	360
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cctgaaactg	aggagctggg	tgatctggta	gtgaaagaag	ctgcaaccgg	taccctgttg	480
ctggatatag	gaaccggtag	cgggtgtatt	gccatcagtc	tggtctaaaca	tattccgcag	540
gctgtgggtca	ccgcatggga	cgtatcggaa	gaggctcttg	ccattgccgg	ggagaataat	600
cgggaattga	aggccggagt	gcatttttag	aaaatggatg	ttctgtctgc	agaacctgtt	660
ggtgatgatc	aatatgatat	gattgtcagt	aatcctcctt	atgttacaga	gagcgaaaaa	720
aacgaaatgg	aacccaatgt	gttagattgg	gagcccagac	tggccctttt	tgtgccggac	780
aatgatccgt	tgcgctttta	tcggcgtatc	gcactcttag	gaagaaaaat	gttacgcctg	840
cacggcaggc	tctattttga	gatcaatcgg	gcttatgggtg	aagaggttct	ccaaatgctt	900
cacgaacaag	ggtacgaaga	actccgtttg	ataaaagata	tatcgggtaa	tgatcgaatt	960
gtaaccgcca	aacgatga					978

<210> 1361

<211> 576

<212> DNA

<213> B.fragilis

<400> 1361

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gcggaagaat	atcgctcgc	agaaacggga	gattacgaca	tttcagttag	tatgctgcaa	180
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atgagtagtt	acttcctgac	ccgtgcagga	aaaggaacca	gtattgagcg	cacaaaggct	300
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actgtcgaac	ccaaaccoga	catcgagccg	atacactata	acagtcatag	cggacaggaa	420
ttcaacctgg	tacttgaagg	ccgcatgatg	atcagtatag	atggaaaaga	cttgatatta	480
aacgaagggg	acagcctgta	cttcaattca	aaactacctc	atggaatgaa	agcactcgac	540
gggaaaacag	tacgtttcct	ggcagtaatc	atgtaa			576

<210> 1362

<211> 185

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (166), (167), (168), (170), (172)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1362

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aaagacagaa	caacaactaa	cgaaatgtcc	tataaagaac	aaatagattt	aaaccggata	120
cctaagcatg	tagtcgtcac	cgccgagtgc	aatgcatgct	ccattnnncn	cnggcctgcc	180
tcccc						185

<210> 1363

<211> 927

<212> DNA

<213> B.fragilis

<400> 1363

caagcagatg	cggcaatatg	tttttcggcg	gctaatacatt	cttacgtctg	ttttttatct	60
atctttgcag	taaacagaat	gaagattatg	agcattgaat	taggaaaatt	caaccagctt	120
gaggtagtca	agcaggtcga	tttcgggtatg	tatctggatg	ggggagaaga	gggagaaatc	180
ctgttgccca	cccgcctatg	acccgaagat	tgtaagttgg	gagactggtt	gaacgtcttc	240
ctttatctgg	ataatgaaga	acggttaata	gctactacat	tgacaccttt	ggtacaagta	300
ggggagtttg	cctgcctgga	agtatcgtgg	gtcaaccagt	tcggagcttt	tcttaactgg	360
ggattgatga	aggatctggt	tgtccctttc	agcgcgcaga	agatgaagat	gcaggtaggg	420
aataaatacg	ttatccatgc	ccatattgat	gatgaaagtt	tccggatcgt	agcttcggcc	480
aaagtagacc	gttacttatc	taaagagaaa	gcttcttctc	agcctggtga	agaagtgaac	540
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ggcttgctgt	atgatagtga	aatatttcag	actttacata	ccggcgatgt	actgaaagca	660
tacgtcaagc	aggtacgcga	agatggcaag	atagatctga	ttctccagaa	gccgggcttt	720
gaaaagatag	atgatttttc	aaagacactt	catcgctaca	tcacagagca	tgggggatgg	780
attggactta	cagataagag	tcttgcgcag	gagatttatg	acacgttcgg	tgtcagtaag	840
aagacattca	agaaggccgt	tggcgatttg	tacaagaagc	gtctgattct	tcttcatgaa	900
gacggcatcg	agttggtacg	tccctaa				927

<210> 1364

<211> 213

<212> DNA

<213> B.fragilis

<400> 1364

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caatatgctg	cctatacctt	tgtctttcat	agccacttcg	atagatgcgg	ctttcaggag	120
gcttttgaca	cttgctactt	cccatggact	gcccgcgaac	acttcaatct	gagaaatctt	180
tctgcttact	atcattttgt	cttaattggt	taa			213

<210> 1365

<211> 1374

<212> DNA

<213> B.fragilis

<400> 1365

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gaggtaaata	aggatataga	gcgatttacc	gttggacgtg	accgtgagat	ggatctttat	120
cttgcaaagc	atgatgtact	tggttcgatg	gctcatatca	cgatgctcga	aagtatcgga	180
ttgctcacia	aggaggaatt	agctcagttg	ctgaccgaac	tgaagatat	atatgcttct	240
gcgagagag	gcgagtttgt	aatagaagaa	ggagttgaag	acgtgcactc	gcaggtagaa	300
ctgatgctta	cgctcgtttt	gggtgatgtc	ggtaagaaga	ttcatagcgg	gcgttctcgt	360
aatgatcagg	tggtgcttga	tctgaaactt	ttcactcgta	ctcagatcag	agaagtagca	420
gaggctgtag	agcaattgtt	tcatgttctg	attcgtcaaa	gtgagcggtt	caagaatggt	480

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tgcaataaga	atcctttggg	ctccgctgcc	ggatatggct	cttcattccc	gctgaaccgc	660
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attaaggtga	acgagcatat	cctcgatgat	gataaatacc	tttttatttt	tagtgtagaa	1140
gagggtgaatc	gcctggcacg	tgaaggtatg	ccattccggg	atgcttataa	gaaagtaggg	1200
ctggatattg	aagccgggtc	cttttcgcat	gacaagcaag	tacatcacac	ccatgaagga	1260
agtattggca	atttgtgtaa	tgatgagatt	tccgcattga	tgcaacgtac	catcgagggt	1320
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<210> 1366

<211> 486

<212> DNA

<213> B.fragilis

<400> 1366

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tggggccttac	cttatgaagt	gattaaccga	atcatcgatc	gtcttggtgt	cgagaagttt	180
attgatgaag	aacgttatgt	tagagcgttt	gtcaacgata	agttccgttt	tgccaaatgg	240
ggtaaaatga	agattacaca	agctctgtat	atgaaaaaaa	ttcctcgtga	ggtaacttac	300
aggatatctga	atgacattga	cggggaagaa	tatcttgcca	ttttaggaga	tctgatagca	360
gcaaaacgta	aaagtataca	tgccaaagat	gaattcgagc	tgaatgggaa	attgattcgt	420
tttgccatga	gtagaggatt	tgaatggac	gatatccgtc	gctgtgtgca	ggtagaagaa	480
gagtaa						486

<210> 1367

<211> 1248

<212> DNA

<213> B.fragilis

<400> 1367

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gtagtggttg	cattcagcgg	aggcctcgat	acctctttca	ctgtaatgta	cctggccaag	120
gaaaaaggat	atgaagtgtg	tgcagcgtgt	gccaacacag	gtggcttcag	cgaagaacaa	180
ctgaaacaga	atgaagagaa	tgcctacaaa	ctgggtgctg	tgaatatatgt	cacactcgac	240
gtcactcagg	aatattacga	aaaaagtttg	aaatatatga	tattcggtaa	cgtactacgt	300
aacgggtacct	atcctatttc	tgtcagctcc	gaacgtatatt	tccaggcatt	ggccatcgca	360
cgtatgcca	aagagattgg	tgcggaagcc	attgcacacg	gttcgacagg	agccggtaac	420
gaccagattc	gtttcgacat	gacatttcct	gtcatgactc	cgggcgtaga	aattattacg	480
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ttcgaagcag	actttacaaa	actaaaatac	tcttataatg	tccgactatg	gggtacttca	600
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caagtaacga	aagagggaag	tgaacttctg	cgcttgaat	ttaagaatgg	tgaacttcac	720
gccgtgaatg	gagaagtgtt	cgaagataaa	attgccgcca	tccaaaaagt	ggaagagata	780
gggtgctgctt	acgggtattg	ccgtgatatg	catgtagggt	atactatcat	cggtatcaaa	840
ggacgtgtag	gattcgaagc	cgcgcgtcca	atgttgatca	tccgtgcaca	ccgtttcctt	900
gagaaataca	cattgagcaa	atggcaacaa	tattggaaag	atcaggtagc	taactgggat	960
gggtatgttcc	ttcatgaaag	ccaatacctg	gaaccgggtg	tgcgtgatat	cgaagcaatg	1020
cttcaagaat	cacaacgtaa	tgtgaacggt	acagccatcc	ttgagctccg	tccgttgtca	1080
ttctctactg	tccgtgtaga	atcacaagac	gacctggtaa	agaccaagtt	tgggtgaatat	1140
ggagaaatgc	aaaagggttg	gacggccgaa	gatgcaaaag	gcttcatcaa	ggtgacttct	1200
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<210> 1368
 <211> 501
 <212> DNA
 <213> B.fragilis

<400> 1368
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 gggggcccgta tcagatttgc tcccgatctc ttattggaaa atatgaagac tttgataaaa 120
 acggcccgaa ctaattttct gattatcgac gggcatcatt gtactgagaa aactgctgtt 180
 atagagacgg taaactcaat gatgctccaa acggtggagg gtgtcatcta tctttttcca 240
 tgttggacac aaacaccggc tgcgtttacg aggcttagag caaaaggagc ctttctcggt 300
 tctgccgatt atgacgggaa gtcagtgggc ggtctgaaaa tctttagtga gaaaggaggt 360
 atatgcagac tgagcaatcc ttggagggga agaaaacttc gggtcaccga gaatggaaaa 420
 cccgtctccg tgaaagaaca aaacaatgtc tgttcattta ttaccgaaa aggaagcact 480
 tatacagatag taggtcttta a 501

<210> 1369
 <211> 1602
 <212> DNA
 <213> B.fragilis

<400> 1369
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 gccttctatt atcttttgcg agctatcgta ttcttattc cgacatcact cgttgcggcg 180
 gaattggctg ccatgttcca ggacaaacag ggtggtgtgt tccgttgggt aggcgaagcg 240
 tacggaaaga aattgggatt ccttgccatc tgggtacaat ggattgaaag tacgatctgg 300
 tatccgactg tattgacatt cgggtgctgta tctatcgctt tcatcggaat gaatgataca 360
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 tggctggcta ccttcatctc actgaaagga atgggatggg taggtaaagt agctaaaatt 480
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 ttggcatccg gagggcattc caaccttgac ttccatagca gcttcttccc cgacctcacg 600
 aatttcgata acgtgggtatt agcgggcaagt atcttctct tttatgccgg tatggaaatg 660
 ggcggtatcc acgtaaaagga tatgcaaaac ccttcaaaga actatccgaa agcagtaatt 720
 atcgggtgcac ttattactgt aatcatcttc gtcttgggta cattctcact aggtatcatt 780
 atccccggcca aagatatcag cctgacacag agtttacttg ttggcttcga caactatatt 840
 agatatatcc atgcatcctg gttatcacgg atcatcgcca ttgctcttgc attcgggtgtg 900
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 cactgggaaa cacaagctaa accacaagtt gctccggcaa caacaactac cgccgggtccg 1500
 gcaacaagca gcgctaccac tatcggtagt acaacttctg ccccatcgac aggttccggc 1560
 tctgtttcat ccgataagga caccacacag aaacaaagt aa 1602

<210> 1370
 <211> 567
 <212> DNA
 <213> B.fragilis

<400> 1370
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 aaagcgttgt atcaagatct gaaagtgaat cgttttgccc gcggagggag taccatcacc 120

atgcagttgg	tgaaaagcgt	atctctgagt	cgaacacaaa	acatagcccg	caaactggaa	180
gaagctctga	ttgtctggct	gatagaaaca	gaacgcctta	cctccaaaga	acgaatgtac	240
gaagtatatc	tgaatatagt	agaatgggga	ccgctcgttt	atggagtgca	ggaagcagca	300
acctattatt	ttaaaaagcg	cccatctcaa	ctgacagccg	aagaatctat	ttttctggct	360
tccattattc	caaagccgaa	gcatttcocg	aattcgttta	acaatgatat	gcaactgaag	420
gagagcctgg	aaggctatta	ccgtttaata	accgaacgat	tagtgaaaaa	aggaatcatc	480
agtgaagtgg	cagccgacag	catccgcccc	gaaattaatg	taaccggcga	ggcaaagaaa	540
gatctgcaaa	gagacagcat	acaatag				567

<210> 1371

<211> 666

<212> DNA

<213> B.fragilis

<400> 1371

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gcacaagccg	gaagaatcag	tggaaataaat	atccaaagct	caggtgaggc	gattcttgct	120
tttgtggatg	gcgagcaaat	ctgcactccg	acgggagactt	gtttcattgc	taactattcg	180
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aaaggcgact	tgctgtttca	ggaatgggtc	tcaaatcccc	gtatgaatat	cagggatatt	300
cgggtgggct	ataatgatcg	tccctgatttc	tgtcccgatc	gtccgggtcg	tcccggtat	360
gatgtagtga	tgaaccgtac	agagttcgac	cgttttctga	gaagtgtgaa	agacaaacat	420
ttcgactcag	accgtaacaa	gctgattgaa	actacacttg	tttcgacagg	cttcacttcc	480
gaccaatgtc	tccaattagt	aaatctgttc	agtttcgata	gtgaaaagat	aaaactgatg	540
caggctatgt	atccacggat	tgttgataaa	cccaatttct	atctgggtcat	cgaaagcctc	600
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<210> 1372

<211> 1044

<212> DNA

<213> B.fragilis

<400> 1372

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<210> 1373

<211> 759

<212> DNA

<213> B.fragilis

<400> 1373

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tcgggacgga	gagatgaggt	gagaagagga	gtgtcccaaa	gagaaagctc	agcttcacgg	660
gataacaaca	gagtgaactc	tgggaatgtt	acccgtaccg	gcagaggaac	cagaagtacg	720
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<210> 1374

<211> 492

<212> DNA

<213> B.fragilis

<400> 1374

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agccaggaaac	gtgtgtacga	gaaacttgcc	gatcttagta	acctggaagc	tattaaagat	180
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tccgaagaag	aatgtaaact	aaaggtaact	attgggctgg	aaatcaatcc	gtttatgaaa	420
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<210> 1375

<211> 981

<212> DNA

<213> B.fragilis

<400> 1375

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aacgccggaa	acaaaattac	tgatgtacac	gagggacttt	acggagagtg	tgacctggct	180
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<210> 1376

<211> 687

<212> DNA

<213> B.fragilis

<400> 1376

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<210> 1377

<211> 783

<212> DNA

<213> B.fragilis

<400> 1377

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caagaattag	aaacactgat	ggccaatcta	ttcagcgaga	tgggtatggc	aatgattttg	480
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<210> 1378

<211> 693

<212> DNA

<213> B.fragilis

<400> 1378

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gttgcacttc	gtaccgggta	tattgaagaa	gaagacattg	caacgttaaa	cgaatggcgc	660
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<210> 1379

<211> 1377

<212> DNA

<213> B.fragilis

<400> 1379

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<210> 1380

<211> 612

<212> DNA

<213> B.fragilis

<400> 1380

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<210> 1381

<211> 1134

<212> DNA

<213> B.fragilis

<400> 1381

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<210> 1382

<211> 1242

<212> DNA

<213> B.fragilis

<400> 1382

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<210> 1383

<211> 1980

<212> DNA

<213> B.fragilis

<400> 1383

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<210> 1384

<211> 483

<212> DNA

<213> B.fragilis

<400> 1384

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gaatctgaca	ccattttggg	aacaattgcc	ggagacgata	ccattatgtt	ggtactacgt	420
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<210> 1385

<211> 1665

<212> DNA

<213> B.fragilis

<400> 1385

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<210> 1386

<211> 1005

<212> DNA

<213> B.fragilis

<400> 1386

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<210> 1387

<211> 2283

<212> DNA

<213> B.fragilis

<400> 1387

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<210> 1388

<211> 345

<212> DNA

<213> B. fragilis

<400> 1388

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gagaagggat	ataataacctg	tgggtgattgt	aaggaaactgg	atgattgtca	gatagtaggt	300
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<210> 1389

<211> 966

<212> DNA

<213> B. fragilis

<400> 1389

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gaggccatta	attggcatga	caaacctgtt	tcaccatttg	acaagacctc	cagagtttat	180
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gatgagtaca	atgcttacga	ccaaataggg	ttcagttata	ctcgtttcta	tgtcgaccac	720
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tacgttgacg	agttcgtgta	taggtataat	ctgaggggaca	tcagcaattc	cgacagactt	900
aactgtttcc	tttgttgcgc	tgacacacgt	tatacatata	agcaaatcag	aaaatcagcg	960
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<210> 1390
 <211> 183
 <212> DNA
 <213> B.fragilis

<400> 1390
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 aaaatgacaa atcgattact tatccggttat tccactcatg attttcaatg ctgcattcaa 180
 taa 183

<210> 1391
 <211> 417
 <212> DNA
 <213> B.fragilis

<400> 1391
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 gtcactccac ttatgattat ccgctctgtc cagcaactcg tttcgggaga aaaagtggta 180
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 gcttcggagg ataaccgctt tgccctctcac aacggattcg acatgataga aatcaaaaaa 300
 gcgatgaagg aaaacgaaac ccggaaaaaa gaaacggggg gccagtacca tcagccagca 360
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<210> 1392
 <211> 1002
 <212> DNA
 <213> B.fragilis

<400> 1392
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 aacaccttcc ggatttaccg gtttgtggta aatcccagga aggcaattat tcaggaactt 960
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<210> 1393
 <211> 969
 <212> DNA
 <213> B.fragilis

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<210> 1394

<211> 867

<212> DNA

<213> B.fragilis

<400> 1394

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<210> 1395

<211> 447

<212> DNA

<213> B.fragilis

<400> 1395

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<210> 1396

<211> 291

<212> DNA

<213> B.fragilis

<400> 1396

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tatatggtct	atcgagccaa	tgtaaagtgc	cctgttatcc	cggaattggt	tgaaactgcc	240
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<210> 1397

<211> 1401

<212> DNA

<213> B.fragilis

<400> 1397

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<210> 1398

<211> 237

<212> DNA

<213> B.fragilis

<400> 1398

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cgtggagtag	cgttgcaatt	ttctgctttc	cttactccta	cgcactatct	ttccgaaaag	180
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<210> 1399

<211> 1206

<212> DNA

<213> B.fragilis

<400> 1399

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<210> 1400

<211> 582

<212> DNA

<213> B.fragilis

<400> 1400

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gcctctctcc	tctcactatc	ggtaaaaaca	gtagagaaag	aaatgacccg	ggcactccgg	540
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<210> 1401

<211> 282

<212> DNA

<213> B.fragilis

<400> 1401

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gagctgacag	atcttaccgt	ggccttggtt	gcagggatga	tatctgcaca	gcctccccgg	180
acggcggcga	tggaagtctc	agtggcctgc	cttagggaa	acgcgaggac	ggggacgaac	240
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<210> 1402

<211> 891

<212> DNA

<213> B.fragilis

<400> 1402

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cctcatgaaa	ccgattgtat	tttgtttgta	atggaaggag	aactggaact	gtcctgtaac	180
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<210> 1403

<211> 372

<212> DNA

<213> B.fragilis

<400> 1403

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gtcaactttc	ctgtttatgg	tctgtcggaa	aacaaacgca	ccogttatcc	aatgatagcg	180
gctcttattg	accgatttaa	tcgtaaattc	ctggcaatac	atatgttgcc	gtatcttatt	240
ttgaccatag	aatatattgc	gaggcgagaa	atcttgatcg	attcccatct	tgtcctgtat	300
atattgatag	gatgtttggc	tgttgaagct	gatatggggg	ccgtttatac	gtatgttgat	360
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<210> 1404

<211> 489

<212> DNA

<213> B.fragilis

<400> 1404

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cagatcaagc	ctttgaaggc	tataaaaaga	aggttaaagt	cactcgggtg	cggtgagata	180
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gtgcagaatc	tgtcacggag	taatatcccg	catggagagt	taatcatgcg	aatccggatg	420
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<210> 1405

<211> 192

<212> DNA

<213> B.fragilis

<400> 1405

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gagccaaatt	ggatacaaaa	gttcagagac	ttctgttggt	tatataatta	caaaaacat	180
gccatatttt	aa					192

<210> 1406

<211> 1287

<212> DNA

<213> B.fragilis

<400> 1406

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tgtaatagtc	gcggggccta	tccattggct	gtgcaggctc	ttcataaacg	gaagaaaaaa	180
gtcttttata	cgggatacag	tattgagccc	tgtcagtttg	attccattag	cggacgggta	240
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gagaaaatga	ccagaatcta	tctgaaggaa	cttgaccggt	cggtagtgga	cgaagtgaac	1260
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<210> 1407

<211> 1572

<212> DNA

<213> B.fragilis

<400> 1407

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gtgaaccgta	agactgtacg	acggtatctg	aatatgacta	tggaggagtt	tgttaaaaaa	180
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<210> 1408

<211> 1437

<212> DNA

<213> B.fragilis

<400> 1408

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<210> 1409

<211> 474

<212> DNA

<213> B.fragilis

<400> 1409

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gcagaggcat	tgccattgct	tatagaccct	aaaaacggac	taataaaaaa	gccggaactt	420
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<210> 1410

<211> 267

<212> DNA

<213> B.fragilis

<400> 1410

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<210> 1411

<211> 189

<212> DNA

<213> B.fragilis

<400> 1411

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<210> 1412
<211> 204
<212> DNA
<213> B.fragilis

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<210> 1413
<211> 1584
<212> DNA
<213> B.fragilis

<400> 1413
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<210> 1414
<211> 564
<212> DNA
<213> B.fragilis

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<210> 1415

<211> 1305

<212> DNA

<213> B.fragilis

<400> 1415

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<210> 1416

<211> 975

<212> DNA

<213> B.fragilis

<400> 1416

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<210> 1417
 <211> 402
 <212> DNA
 <213> B.fragilis

<400> 1417
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<210> 1418
 <211> 969
 <212> DNA
 <213> B.fragilis

<400> 1418
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 tccgatacgg agtccatact ttaccgcaat attgactcgt ttgacagttt cgaggcttac 360
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<210> 1419
 <211> 729
 <212> DNA
 <213> B.fragilis

<400> 1419
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 catgccccga aatcggagggt gcgcatagag gcacggtacg aaaaggagtg gcaatatacc 180
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<210> 1420

<211> 204
 <212> DNA
 <213> B.fragilis

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 cctatccatg caggcactac aacttttcaa aaagagtcga tatgggtggt aagtaagcag 180
 gtaataccgc tatccgtagc ttga 204

<210> 1421
 <211> 651
 <212> DNA
 <213> B.fragilis

<400> 1421
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<210> 1422
 <211> 1296
 <212> DNA
 <213> B.fragilis

<400> 1422
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<210> 1423
 <211> 594

<212> DNA

<213> B.fragilis

<400> 1423

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gaagcgagac	gtatcacatt	tcaactcaac	acgacatatc	atacgcccaa	cgaggtacga	180
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gtaagcatcg	ggaacaatgc	cattgtcgca	gcgggagcag	tagtaacca	agatgtcccg	540
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<210> 1424

<211> 267

<212> DNA

<213> B.fragilis

<400> 1424

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tggatggatt	ccaactgcac	agatgaacag	tacatgtgca	attttgccga	acgttacgtg	180
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<210> 1425

<211> 2073

<212> DNA

<213> B.fragilis

<400> 1425

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caaaacacac	ctaactcgtga	gccactttct	atctctacct	tagataatcg	cttcttgaaa	180
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<210> 1426

<211> 252

<212> DNA

<213> B.fragilis

<400> 1426

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aatcaaataa	aagactccgc	aaaagaacag	tataaatcag	ttaccaacct	ctacttacca	180
cgaacgcaca	aaaactgtat	atgcacgtca	gtcccggaacg	ttaataacca	agaagccaag	240
cctggcagat	aa					252

<210> 1427

<211> 696

<212> DNA

<213> B.fragilis

<400> 1427

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caggcatgtg	gcgttaaacc	ttaccaattc	aaaaaggtgg	aagggtgtagg	ctactcacia	600
tacaacgagt	cggaaacacc	ggaacaaaac	cgctcgttag	aaatatattat	gtacgccagt	660
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<210> 1428

<211> 1275

<212> DNA

<213> B.fragilis

<400> 1428

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agtggagtg	tcaaagacaa	actcaacaaa	aagaaactgg	agtatgtcaa	tgtatcgata	180
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gagtcggttc	aggccaaaga	cattgaagcc	tcacatgtag	gttaacctca	ttcccgtatc	300
cctttaaaa	aagaaaatcc	cacagaacgg	attgtctggc	tactcctta	tgccaacctg	360
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gaatttcgaa	tggaagaccc	gaccagcatt	gacgaccgat	cccagtatgt	catcagcttc	780
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aaacaaaatc	atgtattctc	agacaaagtg	gataacttta	ccagtgacaa	cttttgggga	1200
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<210> 1429

<211> 951

<212> DNA

<213> B.fragilis

<400> 1429

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ggaaaccgtg	gcttcgtgtg	gaacgtctat	aagagaatga	gggacgaggg	cctgcttccc	180
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<210> 1430

<211> 1206

<212> DNA

<213> B.fragilis

<400> 1430

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accaaagcct	gggaaatagg	ggtaggtgga	gctcttatca	actgggacag	agtgactttc	180
tcgaattttc	gtcaggtcga	tggaactat	ctgtatcgaa	tgaatatcga	tcattctttt	240
ggcggtatcc	aactctatgc	agctcgtgaa	ttgaatcctt	ggttttatct	tgattttgcag	300
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tatatggccg	gtccgggact	tcaattccgg	tttaaccccat	tgtttaaatc	aaaatatgta	420
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gctgtgtata	gtgcattgct	gaaacgacaa	gtacctcaac	atatgttgaa	atggcgcgga	1080
gtcggatatc	atgctagtht	agtgccggct	tcaggthtccg	ataaagtcag	gatgggtgat	1140

cgaaaggtgt ctattgagag agtgacgaat tcagattatt ggggttggtt aacgaatgaa 1200
gaataa 1206

<210> 1431
<211> 906
<212> DNA
<213> B.fragilis

<400> 1431
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cctgtcgata ttttattcta ccgtttttta ttggcatata tttgcatctg gtttttctct 180
cctcgtgtgt tgctggctaa gagttggcag gacgaactgc ggttttagg actcggacta 240
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aaataa 906

<210> 1432
<211> 234
<212> DNA
<213> B.fragilis

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acgctccgga acgttcgggtg gaaagaaacg tcagtgtatg ttactccaaa agccatcata 180
aagatcggaa aacttcttcg ggcaggcagt tgcaaaaagc aaccgataaa ataa 234

<210> 1433
<211> 561
<212> DNA
<213> B.fragilis

<400> 1433
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agaatgatta catttttttga aatcacagga ttcaatcccc gctacgcac cgggaatccg 180
acggcactgg tggaaaagag aattgaggac gttgtcagaa tcatcaagtc ccaggaacgg 240
gatatactca agcccgctact tgagaaactc tccgccataa acaacacccc gcaggagtca 300
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ctcaaacgtc tgggcggcct gctgaaatac cagcttgatc cggagaagtt tccaaggata 480
aaatacagcg atgatgtaag agtccccgtc aacaccctgc agttgcttat caagaagatc 540
aacgaggaat atgtattgta a 561

<210> 1434
<211> 459
<212> DNA
<213> B.fragilis

<400> 1434

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acatttctga	ttgaaacttg	ctgggtcgaa	gaacggatta	tggaaagtata	tctaaactcc	180
atcgagatgg	gtaaaggtat	ttacgggtgt	caggcaaccg	ctaaatataa	attttaaactg	240
acagctgcca	aactgaccgg	gggacagtgt	gccctgatcg	cagcaacttt	accaaattcca	300
atacagattcg	actcggcaca	cccctcacct	tatatcaaac	gacgccaagg	acaaattctg	360
cgactgatga	atctggttcc	gaagttccct	cctgttgata	aggaaaaagc	gaaaggacaa	420
gatacaaaaa	aacaaaagaa	taagaaaaag	aagaaataa			459

<210> 1435

<211> 615

<212> DNA

<213> B.fragilis

<400> 1435

ctaataaaga	atacaataga	ctcccccaat	aatgacagat	caattatgta	caaaattata	60
ttcgtatttc	tggcaataat	gggcatagcc	actgcatcat	gtgccaaca	aaaacaaggc	120
gcaaacagaa	agcagcccaa	taacaaagt	cttatagcct	acttctcggc	gacaggaact	180
acagcaggtg	ctgctgaaaa	attgtctaag	gttacaggtg	gagaacttta	tgaaattact	240
ccagcccaac	cctatacaaa	tgctgacctc	aattggaata	acaaacaatc	gcgcagttcg	300
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gattatgacg	tgattttcgt	cggctatcct	atctggtgga	atcttgctcc	acgtattatc	420
aatacattca	tcgagagcta	tcatttgaaa	aacaagacaa	tcattctgtt	cgccacatcg	480
ggaagcagta	gcatcactaa	cagtatggca	actctgaaga	aaagttatcc	ogaactgatc	540
tggaaagagg	gaaaactgct	gaatggaatg	aacgaaaacg	atatccgcga	atggatcagt	600
aaattggact	attga					615

<210> 1436

<211> 279

<212> DNA

<213> B.fragilis

<400> 1436

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aaaaatgagt	tgtataaatc	tgtgcaatct	atagtataaa	agagttttga	aactctctct	180
tttattcttt	gtgaaatctg	ctccgacaaa	cacgaaataa	tattaaatca	tttgtacgct	240
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<210> 1437

<211> 318

<212> DNA

<213> B.fragilis

<400> 1437

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cacaatggcg	accaatggaa	agtaaagcaa	gaaaatgctc	aacgtagttc	tggttaatttc	180
agaacacaac	aagaagcatt	tgagcgtgct	cgtgaaatcg	ctattaagaa	cggtcaagaa	240
gttgctatac	acggattaga	tggacgtatt	cgtgaaaagc	atagctatgg	caatgaccca	300
taccaccag	aaggttaa					318

<210> 1438

<211> 621

<212> DNA

<213> B.fragilis

<400> 1438

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tataactcat	tggtaaaatt	gagaaataat	cgcgaaaacg	catttgccga	cattgatgta	180
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aagattacat	tggaagctta	tccggacctg	aaggccaacc	aaaacttcct	tcagctacag	420
gaagagattt	cggacgtaga	aaataagctg	gctgccgtac	gccgctactt	taattcggcc	480
acaaaggaac	tgaacaatgc	tgtacagaca	ttcccttcta	acctgattgc	caacatgttt	540
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<210> 1439

<211> 1311

<212> DNA

<213> B.fragilis

<400> 1439

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gattttccgac	gaagagggtg	cgggaaggcgg	ctccggcttc	gacgtggatg	tggaacgactg	180
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acagccatgt	tggaagttg	cagcaacgac	gagaccgtgg	aaatggcaca	gtctaaggcc	360
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acagacaaac	cgcttaatcc	tatcaagttt	gaggttgaca	atattactga	ctggaacaaa	1260
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<210> 1440

<211> 222

<212> DNA

<213> B.fragilis

<400> 1440

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cttgctcttc	cttatcagga	atttactaag	ggacctccgg	cccttagccc	gggacgcttc	180
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<210> 1441

<211> 2664

<212> DNA

<213> B.fragilis

<400> 1441

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<210> 1442

<211> 264

<212> DNA

<213> B.fragilis

<400> 1442

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 gaaggcgaag gccggtccat gtcactctca caggaggaaa gacagatact gccggaaacg 180
 agtgtaaaaa gcagaaaatg cgaaaaggca tccttcgagg aatgtaatgt aaaatgggaa 240
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<210> 1443

<211> 204

<212> DNA
<213> B.fragilis

<400> 1443
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gcgacttgcc agaaaaaggg ctga 204

<210> 1444
<211> 186
<212> DNA
<213> B.fragilis

<400> 1444
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ggatga 186

<210> 1445
<211> 516
<212> DNA
<213> B.fragilis

<400> 1445
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cagagattgc aacaggaact gaaggacttt gtttga 516

<210> 1446
<211> 2235
<212> DNA
<213> B.fragilis

<400> 1446
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gagaattatt	ggacttccac	cgtataacg	gaccgggaa	ccaccgctta	tacatatata	2160
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<210> 1447

<211> 1494

<212> DNA

<213> B.fragilis

<400> 1447

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<210> 1448

<211> 216

<212> DNA

<213> B.fragilis

<400> 1448
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tacctaaat cactacctaa aatcaatctt tttattaatg aaaaatacct aatcaaacaa 180
agtccttcag ttcctgttgc aatctctgac gggtaa 216

<210> 1449
<211> 1281
<212> DNA
<213> B.fragilis

<400> 1449
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tgatagaca gtgtgatgag tcaggagtat ctgtgtgata gagatatgtc atcacctgct 180
gctccggact atttccagaa accggaagcg tttctgaaaa aagccgtcgc ttccatggat 240
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<210> 1450
<211> 612
<212> DNA
<213> B.fragilis

<400> 1450
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gaacgttctg aaatactgaa ttttaatgca agcgggtggag tttctaagtc tgttcaagtt 180
atccaaaatt cgatgcctta ctttccaatc agatttccct ttgtactgaa tatgaacaaa 240
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ggaagtactc aaaaaatgct catctacgac ctttccagta atgtaaccga aatcgtagct 420
catattattg acagtatgag aacctatgat gcaaacttta tctcttcaaa tgcaaatatg 480
gggagaatat ggggtgacct tggattatta taccaaaaat tactcaagat tatttcagaa 540
gattatacaa aaggaggcta cgagattcgc ataaattcag tgcttgcaat gaaatttgtt 600
tttgtggaat aa 612

<210> 1451
<211> 1167
<212> DNA
<213> B.fragilis

<400> 1451

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<210> 1452

<211> 876

<212> DNA

<213> B.fragilis

<400> 1452

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aatagtgttt	ctccttgtat	tcttttcctt	cttgatggag	aggtgtctat	tgatagtggg	180
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<210> 1453

<211> 1248

<212> DNA

<213> B.fragilis

<400> 1453

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<210> 1454

<211> 852

<212> DNA

<213> B.fragilis

<400> 1454

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<210> 1455

<211> 1785

<212> DNA

<213> B.fragilis

<400> 1455

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catgccggta	ttaatatgat	attaagagat	aataatcagc	ctgaactcag	cattgacgat	1020
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gctaattttt	gtggacgcat	cattgaggta	tgtgccaagc	aagggtgctt	ggtcaataaa	1740
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<210> 1456

<211> 459

<212> DNA

<213> B.fragilis

<400> 1456

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tcattaaaa	tactgaatat	gaaatttagac	gaaaacattt	tgaagacctg	tcaaggactt	180
gtaatgaact	gtaattgtaa	ggttttaatc	cttaacgtat	tgggtgaaca	ccgtgtattc	240
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caagacatca	ccactcttgt	cttgaatatc	gggcataact	ttgccaatgg	tatgaccgaa	360
cagaccttat	tggaaactgac	ccaatctatt	cacaaggaa	atttcaagtt	tggaaactgat	420
aattacctgt	ggataacaaa	agttgatttg	aatagataa			459

<210> 1457

<211> 2319

<212> DNA

<213> B.fragilis

<400> 1457

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ggaatgtcag	cttatgaatt	ttggaaagag	aatgtagaga	atggagtgat	ttcttggcct	180
aagaaagaga	ctgaaataac	tgattttttt	aagtatttaa	aaggtaagga	cggtctggat	240
ggaaaaagtg	cttttgaact	gtggaaggaa	gaagtagcta	ctgggtgctc	ggataatcct	300
caccgcccgg	gaagtatgtg	gcctgtatcc	cagaataatc	ttagagattt	ttggtattat	360
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gatgctgttc	caccggtagt	tacgatcggg	gataatggta	attgggtgat	tgatggagta	540
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ggagctacaa	tctattcggg	aggagcaggt	agcactttta	tctactctag	caatgtgtct	2220
ttaggagttc	tcaagaagaa	agcagataac	ggtacgtatt	atgttgagaa	tacatataaa	2280
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<210> 1458

<211> 549

<212> DNA

<213> B.fragilis

<400> 1458

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gagttcagcc	acgggggtga	atacgtgtct	ctggcacgcg	gtgccttggc	tggtatggcg	180
caggcgggat	ggttgaacag	cggacacacg	tctgatgaag	ccgtaccgt	gctgtatgat	240
tgtacggtag	aagatttcgg	cacacaggct	ttgggtcggt	ctttcggaat	acctgatttc	300
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ttgaagaacg	gaaaaatcaa	gtcgttcgat	ttcgacgtga	ccgaccaggt	ggtggcgcaa	420
ccgcagggag	gtgtcatcgt	ggtgaagggc	atcgagattt	ccgacgaaga	gggtacggaa	480
ggcggtctcg	gcttcgacgt	ggatgtggac	gactggggag	attacgagga	catcgaactt	540
cctcttttaa						549

<210> 1459

<211> 261

<212> DNA

<213> B.fragilis

<400> 1459

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aagaacattg	catctgcagg	tggaaatatt	gtcgttaatg	cagaagattt	ttcagcgtat	120
gatttaaaga	atattgctga	aaacggagta	gcaacaaagg	caaagctaac	catcaaaaac	180
gcaggtggat	tatctggata	tgattgcaaa	aatattgcat	cagccaatcc	aggggaatgta	240
acatttgatt	ttagcgaata	a				261

<210> 1460

<211> 705

<212> DNA

<213> B.fragilis

<400> 1460

acattgtgga	taataaaaagg	aagtgccttg	atactcgaag	aatcgccaat	tcaacaaaaa	60
gtacaaaacga	ggcacagtgg	gcaacctata	tcaagtgggc	tgttcactctg	tgtgtttgta	120
caagcgtttg	gcgatgcttt	cgagttcaca	cagggtggcag	tccactttct	ttgtaataac	180
gtaattttctc	actggctgtc	tgagaaaaaac	tcgaaaaatt	tcgccattat	gaaaaagtat	240
ttcgttttat	cagtatttat	tatgctgatt	ggagcattta	caaatgttca	aggtaaaaaat	300
tctgcaactc	ccgataaagg	agtgttagtt	catggaaaacg	tccgtttatg	caactatgaa	360
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tacgacggct	cggacaagac	atacggcatc	tatatcaatg	tccgagggga	tattatcaat	480
ttgggtgtca	aatataaaaag	tagcgggaaca	gaatcttata	catacgaagg	aacggacagg	540
gtaacaggac	gaaagggtgt	tgtcgttaaca	aaacaaaagt	tgagttggta	tttgaataac	600

aatggagttg attctcatac agaggttgaa agtccaaagg ggataatcgt tacogttcct 660
gccacttata cagtgttttc agtagttcct attaagaata agtag 705

<210> 1461
<211> 849
<212> DNA
<213> B.fragilis

<400> 1461
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caacttgggtg attttgcccc taaatttgcg gaactcaacg acgatgtcct tttcggcgaa 180
atctggagcc gcaactgaaa actcagtcct cgtgaccgta gtttgggttac gatcacttca 240
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ggggttagatg caaaggccgc tttccagcgt gaaatgatat tcccgatagg agaacctaac 480
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gttaatatct ccaatgtcac gttcgaaccc ggttgccgaa ataattggca cgttcacat 600
gcgaagaaaag gtggcggaca gatgttgatc ggtatagcag gccgcggctg gtatcaggaa 660
gagggtaaac cggcggtaga gattcttccc ggtacagtca tacatatccc tgccaacgtg 720
aaacactggc atgggtgaac agccgaaagt tggttcgcac accttgcatt cgaaattccc 780
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ccccaataa 849

<210> 1462
<211> 186
<212> DNA
<213> B.fragilis

<220>
<221> unsure
<222> (159)
<223> Identity of nucleotide sequences at the above locations are unknown.

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acagagtgcg agaaaacctg ccgtacagcc gaacgttttc tagagcatgg cactgtgtat 120
gagccgggca ttggccatac aggtgcggat gaaagccgnc aaaagaaaaa tgagcttttc 180
cattaa 186

<210> 1463
<211> 225
<212> DNA
<213> B.fragilis

<400> 1463
tatttgatg ttgcaccgga tcacataaaa ttgaacttac agttcaaaaa cggtttttat 60
cacttaaaaa aacaggatga cggatggctc actacagaga taaatcttgt accattttctc 120
tcagtaaagt tcttaactgc actcttgttt atacagaaac ttttctactt tcaggaatta 180
atattgtcga atggatgcaa agcactaaaa actcaaagca attaa 225

<210> 1464
<211> 1911
<212> DNA
<213> B.fragilis

<400> 1464
acctttaatg tgatatttag tatgaaacaa atgatgaaaa aatatctata tatggcagct 60

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gtggctgttg taggtacagg ctctctgatg tgcgtcttcta aagacgaatt tgccggacag 120
aataccaatc cctccacagt ctcaaaaccc aacgtacgct atttattttac tcaatgtgcc 180
atgagttttc agccggccga ttatcttcag tggtttgctg gtttcgatgc aatgtctacc 240
tgggtgcagg caactgcctc aggaggtgga aactccagca aattgaatat ggtaactcag 300
accggctgtg gctatcaggc caacgaggtg ctctcgttata cgaatgaaat aaagcatcag 360
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gaggcagaaa tggcccgtta tgggtgggact ctgactccga aatacgatac gcaggaagaa 540
ttgttcgaac tctggctgaa acagcttgac gagacaatta actatctgag agagaacaat 600
ccgcaagacg tgcttggtgc gcaggatttt atttatagag gaaaacttga taaatgggct 660
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caggggtata cgtatgaagg tgagatgagt aattcacctg tgacgttaag caaagaacgt 1860
gtctggtatg ataaagaggg accggctttt ggtacaggct ctcaacagta a 1911

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<210> 1465

<211> 375

<212> DNA

<213> B.fragilis

<400> 1465

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aaaaaggatc tgaccgagat tatggtaatg atatacagg ctaatgctac gactggaaaa 180
cttccgtata ttgaacgggc aagagatctg gttgtaggag tcaagggtccg ttttagactg 240
ttgcaagata tgcggcatat cagtgtgaag cagtatgcgg cgtttgcca acagggtggag 300
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<210> 1466

<211> 1750

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (2)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1466

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cttgggagta	agtttaaagc	aagaaaccgc	acaggatcgg	catattatat	ttcgccctgag	180
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aatatgtatg	aagaagacgg	tttcggtctt	cgcccgaaca	ttagtttgag	aggaacgaaa	300
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cgtgcagtat						1750

<210> 1467

<211> 186

<212> DNA

<213> B.fragilis

<400> 1467

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ggtacgggta	gcgggggaga	ctaccggggc	ggcgggtacag	gcggatgcga	cgggtggagga	120
gaagatctct	tctgttgccg	tttttctggt	gtcgggtcgac	gggagtggaa	aggaggattg	180
gaatga						186

<210> 1468

<211> 1152

<212> DNA

<213> B.fragilis

<400> 1468

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gtcgacctga	cgcgttatct	gctgatgacg	cgccccctgt	ttgaagagag	caacgggtgtg	1020
gagctcagcg	accaggatta	ccttgattac	gaagatcggt	tcaacgtgat	tttctacctt	1080
accccgatgg	gaaagctgga	ggcgctgaac	attaacggat	ggattatcag	actgaacgat	1140
gcacaactgt	aa					1152

<210> 1469

<211> 879

<212> DNA

<213> B.fragilis

<400> 1469

cgtaaaaaag	aaatgaaaaa	actaaagtac	atgagtatga	tgggggttggc	tgctttattg	60
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gaagcgagag	cttataccac	agtgaaccatt	gccgtaccga	atggtgtggc	ggagacaagg	180
gcctccgatc	cgacggcgga	tactgacgat	acgaatatgg	atatcggttt	aacggatgaa	240
tacaaagtga	cgaaggccaa	tctgtatctg	tttccgggag	gaacgggtag	tagctttggg	300
agcgctaagt	tgacagagat	tatttccatc	agccagttta	cgcaaaccac	cactactact	360
accgaccaga	agaccattgt	atggaccagt	aagaaaacag	ccctgacccc	gggagactat	420
cgtattttata	tagtggtgaa	cggtacggtc	aatggggtgg	gtgacagtga	caagggaact	480
ctgaccgaag	ctgcttttct	cgcaaagaca	acggctgctg	ctacgagtgt	gatagctgct	540
gtaccgagtg	acggactggg	aatggcgagc	cgttctccca	acagtaataa	ctcgaatact	600
cttccttata	ttgccagga	gataaccaaa	gacccggagc	agaccattgc	ggcaacagtg	660
gagcgtgtga	tgggaaagat	tacggtgact	gcgggaggaa	ccagtgcgtc	ttctgctgct	720
actgttaata	aatatacttc	gttttctacc	acagttagctc	agatcaacaa	tattaaggat	780
atcaccctaa	aaactcatta	tgtagtccac	gccggaaaag	agggatatta	tttccgtcat	840
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<210> 1470

<211> 753

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (170)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1470

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ggcaattggg	atctgcaagg	atcaagcgca	tttggcttgt	cgtctttcgg	cactttttcc	120
ggaacttata	cggatatgcc	gggctactct	tccggggcgg	tggaaactan	agtcgccgct	180
tactgctatg	aaaacacgat	gctgaaggat	aaacagaaga	acggatatac	aaccggcatc	240
gtattttaaag	cggaaatagc	tccgagtaaa	atgatgaaaa	aaagggtcttc	gggcgggtgg	300
gtggaagaaa	ctactacaat	tggttcgatt	ggtgaaatct	tctaccattc	cggtatcttc	360
tacaaagata	ttgaagcgct	gaaagaagcc	ggtgtattac	tggcagacgg	aactacttcc	420
agtttcggcca	gcggtgtccc	tgccgacctg	aaaaagaacg	acgtccagtg	tttcaagaaa	480
ggaaataaccg	atggcaagtt	cttttgttat	tatccgtatt	ggatcaaaca	tctcccctcg	540
gatacacgag	aagatgtgat	ggagttcggc	attgtccgca	acaatgtcta	tcaagtaacc	600
gtcgccagta	ttcaagggtg	cggcaaagac	ggtgtaaccg	aaaatatcat	taccgatacc	660
gaaaccgatg	atccgactac	cgtattgctg	aatgtgaagt	taagtatcaa	accttgggta	720
gtgcgtgcga	atagtgcctg	attgggcccgt	taa			753

<210> 1471

<211> 1488

<212> DNA

<213> B.fragilis

<400> 1471

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ttatatgtta	aaataaaaaag	tcttatgaaa	gagaagatac	gatcgaccgc	tttaagaatg	120
tgctttcggg	agatgccgcc	ggcagtggtc	ttcctgacgc	tctttgcaact	gtgcttcggg	180
gcgctgtctg	tccgtgcggc	agatccgtcc	ggaagagtag	ccctttccgc	cgtagcaatg	240
cagcgtgcgg	gtggacaggt	atatgtctcg	tttgccgtaa	agatagcccc	ccgtgcagtg	300
cgtgcccgtc	accgctgggt	gattaccctt	tgtctgggca	acgcctcgga	tagtgtgttg	360
cttgccccgt	ttgtgtgtgac	gggacgcac	atggcgcgcg	aggaaaatca	gcgggcgcta	420
ttggccggcc	ttccggaccg	tgacgtcaat	catcggtgga	ccgcccga	tggagacacc	480
ttcttgtata	ccgatacgtt	gcgctatgcc	ccgtggatgg	agaatggctt	gaacctgcgg	540
ctcgacatcg	accgggaagg	ttgctgccc	gtacagacag	tgggaagcat	cgctcctcc	600
ggcgcttttc	cggtggcttt	gccctatcgt	ccgtcggtta	gtgagctcac	tccgaggggtg	660
agccggacgg	tggcggaaca	tgcggatgac	tatccgttcc	tgtgcgaggc	aggcagccgc	720
ccccctgcag	aaagtggcat	cggtattcgc	ttccgtgcgg	catcggcagt	ggtggatacg	780
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tccgtgcgca	tgaacctgcc	tgtatcgttg	tttgaactga	atgccggagg	agtagactgg	1020
gacaggtcgg	ccgaactggg	gaatgggagt	gacatgacat	ataaggagga	agtgcctcgt	1080
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cgtgtgcagt	atgccaaccg	ccctgacagc	gtggcgagata	cgggtgaaccg	tgcgatagaa	1260
gccattcggg	ggcggaagta	tgaagaggca	ttccggttgc	tgaagacggt	ggaggcggac	1320
gaacgctcgt	ggaatgtacg	gggagctctg	catctgttgt	gcggagacga	caagggaagcc	1380
gggctatggc	tgcatagagc	ggtgaaagcc	ggaaaccggg	aagcgggaaga	aaaccttaaa	1440
aagatgaatg	cggaaacgacg	ggccgctacc	atcgggtataa	cgcaataa		1488

<210> 1472

<211> 339

<212> DNA

<213> B.fragilis

<400> 1472

gccccgctat	tgcctttgtc	aagtcattct	acggacacct	tcttggtgtg	acatgcgggt	60
gggggagaat	ccaacctgag	ccgggtgcac	ctcctttttg	tttcccggtg	ggtttcttcc	120
cgctacgagg	ggtgggcgct	gatgccgggg	ttttcatcgg	gttactcgtg	ggtgctcggc	180
aaacgctgga	atctggaggc	taccataggt	gcagggtggg	tgcattgcca	atacaaagct	240
tttaattgtc	cggtctgtgg	tgaatatcgg	ggagcgaaca	agaaaaattt	tctggcgccg	300
accgtagcgg	gcatcagctc	gatttatatg	ttaaaataa			339

<210> 1473

<211> 1035

<212> DNA

<213> B.fragilis

<400> 1473

cgtactgcgt	cgccgtttctc	tccatccggc	acggcgtctg	tgaacggaag	atctatgaaa	60
tcgtcgggaag	attcaaaaag	gagtgtagcg	tccatgcagt	ataaatgccc	tccgtttttt	120
gttttcatgg	gaaaaactga	agaattttgc	tgcccggaaa	tacaaacaca	tatattacac	180
gacaaaatga	ttatgaaaaa	ggaaaagact	tactcccgtg	ctccgctccc	tttcgtgggg	240
cagaagcgca	tgttcgtatc	ggaattcaaa	aagatcctga	aacattttga	tgacaaaacg	300
atatttgtcg	acctgttcgg	cggctccggc	ctgctatcac	acattaccaa	acgtgaaagg	360
ccggatgcgg	tggtcatata	caatgacct	gacaactacc	gcgagcggtt	ggaaaacatt	420
gaccggacca	atacctgtct	gagagatctc	cgtaaaatag	tcgggatata	tccccgccat	480
cagaagatta	ccggaaaaat	gcgcgaggct	ttccttgaac	gcatcaggct	ggaggagaca	540
accggtttcg	tggactatct	tacctctctc	acttccctac	tgttttccgg	aaaatacgca	600
caaaacatgg	aggaacttga	aggattgtat	ttttataaca	agatacgcca	gtctgactac	660
cgggtgtgacg	gctatctgga	cgggcttgag	gtagtctgct	acgactataa	ggaactggca	720

gacacatacg	gggtgtttcc	gggagtggta	ttcctggttg	atccccocta	tatgggaacg	780
gatatcagta	catacaagat	ggactggaag	ctggcggatt	acctggatgt	cctgctggta	840
ctgaaaggac	acccgtttgt	ctatttctact	tccgggaaat	cccccatact	ggatTTTTgc	900
cgctggatgg	aagagcatcc	cgggatcggg	aatcctttca	agggagccgg	ccgggtccaca	960
cttaccgcac	ggatgaatta	caactcctcc	tataccgata	tcattgctcta	caaagacctg	1020
ccaagggcgg	cctga					1035

<210> 1474

<211> 264

<212> DNA

<213> B.fragilis

<400> 1474

gcgcgcgcca	caaccacata	catacagttc	attacacttt	ccgcccattc	aatgggtacgt	60
gcgacaacgg	ttgcaccatc	cttgctcttc	aaggtaatac	ccgtacaggc	tcccgcgggt	120
atTTgcggaa	cgctacataa	aactgacatc	aataatgctg	ataattttgt	attcatactt	180
tctatttttaa	tggtcgttta	tggtagtgta	acacattcca	ttcccgaaag	gttgattaca	240
atagagagta	attatttcatt	ttaa				264

<210> 1475

<211> 435

<212> DNA

<213> B.fragilis

<400> 1475

aatttgaaaa	cgcataaaga	agtaacttca	aataaaagta	aaacactgga	ttttgtaata	60
agtaaaacaa	tgaaaatatt	tagatatata	ttgctcgctt	cgcttacctg	tacgcttttc	120
tcattgcggcc	cggatgaact	gataccggaa	tccgtgccac	cggtggtgaa	tcccggggat	180
aaggacgagc	cgggtgaaga	accggaggag	ccggaagagc	ctgaaaagat	acagttagcc	240
atcaccgcat	cattgcagaa	catgcagcag	accaggggaa	tcatagaggc	ttttgctccc	300
ggccatgaaa	tgggagtctt	tgtcggaaaca	agtcagacag	atgaagcagc	aggtataaaa	360
aacgcctcct	atctttttga	tgggaaagta	tggaatgccg	gacaggatgt	accggtggaa	420
gcggaacgcc	gtctt					435

<210> 1476

<211> 351

<212> DNA

<213> B.fragilis

<400> 1476

catacagatg	cgcatacccg	cacgaccggg	ggtaaatacc	cttgctcgcg	gatgcgcttt	60
tatctgtata	tgaatgattg	gctttgcaaa	gataaaaaaa	tattcgctat	gacactattt	120
gagatTTTTaa	atTTtaatat	agaactactg	gaacgtctga	cccgcattgg	tttcaaaccg	180
gatgactata	aatatatcga	cctgtacaag	gagtatgaac	agatgcgccc	gcaggggtgat	240
aaggtgacgt	actgcgtcgc	cgttctctcc	atccggcacg	gcgtctgtga	acggaagatc	300
tatgaaatcg	tcggaagatt	caaaaaggag	tgtacgctcc	atgcagtata	a	351

<210> 1477

<211> 1101

<212> DNA

<213> B.fragilis

<400> 1477

acgaccatta	aaatagaaag	tatgaatata	aaattatcag	cattattgat	gtcagtttta	60
tgtagcggtc	cgaaaatacc	ggcgggagcc	tgtacgggta	ttaccttgaa	gagcaaggat	120
ggtgcaaccg	ttgtcgacag	taccattgaa	tgggcggaaa	gtgtaatgaa	ctgtatgtat	180
gtgggttgtgc	cgcgcgctca	agagttgcag	tactgactc	cctccggtat	ggatggactt	240
aagttcaggg	caaagcatgg	ctttgtgggc	ctggcggtag	agcagaagga	atTTgtgggtg	300
gagggcatga	acgaaaaggg	actttccgcc	ggattatact	atTTtccgaa	ctatggtagg	360

tatcctgttt	atgatgcggc	acagagggac	aagagtcttg	cggattttca	gttggtatca	420
tatgtgctgg	cagaatgcag	cacgtagat	gaagtgaagg	aggcccttcc	gcaggtgcgt	480
gtcatcaata	ttgatccccg	ttcgtccacg	gtgcattggc	gctttaccga	agcatccgga	540
agacaggtgg	tgttgagat	tgtaaatgaa	atgatgaact	tctacgacaa	tccattgggc	600
gtgtaacca	attcacggg	tcttgaatgg	cattggacca	atctgaacaa	ttacatcaac	660
ctacaaccgg	gcacgttacc	tgaacataac	ttcgggcccgt	tggagccgaa	gtctttcggg	720
catggcagtg	gtctgctggg	acttcccgtg	gattttacac	ctccatcccg	ttttgtgcgt	780
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gcgttccata	ttctgaacaa	ctttgatatt	ccgacgggta	gtgaacagcc	ctggggaaag	900
gcgtcagcca	atgtaccgag	tgccaccag	tttaccgttg	cgtgcgatat	acggggaccag	960
aagggtttatt	atcgtaccat	gtacaacagc	aacatccgtt	gcattgattt	gaaaacgata	1020
aatttcgaca	atgtaaaata	tcaagcggat	cctttgggatg	aaacgaagga	gcaaccgggtg	1080
gaaatgaaag	tgataaaata	g				1101

<210> 1478

<211> 189

<212> DNA

<213> B.fragilis

<400> 1478

aagggtgaca	aattgaatca	aattgctctt	ctgtatatct	caaccctgtg	tggactgtat	60
acgtcatttg	ttgctttcgt	tgtgctgcaa	catagccaat	ctgctaacca	cagaactgta	120
tacatggcaa	atggtaaaga	gaatgtcaag	cgtaaccgta	tgaaagggtc	ggacaagaca	180
aagtactaa						189

<210> 1479

<211> 426

<212> DNA

<213> B.fragilis

<400> 1479

ctcaataaga	agaagctaag	ttttctatct	ctaaagggtga	taattacaga	agctatcaaa	60
caactttttt	cttctcacac	attccaaacg	ctctcccttg	aaagtaggac	attattagac	120
gaatataatt	tcacaaaatc	catgatagca	aatcttttgg	ataaacaaga	aaaactctac	180
cttgtagcct	ctactaaaaa	ggaaaatgaa	cttttagcag	ggattatcct	taatgatgaa	240
attatttate	tactaaaatt	ttcaaaggca	tctgataaca	tttatactct	ttacaacgaa	300
acaaacgaac	ctatatgcga	tgtcaaatat	gattttgaaa	aacaaaatat	agttattatt	360
agcaactatg	gaaatgatgc	tatccccct	acaacacaag	ttggtacagt	tttgtttgta	420
atatag						426

<210> 1480

<211> 816

<212> DNA

<213> B.fragilis

<400> 1480

tcaaggagat	gcaaacgtat	gaaaacaatt	acaacggcat	gtgtgaacca	taaggagggt	60
gtcgcaaaga	caacctcgct	gctgaacctg	gcagccggga	tcgcacggat	gtataagaaa	120
agggtctgca	ttatcgatgc	ggatccgcag	gcgaatacga	caatggcagc	gttcggggag	180
gaaatggcaa	gccttccccg	ggaggttctg	ctcgagagtg	cgctacagga	ctgtatgcag	240
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ttcagggaaa	tagtaaaggg	gctggaagag	aagtatgacc	acatacttat	cgactgtccg	420
ccatcattgg	ggatcatcac	gcagaacgcg	ctgatggcaa	gcgattacgt	gatcatacct	480
acggacggga	attacttcgc	catgaaagga	attgaaaaga	tacactatat	catcggcctg	540
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gccaggagaa	agctggatat	ggatatcagg	gagagtctgg	taagaagttt	gggagatggt	660
gtcttcgaaa	cggtaatacg	cagcaatgtc	gccctgggag	aggcacaata	caaggcacag	720
agcatatctt	actatgcgcc	ttcctcaaac	ggggctgatg	actacaggga	gctggtcaag	780

gagttcctgg gcagaattaa aaaaataaat aaatag

816

<210> 1481

<211> 294

<212> DNA

<213> B.fragilis

<400> 1481

aagaaaggca	ggattatgaa	agactttaca	tcgaaaggaa	tatccctgga	aaacatgggtg	60
ggagaaaccc	cgggaaaaga	aaaagggtatg	acaggaaaaa	catcacccaa	aacgaaccag	120
accgttgac	tgacggaaga	tctgaaatgg	gagttacgga	cgttcgcttc	ggaccatcgc	180
tgcaggggag	tcaagacact	gcttgaaacg	atgatagaat	gtttcgtcag	ggaagacggt	240
acgcttgacc	gtgacaagtt	agaaggcttc	tggcgggaat	atgtcgaaaa	ataa	294

<210> 1482

<211> 1569

<212> DNA

<213> B.fragilis

<400> 1482

ttgtatacca	tgaaaaaaat	atcaatttta	attgcggctt	taaccctcag	cataagcctg	60
aaaccacttg	ccgctcagaa	taaaaagggtt	tttatcatcg	ataaacagac	cgtctatcaa	120
gaaatagaca	acttcagcgc	ctcagacgct	tggcgtctgc	ccttcattgg	taaaaactgg	180
cctcaagaga	aaaaagaaaa	aattgccgac	ttactattca	aacgtgaatt	tgacgaaaaa	240
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cgtgaacgag	gcatgaacaa	ctttctgttt	ttcacgaact	cagctcccta	ctttatgact	480
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gatgactttg	cccgtttctt	ggtgaagagt	gcccaacatt	tcctggaaca	aggctttcac	600
gtaaattaca	tcagcccga	caatgagcca	aacgggcaat	ggcatgccaa	ttccttccaa	660
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gactattggg	cggcctaccc	cgctaccttg	ctgggtggata	tacgtaaccg	aattcacaaa	960
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gtagcccgta	tcattccaaa	tgatctaact	ttggcgaatg	cttcggcttg	gcaatggtgg	1140
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ggattgtcac	tacaatatga	cggtgaaatc	tctaccacca	aaatgctgtg	gactactgcc	1260
aactacagtt	tctttgtgcg	tccgggtatg	aaacgtatcg	ccgtaaaacc	tacctataag	1320
gtaagtgact	tggaagccgc	tacttcaactg	atgatttcat	cgtatactga	tgggaaagaa	1380
gtggtgaccg	tagccatcaa	ctattcaaag	gaaaatcagg	tgattagcct	aaactgtgac	1440
catgcccaca	aaggaaaagt	ttatctgacc	accatcgaca	agaatctgcg	atacatgggt	1500
gaacaaccgc	tgaaaaagtt	acagctgcc	gcacgttcgg	tagctaccat	tgtagtcgaa	1560
gacaactaa						1569

<210> 1483

<211> 222

<212> DNA

<213> B.fragilis

<400> 1483

agcgtgtttg	ttgccagcat	gaaacggcag	ggtgtagaag	tgcatttcag	gcacatggaa	60
cagagcaata	agctacagga	catcgatttc	actatggaca	gctaccattt	caatggttcc	120
aaagtgggca	ggcgtttcag	ttattctaag	tttggtacaa	ctcttttttc	gtgggctgta	180
ccgcctctgt	ttgccagtgg	aagcctctgc	tgccggatat	ga		222

<210> 1484
 <211> 1269
 <212> DNA
 <213> B.fragilis

<400> 1484
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 ccagaaactg atgtagtgga attcatcctt gatgaactaa atgacatcac caaagacgga 180
 gcactggacg taagtccaaa acagaaagga agaattacac gcgggtgctgc tttggccttg 240
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 gactacaaaa accaaacccat cattgaattc tgaacgtaa ttgatggcgg ttggtcggca 480
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 caagctaaac tgagagaatt gctcagaaga gagcgccgtg tagaatttgc tttcgagggc 1020
 ttgagaagag atgatatcat ccgttggggac attggccaagg acgtactgaa tgggtccaatc 1080
 tatgcttcta accaagggtac cgtagatatg gatacaagca ttccccaaga ggagcgtgct 1140
 acaattttcc aagggtgaaaa gaaccagggtg gtactcgaga tccgtaaatt caggaaccgt 1200
 tacatgccga ttccacaagc tgaattggat aagaaccgga acttgaaaca aactaacttc 1260
 aaaatataa 1269

<210> 1485
 <211> 246
 <212> DNA
 <213> B.fragilis

<400> 1485
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 ggtataaata aatggactta tttattttata aaatcgacca cccggccgat ggcctatcag 180
 ccgatggag atagagggtca aaacttaaat ccgatcttaa atgtcggagc ggccagcaca 240
 ctgtag 246

<210> 1486
 <211> 459
 <212> DNA
 <213> B.fragilis

<400> 1486
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 tacataagtg aagtgataaa acagggtcata gccgaaaagc aggtgacaaa ggccgagctt 180
 gcccgtaggt tgggggtaaa accacagagt gtggactatc tgctgacacg gaaaagtatc 240
 gatacgggata cctgttatag cttgtcgttg gcgctggatt atgatttcgc tgttttatat 300
 tccataaaga aagaacatgc tcttgctacg gacgaagagt ctccgtttta agtgggaaat 360
 gcaaagatca gtttagagat cgagttgcgt cccgatgaaa tgttgaaatt gaacctgaaa 420
 cagaagattg cagacctgtt ggaaggaaa ggaagtgaa 459

<210> 1487
 <211> 2250
 <212> DNA

<213> B.fragilis

<400> 1487

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cgccatccaa	tgaccgttat	aagatgcgc	atcttttttg	tccaccagtt	cgggtcccggc	180
aatgcttcc	ttagccccgg	tctgattcag	gaaattgata	accgtggcac	tcaacgcaag	240
atgcttggtc	accgtccagt	tgataacctcc	gaagggttcc	cagcgtccgt	tgaaatagta	300
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aatatccct	gtggcatcga	tctccccac	cgtaccgtct	ttaaagggtca	cactcgtttc	480
atacttcttg	taagtcggac	tttgataagt	gaagaggaag	tggaaagtga	agcccttaaa	540
cggcttgatc	actgcatccg	tctgccagcc	gatggtttgg	atgtcataac	tcaacggggc	600
ggcgagaatc	tcagtctggt	cattcggatt	aatcagggtc	agtgtcgagt	tgttattcgt	660
cttcgagata	taagagaaca	gagaggtcag	actgatccaa	tccgtgttat	aatagatccc	720
ggcacgtccc	aggggaacag	agattttatc	ggtattgggc	atagtggccg	gtgcaaagtt	780
cgacaagccg	ggacgctgtg	tgttgtaagt	gaaatcggcg	gtaaaaccaa	attcacgggt	840
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atttacatta	tgccgattag	aggatatagac	tacggggagt	cgtttttcga	gtacattttac	2160
gtctccacct	ggcaagccga	tagagatttc	gcggggacca	ttggcgctcg	aagcgttcag	2220
cataacatta	cgattgcctt	cttcctttga				2250

<210> 1488

<211> 411

<212> DNA

<213> B.fragilis

<400> 1488

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tactataaag	ctgatacataa	ctattctggt	cagaacacat	tggcttatac	attacaaact	180
atagctgatg	gcttggctga	ttatgatcag	ttgattttag	tccagaaaca	agctattgct	240
gctgctgatg	aaaatatagc	taatgccgct	tcagttgtat	caaaggaaca	ggctattgct	300
aatcaggaga	aaaccattgc	tgaccttgaa	aatagtttgg	ctgtaaataa	acctattttac	360
aatgattatt	tagctcagat	caaagcttta	gtaggtgact	ctgcagaata	a	411

<210> 1489

<211> 786

<212> DNA

<213> *B. fragilis*

<220>

<221> unsure

<222> (510)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1489

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gtagcagcta	ctgttgata	caatagttac	acaagtgtca	cagccccttc	ggggctgctg	180
actgactatg	aagtcagagc	gctctcaacc	aactgggcag	acaaaaagct	gatgggtggg	240
tttgaaggag	gctggttctt	caaagatcag	tggaaactaa	atttgggtgg	cggtgtcagc	300
ttcacgaata	accccggtta	tccggctggt	cccggcacaa	tagacgattc	gaataagaat	360
aactcggctg	acgagaatat	gggagagatt	cctaattatc	gtgccgtagc	cgatgctcag	420
tcggttcgcct	ataatgtgtc	agcagggtgt	gatcggttatt	tcaacatcaa	gcgtgttcct	480
aacctgatgt	ggtatacagg	tattcgcgtn	aggtttgctt	acggtgaaaa	tgaaatgaag	540
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ttgactatcg	gtgtcgacta	ctttgttttt	cctgcactct	atatcgggtc	gcagatcgat	660
ccgtttgctt	atacgtacaa	caagactacg	tataatccgc	aagcaggctc	tggcgatctg	720
tcggcgagaca	gccacaacta	cagtgtgctg	gccgctccga	catttaagat	cggatttaag	780
ttttga						786

<210> 1490

<211> 795

<212> DNA

<213> *B. fragilis*

<400> 1490

aaataccatg	ttatcatgaa	aacaactttt	atgaatgtaa	gtagaggagt	gatcgggtgct	60
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caagaaggcg	acagccttac	ggtgatccat	attacaaatc	ctacacagta	tttacttttg	180
cccgtcgagg	agaagactcc	cgaagcacag	gtctgcattg	cttcggactc	ggttccggta	240
gacatggacg	tacgcctgtc	aagggagaaa	gtggactatt	ttgttccttt	tgttttgctt	300
aagggagaga	aagaggtagc	cgtgcgtatc	cgtcacttgc	cgaaggaggc	tttgtgttgg	360
aaagaactta	agctttcgga	tacttttgat	acgaccaata	cagaccaata	ccgtcccttg	420
tatcaccata	ctccgctcta	cggatggatg	aacgatgcca	acggactggt	atataaagat	480
ggtgagtatc	acttgttcta	tcagtataat	ccttacggct	cgatgtgggg	caacatgcac	540
tggggacatt	cggtgagcaa	ggatctggtg	cactgggaac	atctggagcc	ggcacttgcc	600
cgcgatacgc	tgggacatat	tttctccggc	agttcagtag	tggatgatgc	caatacagcc	660
ggatatgggg	caggggccat	cgttgccctc	tacacttcgg	ccagtgataa	gaacgggcag	720
atacaatgta	tggcctatag	cactgacaac	ggacgtacgt	ttaccaataa	tgaaaagaat	780
ccgtcttcac	cacgg					795

<210> 1491

<211> 2373

<212> DNA

<213> *B. fragilis*

<400> 1491

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gcttgcttgc	tgatagcggg	cttcacagct	gcacaggaaa	agaaagaatc	tgctcaaaca	180
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ctccccgtag	tctatacctc	taatccgcat	aatgtaaata	cgcactggcg	tggagacagc	360
agtctcgggc	acgtcgggtt	gctcaaaatc	tccgaaaccg	ccattactac	cggcaatatc	420
ggttatgctg	taaactcttt	taccagttg	ggaacagaaa	agtttcgtgg	aatcgtcaat	480
tatagtacca	atcacttttg	caagcagcag	ttcgatgcta	atatcagcgg	tggtatgggg	540


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aaaggatggt tctacagtgg aagcgtttac caaaattttg atccgggcag tttcaaactg 600
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aaaaaagatg cggcatctta taacggtcat tggatggcgg gcagttatat tcgtccgttt 2340
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<210> 1492
<211> 384
<212> DNA
<213> B.fragilis

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<400> 1492
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gtggtcgtca atcttcggga ctttgatttt aaacaccaac ttcttcattt gaactactat 180
cctctaaatc ctttaggttg aaaaatttta ctcaagtgtt caaccagccg tttattccgt 240
tcttcgtttg caggaatat taatccttta ctggaaaaat cccgttgtca acagactccc 300
actgtcaaga ccctatttta ccgtaccgcc ttaacaatac gcctggcacc tggttcatgg 360
aacaatccct acaccctctg ttaa 384

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<210> 1493
<211> 1203
<212> DNA
<213> B.fragilis

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<400> 1493
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aaaaatgaca tgataagcaa tatcatgcc ttttggtatg aatatgggtg ggatcgcaag 120
aacggagggtg tttataacct cgtcgaccgt gatggctcag tgatggatac caccaaatct 180
gtttgggttcc aaggagatt tgcttttaca tgttcatatg catataatca cattgagcgt 240
aatactgaat ggttggcagc tgcgaaaagc actctcgatt tcatagaagc acattgtttt 300
gatacggatg gacgtatgtt ttttgaagta accgagaccg gattacctat tcgtaaaccgt 360
cgttatgtct tttctgaaac atttgcgtct attgcaatgt ccgaatatgc cattgcatca 420

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ggagatcata	ggtatgctgt	aaaagctttg	aaattgttca	atgatatccg	tcacttcctt	480
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gcaactctat	atgcgtatca	agctactaaa	aatgaaaaat	atctggctat	gcataaacag	1020
atcagtgact	ggacttatgc	ccatttttct	gacgcagagt	ttggtgaatg	gtatgggtat	1080
ctccatcgtg	acggaacgat	ttctcagcct	gcgaaaggaa	atctgtttaa	gggaccattc	1140
cacattccta	gaatgatgac	gaaaggctac	gcactttgtc	aggaattact	gtcagaaaaa	1200
taa						1203

<210> 1494

<211> 222

<212> DNA

<213> B.fragilis

<400> 1494

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aaagtaggtc	gtatcgaaat	atctggtaaa	ggtattgtga	agaaatcgcc	ttgggggtgc	120
tgcggatcta	tcctttctaa	tatgtatcaa	attcgggatt	tcaatggagc	attattgaca	180
atgggttgtt	tcttggaaac	agtagacggt	cgttattcct	ag		222

<210> 1495

<211> 1254

<212> DNA

<213> B.fragilis

<400> 1495

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atgcaggtag	atattgtgga	acttcagtcg	gcaaccaatt	ttggccggtt	aatggctggt	180
ttcctttgga	tttatggcct	tatgagcccg	atttcgggta	tgattgccga	tagattgaat	240
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ctttatatct	cggccgggtc	ttctcttatt	gccgattatc	atactgaaaa	gtcacgttct	420
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agttttgttg	ctggttgtgg	agccggatta	ttattcggta	tcggttatgg	tatttttgat	1020
gctaataata	tgctatttct	ttgtcagttt	gtctcttcaa	agtaccgtgc	gacagcatat	1080
ggatcatatg	atatgaccgg	ggtatttgca	ggagcgttta	tcacggattt	gttgggttaag	1140
tggaccgatg	gaggaaaatt	agggttaggt	tttgccatgt	tagctatcat	cgtattttatt	1200
gctttggcag	tgcaactcta	cttcctgcgt	ccgaagacag	ataatatgga	ataa	1254

<210> 1496

<211> 450

<212> DNA

<213> B.fragilis

<400> 1496
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 atccttccat gcctagctat gggaggtccc cagggaggta ttggaggaaac tgccaactac 180
 aatggtgtaa atctggttgg tattatagaa gcatggaaag caggtgatct tgagaaagca 240
 cgtgaattac aaaatttctc tcaggaagtt attaatgtca tttgtcattt ccgcgaaaat 300
 atcgtagggtg gaaaacgaat catgaagttg ataggattgg atttgggtta aaatcgtact 360
 cctttccaga atatgacgga cgatgaagaa gtacgtatga agcccgaacc gcaagccatt 420
 catttcttcg atcgttgcaa taagttttaa 450

<210> 1497
 <211> 453
 <212> DNA
 <213> B.fragilis

<400> 1497
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 tttaaaactc tgtttgatta cgtaaaaaca catgatttat ttcatgccga attaggacga 120
 attgagatag atggtgataa tttattttatc aataacgtga atcctgagtg tgttgacagt 180
 gacaagcaag ttttggaact acatcgcgat tatattgatg tacatatattt gttggaaggt 240
 actgagacta ttggttgga ggctatcgaa gatctgaaag atgaagtga accttatgag 300
 gcgaacgggtg attgtgctct ttactctgat gcacctacca cctttgttga tttgcttcct 360
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<210> 1498
 <211> 2094
 <212> DNA
 <213> B.fragilis

<220>
 <221> unsure
 <222> (2002)
 <223> Identity of nucleotide sequences at the above locations are unknown.

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<210> 1499

<211> 222

<212> DNA

<213> B.fragilis

<400> 1499

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<211> 990

<212> DNA

<213> B.fragilis

<400> 1500

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<210> 1501

<211> 351

<212> DNA

<213> B.fragilis

<400> 1501

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351

<210> 1502

<211> 609

<212> DNA

<213> B.fragilis

<400> 1502

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<210> 1503

<211> 1298

<212> DNA

<213> B.fragilis

<400> 1503

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<210> 1504

<211> 1341

<212> DNA

<213> B.fragilis

<400> 1504

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gggcccaatc	ccgacagctg	gtatacccg	cagattgctt	tgcaaaaaaa	gacccctgaag	180
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<210> 1505

<211> 903

<212> DNA

<213> B.fragilis

<400> 1505

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<210> 1506

<211> 219

<212> DNA

<213> B.fragilis

<400> 1506

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<210> 1507

<211> 3000

<212> DNA

<213> B.fragilis

<400> 1507

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<210> 1508

<211> 207

<212> DNA

<213> B.fragilis

<400> 1508

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 <211> 864
 <212> DNA
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cagggtggga	tgaatttctt	tttctacacg	cgggacgcca	cgtcttcccg	gtacaaggca	240
aagaagttca	gtcactggct	tgctccagcc	gagctccgtt	attggacctg	tgacgttttc	300
aacggctggg	tcttcgggtt	gcatgcccat	ggcggccaga	tgaatatcgg	aggtgtcgat	360
gtcccttctg	tgcttcagaa	aggggacgga	aacatgaagg	accaccgtta	cgagggttat	420
ttctggggag	gcgggttgag	cgccggttac	cagtgggtgc	tttccaaccg	tttcaatata	480
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gataaaaata	atatatctat	aaatcttgcc	aagaagaata	ttaatcatct	aaggcaaaca	180
aattatctaa	ttaacaacaa	tatatattat	gaatataata	cgcagcccat	tatttattgt	240
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<213> B.fragilis

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atgcatataa	gtttatgctt	cctttccagg	aaacaaggaa	gcgtcaaagt	tctaactaat	180
aaaaaactta	tggcaacagt	taaaacagta	ttggtaaaag	gaaggagcaa	ccggtccggc	240
aaattcccggt	tagtcgtgca	ggttcttcac	aagcgaagga	aaaaggttgt	ttatacagga	300
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gaattcccg	tgagacttca	cgcggcccg	cattcatggg	ccacgatagc	caaggtgaac	1260
ggtgcctcgg	ttcatgttat	tggtgagtg	ctggggcata	cgtcggaaaa	aacgacccga	1320
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<211> 1461

<212> DNA

<213> B.fragilis

<400> 1513

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caggttcaga	tcccagtttt	tataagacag	ggagttattc	catcccagg	tgaaatcggg	240
attggccttg	ccgatgacct	tgcggtcgcc	accgtctatc	atctgatttc	catctacatc	300
cgtgtaagt	tcatgtccgt	tttcatccaa	gccggtccat	tcatatcccc	aaaaagtacc	360
gatggcctca	cccggtttga	taatgggtgg	ataatcaacc	ataccggcag	ccggactgga	420
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accgttcaag	gtggaggtcc	attggaaccg	gtcattctgc	ataatccggg	cggtcacgct	540
caaatcaata	ccacgattac	tgatttcgcc	gtcattcacc	caaaaagagt	taccgccgac	600
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atccttcatg	aaatcctcat	tgctcaacgt	ccaagctcgg	gcaatagaag	gaaagtaccc	960
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ttgcagcatc	agacgataag	tatcgttatt	gcccatacca	ctcttggtcc	ccactcgttt	1320
ggagctgaaa	ctataacttt	tcccgtcata	atagtccacg	ccattgggtg	tggtgaatgt	1380
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 <212> DNA
 <213> B.fragilis

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 aagaacaaac tgcattgagga cccggcaaaa atgaccgtcc gcctcgttga atgccacctg 180
 cacgctgact ggaacgagat acagaaggcc ggaggtcccc accaaaatcc ggaatccccg 240
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 ggaaacaact ttaccccgcc cccggtttac ctgatgttta tctattacta caattccaaa 420
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<223> Identity of nucleotide sequences at the above locations are unknown.

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cgaacaggca	cgccgcaacc	cacaacccca	gaccgcgcgcg	cgcgccgcgc	acgggggagca	180
agggagagag	ggaggaagag	acggaggaan	acgcgaaaaa	nnaaggaaga	aaaaaanaaa	240
anaaccaaga	naaannaana	aaannnnnaaa	naaaaaaaa	agaaaaaaan	nnnaaaaaaa	300
anaaaaaaaa	aaaaaaaana	annnnnnnaaa	aaaaaaaana	aaaaaaaana	aaacaaaaana	360
aaaaaaaaaa	aaagggnana	aaaaaaaaaaa	aaaannanaa	naaaannaan	naaaaaaaa	420
aaaaaaaaann	naaaaaanna	gnnnnnaann	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	480
nanannnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	540
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	600
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	660
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	720
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tga						783

<210> 1517

<211> 330

<212> DNA

<213> B.fragilis

<400> 1517

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tgctctgaca	aacggggaga	gcgtaaagag	acagatggta	caatttttcag	gagaatcgtg	180
acgggagtg	ccctgttcgt	tatgggatac	gcacgaatgt	tccccgtgaa	catgaaaagc	240
tttcacgagg	aaaaagggca	tcaatgtcag	caacaacata	catgctatga	cagcccgtg	300
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<210> 1518

<211> 780

<212> DNA

<213> B.fragilis

<220>

<221> unsure

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cgcgaaacagg	cacgcccga	cccacaaccc	cagaccgcg	ggcgcgccgc	gcacggggag	180
caagggagag	agggaggaag	agacggagga	anacgcgaaa	aannaaggaa	gaaaaaaaana	240
aaanaaccaa	ganaaannaa	aaaaannnna	aanaaaaaaa	aaagaaaaaa	annnnnaaaaa	300
aaanaaaaaa	aaaaaaaaaa	naannnnnna	aaaaaaaan	aaaaaaaaaa	aaaaacaaaaa	360
naaaaaaaaa	aaaaagggna	naaaaaaaaa	aaaaaannan	anaaaaaanna	annnaaaaaaa	420
aaaaaaaan	nnnnnaaaaan	nagnnnnnna	nnnnnnnnnn	nnnnnnnnann	nnnnnnnnnnn	480
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnnn	540
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnnn	600
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnnn	660
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnnn	720
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<210> 1519

<211> 1539

<212> DNA

<213> B.fragilis

<220>

<221> unsure

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<223> Identity of nucleotide sequences at the above locations are unknown.

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aacatgcagc	tgtcccagtg	gcagggggat	gatataacga	ccaatccggg	gagcaacaaa	180
cagtctgccg	cagaaatgga	caagtttgcc	gcagcaaaca	acaacaaggg	tgtcaaagat	240
gcgtggaaca	tgcatattgc	cattgttaaag	gctgccaat	tgatcataca	gggggcttct	300
aaaacacct	ccactcaaga	tgagataaat	atcggcctcg	ggcaggctaa	attctggagg	360
gcatacgctt	attttaccct	ggtgcgactt	tggggaccgc	tgccgatgaa	tctggacaat	420
gtcaacgatg	attataccaa	acctctatcc	cccggtggaag	aagtgtatgg	tcatattgtg	480
caggacctga	ccgaagctga	ggccgtattg	cctacggggt	acagtggcag	ccccgccttt	540

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aaggcgaagg aggtcattga ggggtgtgaac agaggtgaat acgagtataa gctcgataag 720
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<211> 837

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<223> Identity of nucleotide sequences at the above locations are unknown.

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 <212> DNA
 <213> B.fragilis

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 <213> B.fragilis

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 <212> DNA
 <213> B.fragilis

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<212> DNA
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<210> 1534

<211> 189

<212> DNA

<213> B.fragilis

<400> 1534

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<211> 711

<212> DNA

<213> B.fragilis

<400> 1535

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<210> 1536

<211> 1353

<212> DNA

<213> B.fragilis

<400> 1536

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<210> 1537

<211> 255

<212> DNA

<213> B.fragilis

<400> 1537

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gcggagcgta	tttttgatgt	aaaactttgt	atagaatctg	atttatcgtg	tatcagggcc	180
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<210> 1538

<211> 1290

<212> DNA

<213> B.fragilis

<400> 1538

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<210> 1539

<211> 1578

<212> DNA

<213> B.fragilis

<400> 1539

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<211> 429

<212> DNA

<213> B.fragilis

<400> 1540

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<210> 1541

<211> 1341

<212> DNA

<213> B.fragilis

<400> 1541

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<210> 1542

<211> 864

<212> DNA

<213> B.fragilis

<400> 1542

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<210> 1543

<211> 1080

<212> DNA

<213> B.fragilis

<400> 1543

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<210> 1544
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 <212> DNA
 <213> B.fragilis

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<210> 1545
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 <212> DNA
 <213> B.fragilis

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<210> 1546
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 <212> DNA
 <213> B.fragilis

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caatatttgcg	agctatga					1518

<210> 1547

<211> 240

<212> DNA

<213> B.fragilis

<400> 1547

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aatgaagaac	atgataaaga	gtttcacaag	tataatgagc	cacagggtac	gtccccagg	180
tcatgcttcg	aaagccttct	acatagaaat	tccagatgtg	gagcagtgta	ttcttcataa	240

<210> 1548

<211> 2073

<212> DNA

<213> B.fragilis

<400> 1548

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ccttatcggg	ctagtggaaa	ctttatggta	caatgggatt	gtccgggatt	aaagtggcc	540
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cgttcgggttc	aagagagtgt	taagaccgtt	gacggacgtg	cgaaagtgt	tgccggactg	1920
atgtttcccg	atataaagaa	cgattttgag	aaagcattgg	atgaagcatt	tgataacggt	1980
gcatccgggtg	tttcatttctt	tgacggacca	tcagacgaat	atctgcatcg	gtttaaagcc	2040
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<210> 1549

<211> 894

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (778)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1549

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aaagcttttc	cggtaaaaaa	agagattcct	ggcaagaaaa	gttttcttga	attcgatggc	180
gtatttcaag	aagcagagat	tttcgtcaac	ggacacttgg	caggcactca	caaaggagga	240
tataccggat	tttccatcga	catatcagct	tacctgaaag	aagggaaaaa	cctggtagcc	300
gtccgagtaa	acaactgttg	gcgcctgat	cttgccccgc	gtgcaggcga	acatgtattt	360
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cacatacggg	cagacgtatg	taatgcttca	ggaaaaacag	acacttaccg	actcctgacc	540
accgttgtcg	atgcacaagg	caaagaagtg	tcttcggttt	ccacatccca	agtattgccc	600
gacaatgcaa	cctacacatt	taaacaacaa	accaaagaaa	ttcaggcacc	tcaactgtgg	660
catcccaatc	atccggcact	atataaagtg	ataagctcac	tctatcacgg	acaagaattg	720
atagaccgtt	acgaaacaac	attcggattt	cgctgggttc	aatggactgc	agaccggnga	780
tttttcctga	atggggagca	cctttatttt	aaaggagcca	atgttcacct	agatcatgcc	840
ggatggggag	acgctgtaac	ccaaaaccgg	aatgccaaaa	aaaatctccg	gtag	894

<210> 1550

<211> 1026

<212> DNA

<213> B.fragilis

<400> 1550

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tattttatca	aagcgggtag	aagcctcggg	gcggaacact	gctttgtcac	ttatgacgag	120
ttgtcggccg	ttcttcccgga	ttgtcgcgat	acggttgtaa	agctggagcc	tccggtgttt	180
cgggaggcgg	actttcggaa	atacaatttg	ctctgcgagg	agtatagaag	tctgttgctc	240
cgactggccg	atatggataa	gtcggaaagt	gtacactttc	tgaatgaacc	ggctgcaatt	300
ctttgtgcac	tcgataaagt	gtatactcag	cggaaactga	ccggggcccg	cctgaaaaca	360
actccgttgc	tttcgggatgc	gcttagcaca	tttgatgatt	tggccgccat	actttgccgg	420
cagaagaggg	gaggatttct	gaaaccccg	tatggttccg	gggcccgttg	gattatggct	480
gtcagggtata	atcatcgccg	ggatgaatgg	gtggcctata	cgacgatgtc	ctgggaagga	540
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gccatgaagg	ccttggggct	gcgatatgcg	ggcatagacg	tgctgatagc	ccggaatacg	900
gacacacctt	atattataga	ggtcaatggg	cagggagacc	atatctatca	ggatatgtat	960
acggaaaata	agatatatgc	caatcagata	aaaacgatag	aatcactttt	caatggaaat	1020
agatga						1026

<210> 1551

<211> 1236

<212> DNA
<213> B.fragilis

<400> 1551

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gcaggcggag	gggtttggct	ctttggcggt	tctacggcca	agcacaaagt	gacctatgcc	120
acggcaaccg	taagcaaagg	cgagatatcg	gagtcggtaa	ccgccacagg	aactatcgaa	180
ccggtaacag	aagtagaagt	cggtacacag	gtatccggaa	ttatcgacaa	aatctatgtg	240
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ggcgataatg	acatagtga	ggactgtgag	ggcgaaacata	aaatatggac	acgtgaagga	1020
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acccaaggtg	cttcggaagg	catggtagtt	gtcaccgaag	ccaccattgg	aaatatgcog	1140
ggcggcaatg	tatcgctgag	aggcggacag	gaaggcggag	gagaacaaag	tccgtttatg	1200
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<210> 1552

<211> 621

<212> DNA

<213> B.fragilis

<400> 1552

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tttgacagcg	acaaggcgca	gcaggccgtg	caggagctca	gcaagttgct	acgctatgtg	180
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gccttttaaac	acggcatctc	ccccaccgaa	ctgagtttca	tccacatcct	catctctgaa	420
aacaaagagg	agatccggtg	tgagatacgc	aatagttatc	atcccaaaaac	caacacggat	480
aaaagcggat	cgggtatcgg	gctcgaacag	gtaaggaagc	gcctcgaact	ctcttatccc	540
ggacgttatc	aatgggataa	agccatctcc	ccggatggca	aagaatatat	atcgaaatta	600
ttaatatatta	atcatccata	g				621

<210> 1553

<211> 780

<212> DNA

<213> B.fragilis

<400> 1553

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gaacgactga	aagtgttttg	ggtagatgaa	cgttgtgtgc	ctcccgaaaa	ttcggacagt	300
aattatggca	tgatgcggtc	gttggttgctg	agtattgtac	ctattccgta	cgagaatgtg	360
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atgaaagaag	tgccggtgga	gaatgagttc	ccgctatattg	acgtagtgtc	gctgggagca	480
ggtaatgacg	gacatacgtc	gtctatcttt	cccggacagg	aagaattgct	ttcaactgat	540

catatatatg	aggcgaattt	taatccgaat	aacgggtcaaa	agagaatagc	tttgacagga	600
cttccgattt	tgaatgcccg	aaggatcatc	ttcctgataa	caggaagggt	gaaaagtccg	660
gttgtagaag	atatcttcta	ttcgggagat	accggaccgg	ccgcctatat	agcgcatcat	720
gccgataacg	tggaactatt	tatggataat	gcagctgctg	aaaaagtcac	tcgcgataa	780

<210> 1554

<211> 1281

<212> DNA

<213> B.fragilis

<400> 1554

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gaagaacagg	aacctcaaca	ggagaaacag	gataaggaaa	aatggacaat	gcagggttgc	180
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<210> 1555

<211> 1260

<212> DNA

<213> B.fragilis

<400> 1555

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acttccgtta	cgcgtaatct	gatgacatca	gatgggtccc	gttttaagat	cgatacagtt	180
acgtacgata	aaattccggc	tgaatatgcc	cggaaaatat	tgtctcttga	agaacctact	240
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aaagcaaatg	atcaattgct	ttcaattacc	agctattccg	ccaagacggg	ttatgatctc	360
atacttgaag	tctatgtaga	aggtgggtcc	cagtatgttc	ctattgctta	tctggactcc	420
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aatattttct	tttcaaatta	tgattggaaa	ccgggggtatg	aaagtgggtc	atggcgcgag	660
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agagggaatg	attggctgct	atatacggat	cggaatctgt	taggttttca	taagccggaa	1140

aacgcgaaat	atcgtgatgg	tggaattgac	cctgataaac	tgaatgataa	taagattctg	1200
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<210> 1556
 <211> 477
 <212> DNA
 <213> B.fragilis

<400> 1556						
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gacgtacag	gagacagtat	caattggcat	gcctatctgc	gtcattctgc	cgtacccctc	180
tcttttgtca	ccgtattcta	tttaaactat	ttcctcctcg	ttcctcatct	cctcttcacg	240
gaacagaaga	ataaatacat	catctacaac	atcttattgg	tctgcctcat	cggactgctg	300
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cccggatggg	atttttttcg	taagagacat	tctaagcctc	atcttcacca	tccgactgag	420
tgccggcatc	cgcatagagt	ccccgttggg	gacaagctga	aaccccgccc	gtcgtga	477

<210> 1557
 <211> 1548
 <212> DNA
 <213> B.fragilis

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<210> 1558
 <211> 1188
 <212> DNA
 <213> B.fragilis

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<210> 1559

<211> 450

<212> DNA

<213> B.fragilis

<400> 1559

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<210> 1560

<211> 960

<212> DNA

<213> B.fragilis

<400> 1560

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<210> 1561

<211> 804

<212> DNA

<213> B.fragilis

<400> 1561

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<210> 1562

<211> 864

<212> DNA

<213> B.fragilis

<400> 1562

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<210> 1563

<211> 1299

<212> DNA

<213> B.fragilis

<400> 1563

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<210> 1564

<211> 1608

<212> DNA

<213> B.fragilis

<400> 1564

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<210> 1565

<211> 1425

<212> DNA

<213> B.fragilis

<400> 1565

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<210> 1566

<211> 555

<212> DNA

<213> B.fragilis

<400> 1566

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<210> 1567

<211> 186

<212> DNA

<213> B.fragilis

<400> 1567

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<210> 1568

<211> 1512

<212> DNA

<213> B.fragilis

<400> 1568

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<210> 1569

<211> 213

<212> DNA

<213> B.fragilis

<400> 1569

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gttgtgctca	tctatatctc	taattatata	tccttattct	atagggtata	cctaaactct	180
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<210> 1570

<211> 330

<212> DNA

<213> B.fragilis

<400> 1570

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<210> 1571

<211> 618

<212> DNA

<213> B.fragilis

<400> 1571

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618

<210> 1572

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<212> DNA

<213> B.fragilis

<400> 1572

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<210> 1573

<211> 948

<212> DNA

<213> B.fragilis

<400> 1573

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<210> 1574

<211> 185

<212> DNA

<213> B.fragilis

<400> 1574

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 <212> DNA
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 <211> 270
 <212> DNA
 <213> B.fragilis

<400> 1576
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<210> 1577
 <211> 189
 <212> DNA
 <213> B.fragilis

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<210> 1578
 <211> 288
 <212> DNA
 <213> B.fragilis

<400> 1578
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 aatgttactg ccatccggat cttactacta acgttctact atctttattg taaaatccaa 180
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<210> 1579
 <211> 1164
 <212> DNA
 <213> B.fragilis

<400> 1579
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<211> 2400

<212> DNA

<213> B.fragilis

<400> 1580

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<211> 204

<212> DNA

<213> B.fragilis

<400> 1581

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<211> 2865

<212> DNA

<213> B.fragilis

<400> 1582

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<210> 1583

<211> 1032

<212> DNA

<213> B.fragilis

<400> 1583

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<210> 1584

<211> 231

<212> DNA

<213> B.fragilis

<400> 1584

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cggtcagccc	ggattaagac	agaaaagaga	tcagcacccc	tgccgctacg	gcagacccga	180
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<210> 1585

<211> 432

<212> DNA

<213> B.fragilis

<400> 1585

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agtgaggaga	tcattgtcaa	tattctcaat	tacgcttata	cgcagcaggc	agaagggtat	180
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<210> 1586

<211> 1551

<212> DNA

<213> B.fragilis

<400> 1586

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<210> 1587

<211> 453

<212> DNA

<213> B.fragilis

<400> 1587

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caaaagccat	acgaacctgt	tctatgtgac	aggcagaaac	cgaccggcga	tttaagctgg	420
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<210> 1588

<211> 1065

<212> DNA

<213> B.fragilis

<400> 1588

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gaaagtaata	tactggcaga	accctgtccc	agaaatacag	ctccctgcat	tgcgtatgcc	300
tgctggaaaa	taaaaaagaa	atatccggaa	gccaacattg	tcgtgactcc	ttccgatcaa	360
gtggtaaatcg	ataccactga	atttcgcagg	gtgattgaga	aagcgctttt	gttcaactgat	420
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<210> 1589

<211> 1110

<212> DNA

<213> B.fragilis

<400> 1589

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<210> 1590

<211> 1752

<212> DNA

<213> B.fragilis

<400> 1590

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<210> 1591

<211> 318

<212> DNA

<213> B.fragilis

<400> 1591

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<210> 1592

<211> 1944

<212> DNA

<213> B.fragilis

<400> 1592

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<210> 1593

<211> 1152

<212> DNA

<213> B.fragilis

<400> 1593

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gattatgaaa	aatccaacta	ctatggccta	acattagttc	ttcgtggcta	caatttcaaa	1080
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<210> 1594

<211> 1650

<212> DNA

<213> B.fragilis

<400> 1594

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aagtttatac	gtaaatactg	ttcgagtagt	ttcccgctcaa	agctgtttga	ctataaaggg	480
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attctttctg	cacaatttac	ttgtacggac	ggaattgtat	atcccaatgt	ggtattgatt	1620
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<210> 1595

<211> 204

<212> DNA

<213> B.fragilis

<400> 1595

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gcctggccgg	aggaacacac	acaaacaaaa	caaataaaaag	cagtcacgat	tcgcatcggg	180
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<210> 1596

<211> 1473

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (145)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1596

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gaggatatgg	aggatgtgtt	gttcngaaac	cctgaacaat	ttcgtcgggt	ggctccttac	180
tttcccgaag	aggtgtttga	gcatttgcct	gatctgcttg	cgcagggggg	gaaggcggcc	240
ggcaattatc	gggaacgcga	tatggtgctg	atggcgatga	tcaccaatat	cagcgccctgt	300
ctgcccaggg	tgcgtgtatt	gtacgatcag	gtgtattact	cgccgcactc	gtattacatg	360
gtgatagccc	atgcggggagg	cggaaaagggg	gtgggtgtctc	tggccgggctt	ggtgcccggga	420
gagattcacc	gctattatga	gaagcagaac	gaggagatgc	gcctggtgta	tgataaggcc	480
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gagctggaca	ttgtgtcggg	agctatccgg	aatgattacg	gaaagcacga	tgatgtgttt	720
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tatgatgcga	tggatcgtgc	tgtagagatg	gggatctcgg	tacctacttt	taactgctta	1440
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<210> 1597

<211> 1380

<212> DNA

<213> B.fragilis

<400> 1597

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ggacatcccc	acacagcatt	tcaaagcatt	cacattgcag	ggaccaacgg	aaaagggtcc	180
tgctcacata	cattggctgc	cattctgcaa	tcggccggat	atagagtcgg	gctctacact	240
tgcgcccat	tagtagattt	tcgagagcgt	atccgcatca	atggcgagcc	catcccgcga	300
gaatacgtca	tccgctttgt	ggaagaccat	cgtctgttct	ttgaacctct	gcatccttct	360
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cagtctgcgc	taaaggccgc	acaagaaaaa	agcctcccg	aagacctgat	cttcgttagga	1320
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<210> 1598

<211> 267

<212> DNA

<213> B.fragilis

<400> 1598

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ggttataatt	gtcctacgaa	aattttctgg	aagccgctgc	taatttttta	tcataattgat	180
tctgctcata	agcaggacca	ttataacgtt	tggcaaaactc	tgcccagctc	ttggcttgca	240
aagcggaaaag	cattccggat	tgtttga				267

<210> 1599

<211> 1065

<212> DNA

<213> B.fragilis

<400> 1599

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catgccgatt ttcaggctct tggtatgcct gacaggacag aaatgacaat tcttccttta 180
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cagtgtgcat tctttttaat tggatctat acttttacaa tattgattgg cattgaacca 360
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<210> 1600

<211> 1266

<212> DNA

<213> B.fragilis

<400> 1600

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gaaaatatcc ggaccattga aacgggagga acgactgttg ccgcctttga ggacaatgta 180
tacagaggaa cctaccgcgg agtgggaaaa gcaatcatcg caggaatgga agggatgggc 240
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ttttaa 1266

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<210> 1601

<211> 753

<212> DNA

<213> B.fragilis

<400> 1601

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aacgcccatt catataatac agcgtgaaa gatgccgggt ttgcagaagc cttgctcaaa 180
ggcggagcac tgattcctga cggggcaagc atggtattgg cgttttagatg gctccgaaaa 240
gagagcatag aacgtactgc cggatgggat ctctttgaat atgaaatgga acggctgaac 300

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cggaagag	gtatttgc	ctttctgg	agcagcaaaa	atacacttaa	attgatcaaa	360
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ccggaatt	cagaagaaga	aatcaaatg	atgatagatg	ccataaatgc	ggtaaagccg	480
gacttatt	ggataggat	gacggctccc	aaacaagaga	aatgggctga	tacgcatctg	540
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ggtacggttg	aacgtgctcc	ggtccgggtg	caagagcacg	gactggaatg	gctatatcgc	660
ttgatcaaa	agcctaggcg	catgtggcgc	cggatatatca	tccgggaatgc	cctgttctctg	720
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<210> 1602

<211> 813

<212> DNA

<213> B.fragilis

<400> 1602

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tgggcagagt	ttgccaaacg	ttataatgg	cctgcttatg	agcagaatca	atatgataaa	780
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<210> 1603

<211> 195

<212> DNA

<213> B.fragilis

<400> 1603

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<210> 1604

<211> 756

<212> DNA

<213> B.fragilis

<400> 1604

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gacttgtaaa	aagagctgtt	tactgctctg	aaaggtagcg	tgattcctgt	tcagcgtgtc	180
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gtcaagattc	cgatgctggg	tagcattgaa	tcactcaatg	tatctgtagc	cgcaggatc	720

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756

<210> 1605

<211> 831

<212> DNA

<213> B.fragilis

<400> 1605

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aatatgcctg	aagaagcgat	acacagtttt	aagatcaagt	tcagccctcg	caattattca	780
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<210> 1606

<211> 537

<212> DNA

<213> B.fragilis

<400> 1606

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gtattcatct	tcttcatctc	cggatttgac	gaaccggcaa	gagagtacaa	atgggaaagg	240
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acactgatga	cagaaaagta	catacaacag	ctgaaaagac	tggaatacaa	cgtgtgtaaa	360
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gagatgaatt	cggaggaact	gaaaaaggag	acagaaaaaa	tggcagcata	catagaatta	480
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<210> 1607

<211> 192

<212> DNA

<213> B.fragilis

<400> 1607

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gtgagaaaaa	aa					192

<210> 1608

<211> 243

<212> DNA

<213> B.fragilis

<220>

<221> unsure

<222> (145), (184)

<223> Identity of nucleotide sequences at the above locations are unknown.

<400> 1608
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 ttaagtcttt tcggaaaagg ctttaagagt tgtcatataa tcattgggtg gtccgggtgt 120
 ttccaagggc aaaagtccaa agggnaactc tatgagtcag tttccggcaa gccccgcgga 180
 gttntgatat acatatctcc atctttatca attattttta agctctatag tctcatgaa 240
 taa 243

<210> 1609
 <211> 606
 <212> DNA
 <213> B.fragilis

<400> 1609
 agagtaggaa aaaataataa gaaatatatt atggatgaga aattattacc ttactttgag 60
 aatgttaatg atggaggaga acagggcaaa tacttaaaag aatttggaaa tgaagaaacg 120
 caaggaggta tttgtctaca cttatcaatt acttgggtat atctatggca taacagcaca 180
 aataaagctc cgaatacgat atggcaggaa atgaaaactc ccactttaat tcaacaaata 240
 gcaagcaacc aaagaagtta ccaacaatat tatccgaata ttgcagataa tgtatcttta 300
 gctactcgta actcccttca tgtaacaggg actaacgcag gagaaattta tcagataacg 360
 accaatgcac tagtcaagag taacatgctt ttgtatgtca tcaatttaga aaaagaccat 420
 aagccagtcg gaagacatgc cattgcagca attgcaacaa gaggacgttt ctatttgtac 480
 gatacctaag ttggtgtaat gtcagtgcct atgccaata tgaaagaact aatagaaaaa 540
 atcccttata tatatggtaa gcattctctc aatattagtc agacttctgt ttataacata 600
 tcttaa 606

<210> 1610
 <211> 345
 <212> DNA
 <213> B.fragilis

<400> 1610
 aagagtatga atcctatatt gaataaaatg ggcgcaaatt ccaatgaaca gaaaaaactc 60
 ttgatggagt gtgtgtcaat gcttgaaaag tatgtgaaca gatttccggc agaaaagggg 120
 tgtgtctcat tctccggaga agatatgaag ctgtggaagg aagtttattt tccgaaactt 180
 gttcagacgg atattttgtt ggacggtaaa tttttctgtg gcacgtcgtc cggtaatatg 240
 ggtattggta cagacggtta ttttaccggt tatgaatttt tccagtttat ttatcgtgcc 300
 tacaaggcac tttatgaact ggaaaaggct tcacaaatga gatga 345

<210> 1611
 <211> 972
 <212> DNA
 <213> B.fragilis

<400> 1611
 tactcaatga aaaagagaga gtttaaaatt tcctttttcc tccatgtgtg ggaaaggaaa 60
 gcggaagaga tttcgttgga agagtttcat aatgacctca ggggagcacg ctggaagggtg 120
 cttgccgagt cgtaccggcg gtggatgcgg acgggcatga cagaggaggg caaaaggctg 180
 aaaggggctc tgaatgcggt ggtcgtggcc ggcaagtgcc ggggcggaac tgcggcgaac 240
 caggtgaccg agctgaacgg actggcgctg ttcgactttg atcattgcct cgagatgctg 300
 gccgggatga aggagaaggc cggggcgctg ccttatgttg tgggggcttt tgtcagtatc 360
 tcgggtgaag ggctgaagct gattgtgcgt atcgatgccg agaatgccgg gcagtatgcg 420
 gtggcttatc ctgtcgttgc ccgtgagttg gagcgggtgc tggggcatcc ttgcgatatg 480
 tcgtgccgag atctgggacg ggctgtctac gcttcgtatg atccggaggc gtactataat 540
 cccggtgccg ggggtgtttc gtggcgggag caggtggacg ggctgttgca ggcggaaggg 600
 gagtgttccg cgcagtcggt gggcaaggct tgtccggcgg gcgttgcttc cgaagcgggg 660
 gatggcttta tgcagggttt cctgaatgat tttgatgccg ggaatccgtt tgtggcggga 720
 gggcgccatg cgtttgtgct gaagctggga cgtgttgccc ggtataaagg tttttcgcgg 780
 gaagaaatgc ggctgttgca aaaagcagtg gttgagaaat acgcgcaggc tgatttcggg 840


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agcggagaaa tagaaaaaac attatcgtct gggtatcagt atgtttctgt caggaggcg 900
gacgctgtca tggcgagtca ggggccaaaa gtccaagggc cactctatgc tctcagagga 960
gggggagagt ga 972

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<210> 1612
<211> 246
<212> DNA
<213> B.fragilis

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<400> 1612
attaagatga agcggataac ggacaggaca aatttttccg tcataaatac ggtgggtgaac 60
tatagcgaag ctccctatgc tgtctgtccc caatgtaata tccggacggc ctgcagaaga 120
tttccatctt ccatacattc cgtccggcat ctgtacccgg acaggtcgac aacccaaaag 180
cacaaatatg ataaagacaa aatacaaaaa aaagctgtaa tgattcctat ttttaccat 240
atataa 246

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<210> 1613
<211> 1350
<212> DNA
<213> B.fragilis

```

```

<400> 1613
aaagtatcga aaaagagaga aacaaaaaac agttttaata ttttcttaat gacaaaaatg 60
attatgaaaa agagtgaactt atttaaaata ggtgtgttgc tgatggcaac gaccttggga 120
acaaccggat gctcttttcgg agaagacgag aagaaaccgg aaattgtagt ggatcctgcc 180
gaaaaaacaa tagaataacta cattgcagggt aaagtgcagg aaggaacgac cgcgctgtcc 240
ggtgtagaag tgaaagccgg tgaagtaacg gctacgacgg atgcggaagg ggcttataaa 300
ctgacagtgg acagcaagaa ggtgtacacc gtgacattca gcaagaagg gtatatgagc 360
atagacaatg caacggcaac catcgcagac aatgcggcaa accgcagtat ggtgagtctg 420
agtgtgaaat taagcaagaa agtccggaa aaagaagtga aggccgatgc ggaagaagaa 480
gtggtggtaa ccgataaagg agacagcaat atttctcagg cagaagcagc tgtaattatt 540
cctcccaaag ccatagaaac aactacaacc gtaagcgtga ctccatatga agaaccggct 600
gccgtgacaa caaccgtaac accgggaaat aatgtggaga ctccggtagc gatcgcaaac 660
atcgaagtgg aaacagccca agaggtcact ctggccaaac cggtaacact ggcaatcata 720
aacaagctt cggaacatac aacgttcgaa aatgtggaag tgtacaatca gaaaacaacc 780
acaagggccg gagaaaactg gaacaaagtg gcagatgcca tttatgactc ggaaacgaac 840
agctataaat tcacattgcc cgcaggcgca tcaactgtcc gaaaatattc gatgctgtc 900
aagagtagca agaccacagg aaaagaacgg ataggcgaga caaacaagga agagaaaaaa 960
agcaatgaag gcaatgatc tgccattccg gaatacaaaa tcaactttga ggctacggcc 1020
ggatgggaat atactgtcag tccggaaaag gcgctgatga atgcaggcgt agacgctgcg 1080
gatgcccgaag gcatgggcac gacgatcaac agtgccattg aagcgcagga aggaacgacg 1140
ggaacttata aagtggctca cgaactgata gcgggtatca gcggtaacca taccctttat 1200
tacctgaatc aggctaaata ttgcgaaaag acatatacat tcaaatcag tggcggaaga 1260
acagtgacca tcaccctgaa attctatata ggaatgcaga ttacttacac caacgtggaa 1320
gcaagccagc actcgggagg taagatttaa 1350

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<210> 1614
<211> 1212
<212> DNA
<213> B.fragilis

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<220>
<221> unsure
<222> (250)
<223> Identity of nucleotide sequences at the above locations are unknown.

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<400> 1614
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atagctgcct ataaagcttg ttacatcata cgtggcctga tcaaacaggg agctgaggta 120

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caagtcgtaa	ttactccgc	cggaaaagaa	tttatcactc	cgataactct	ctctgcgttg	180
accggcaaac	ctgtcatcag	tgaattcttt	gctcaacgtg	acggtacgtg	gaatagccat	240
gtagacctgn	gattgtgggc	ggatgctatg	ttgatagccc	ctgccacggc	ttctaccatc	300
ggaaaaatgg	cgaacggcat	agccgataat	atgttgatta	cgacttatct	ttctgctaaa	360
gcgcgggttt	ttgttgctcc	ggctatggac	ctggatatgt	ttgccacccc	cagtactcaa	420
aagaacctgg	atacgttcg	ttcgtatggc	aatcatatca	ttgagccggc	ttcgggtgaa	480
ttggccagtc	atctggtagg	aaaaggccgt	atggaagaac	cggagaatat	aatccgggta	540
cttgatgaat	tcttttcac	aacgggcgaa	ctggcgggga	aaaaagtgt	gatcacggcc	600
ggaccgactt	atgaaaagat	tgatccgggtg	cgcttcacgc	gcaattattc	ttccggtaaa	660
atggggtttg	ccttggctga	ggagtgtgcc	cgctcgggag	ccgatgtggg	actgattgca	720
gggcccgtac	aacagaaaac	atatcattca	catattaccc	gcattgatgt	ggagtccgct	780
caggacatgt	atgaagcagc	catggcgcaa	tacccttgg	togatgccgg	aatactgtgt	840
gcagcggtag	cggattttac	tccggacgct	gttgctgaca	agaagataaa	acgggaagga	900
gacgagttgt	tgctgcatct	taaacccact	cacgatattg	ctgctgcatt	gggcaagata	960
aaaactccgg	gacagaagtt	aatcggtttt	gctcttgaaa	cgaatgacga	gcagcgcaat	1020
gccgaaggaa	agctgatccg	gaagaacttt	gatttcattg	tgctgaattc	gttgaatgat	1080
gctggtgcgg	gattccgtta	cgataccaat	aagataagca	ttcttagttg	caggggcaga	1140
accgattatc	cgtaaaatc	gaagacggaa	gtagccagag	atattattga	tagaatgata	1200
aaagaaatgt	ga					1212

<210> 1615

<211> 1368

<212> DNA

<213> B.fragilis

<400> 1615

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tatacattgc	cgccaaggca	aaagatgatt	aacctgctgt	acgtgggtatt	gattgctatg	120
ctggccatca	atatatcgtc	ggatgtctta	gaggggtatg	gacaaatgaa	caacgactac	180
cttccacaaa	taaaaaagct	ggaagaatat	aaccggactt	tactggaaaag	aattaacagc	240
cgaatgata	aagcggcttt	atctgcacag	aacatagatg	cggcggcagg	aaaactaatg	300
gatacactgg	aggaactgaa	agaagatatc	gcccggaag	cggacaaaag	gaaatatgaa	360
gccggcaagc	taaaggcaaa	agatgacttg	aacgctgtgc	cggagggtatt	tctgtcggtc	420
accgggggga	aagggaaagc	actcaggctc	tactgggata	cattcaaaga	agacgcttta	480
tcgctgatca	agaatgatgc	acacagacaa	ctggtaggca	cttacctcaa	tacggaaagt	540
ccgggtaccg	gaatatcctg	ggaaaaggaa	accttctctt	atcttcctgc	catcgggtga	600
gtgacattta	tcaataaaat	gcaggaagag	gtgttgctgt	gcgtgaatga	agtatatcgg	660
tactgtctgt	acgaagaggc	agaagatgga	aaaggcggag	cttttgtatt	catcaatgaa	720
gaccagatga	tagtaaaata	agatggaacg	gtggacctgc	ctgtagtaca	gatcacaccc	780
gccttaacaa	gtatcttgta	taccgactat	gaaaaccgcg	taaatatact	gactgcccga	840
ataccgttca	acgaggtgac	attccggatg	acgaacggaa	agatactcaa	aagaggaaac	900
cattgcatag	ccgttcccga	cgaaaaagca	cagacagcga	cagttaccgc	cacacagata	960
aaaaacgggg	tggcaaggca	actggccgaa	taccggtata	ccgtaaaggc	actgcccgat	1020
ccgacacctt	atatactctg	cacggatgaa	aacggggagaa	cggtaacaata	ccgggggaaat	1080
gtgcccatta	acaaacggct	ggtatccaac	atgacacagc	tgggagcttc	aatcagcgat	1140
ggtccgaaag	ccaactacga	gatcagcagc	tttgaaatgg	tattgatcaa	aggaagcagt	1200
aaagcggtaa	cttcaatacc	caacaccggg	aacaaattct	cggccaggca	aatggaactg	1260
atcagacaat	tggagaaagg	agataaattc	tatatcactt	cgattgttgt	gaccgggtccg	1320
ggaaacaaaa	agaaacagat	tgcataaatc	aatgtcgtat	taatataa		1368

<210> 1616

<211> 1257

<212> DNA

<213> B.fragilis

<400> 1616

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ttcagcaata	ttgttgccga	accgcagttt	ctgggtgatgt	atgtcattgc	cttcgttctc	120
ttgtatctgg	gtataaagaa	acaatacagag	cctctttttat	tggtgccgat	tgccttttga	180

gtgctgttgg	ctaacttccc	cggcggagga	atgggagtga	tacaggctga	cgagaatggc	240
atgacccctg	tgaacggagt	aatgaagaat	atctgggaga	tgccctctca	tgatattgct	300
catgaattgg	gactgatgaa	ctttgtgtat	tatatgctta	taaagacagg	gttccttccc	360
ccgatcattt	ttatgggagt	gggggccttg	acggacttcg	gaccgatgct	tcgcaatctg	420
cgtctgtcta	tattcggggc	tgccgctcaa	ttgggtatct	ttactgtgtt	gttggttagct	480
atcctgatgg	gatttacacc	cagtgaagca	gcttccttgg	gaattatcgg	tggcgcgac	540
ggacctacgg	ccatctttac	caccatcaag	ttggctccgc	atctgttggg	cccgatcgcg	600
attgccgcct	attctttatat	ggcattgggt	ccggttatca	ttccactggg	cgttcgtctt	660
tttgtgtacca	agaaggaact	gagtatcaat	atgaaagagc	aggagaagaa	atatccatcg	720
aaaacggaaa	ttaaaaacct	ccgtgtattg	aaaattatct	tcccgattgt	ggtgactacg	780
gtcgtggctc	tgttttgtacc	gagtgcagtg	cctttgatcg	gtatgctgat	gttcggtaac	840
ctgggtgaaag	agatcgggtgc	caatactttc	cgtctgtttg	atgcccgttc	gaatagtatc	900
atgaatgcgg	caaccatttt	cctgggtttg	tcggtaggag	ccacgatgac	aagtgaagct	960
ttcctgaact	ggacgactat	cggtattgtg	gtaggaggat	tcctggcttt	tgctttgtca	1020
atagcaggag	gtatcttctt	tgtgaaactg	gtgaatctgt	ttacgaagaa	aaagattaat	1080
ccgctgattg	gtgctacggg	acttagtgcg	gttcctatgg	ccagccgtgt	agccaatgac	1140
attgctttga	aatatgatcc	taaaaatcat	gtattgcaat	attgcatggc	cagcaatatc	1200
tcgggagtga	tcgggtctgc	cgtagcggca	ggggtgctga	tctcttttct	gtcttaa	1257

<210> 1617

<211> 1197

<212> DNA

<213> B.fragilis

<400> 1617

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aatttactgt	tattatatac	attctggaaa	gccggtagaa	atatctcgca	aagcatggat	120
tactggcata	atgccggatt	gtgcgtaatc	ctattctcta	ttgtacaagg	ctgccgattt	180
gccagaggaa	atgattactt	tgcgtaactc	agaattttcc	gtgaaggtag	cctgcatgtc	240
gaaaatccat	ttttctcagt	cattaatgaa	ttactcagaa	tagttggtat	taatgagtat	300
agttgtttta	tggtgtatgc	gttcacatct	gcattgtgcg	ccatgatttt	tatgaaagac	360
tatcgacagt	atgccagata	tatgttccca	ctattcttga	taggcttcat	gaacttcgaa	420
gaaagcatga	tacgccaggc	attcagctac	tcttttttct	tcctatattt	gaaatatctc	480
tttaagttga	aatttaacaa	gccaaaggat	atattgcata	accataaaaa	attaatatac	540
tgcataatat	ttgccatact	aacattagcc	atacacactg	gcaatattat	aagcttattt	600
gtaatcacca	ccctctatat	attttggcgt	aaacctttcc	agccacagtt	tgccataccg	660
atatatgttg	cgtgtgtcta	catattacca	catataatta	atttcaattg	gctggaaccc	720
attttaagct	ttgcagcaga	cacaaacgaa	cgtgcagcag	aatatgtgaa	gaatgctgac	780
tattggtttt	cagaaaaggg	tgagaacgat	cagtatgata	aaaattttat	cgtggaaatt	840
attcaagtga	taggtctctc	tgcatgtgat	tatttcggat	atagactaat	catagaaaag	900
ttacccaaac	attatgctct	gataacaatg	cttaatacct	ttattatttg	tttgtgtata	960
gagtctatat	tcgtaaaact	agaaattttg	catcgtatag	gacaaaactc	agatattgta	1020
ggttactttg	cttttagcaat	agtagtatcc	tataaaaaca	ttaaactaaa	acctatccaa	1080
aaagtagcct	atgtctgtct	cctttgggtt	gtttattact	acgtaaaata	cttattcttc	1140
agtgggcgta	ctatgttcat	ctgggatacc	cattatcctt	ttttcaaatt	tatataa	1197

<210> 1618

<211> 1182

<212> DNA

<213> B.fragilis

<400> 1618

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ttacttacc	agtacttcag	gcgacaaata	cgaaaagggt	aatacgagtt	cgcttttgcc	120
cataacgggt	tggaagcttt	acagaaaactt	ctggaaaactc	ccgatttcga	tatcatcctg	180
agtgatatta	atatgccgga	gatggatggg	ttgacctat	tggtctaagg	caatgaactg	240
aaaaatccgg	caatgaagtg	tataatggtc	tctgcttatg	gagacatgga	taacatacgt	300
tctgctatga	acaagggagc	gtttgatatt	gcaaccaaac	cgatcgattt	ggatgatctg	360
tcgcgacta	ttgaaaaggc	gatcgaacag	gttcgctata	tccgtgagtc	acagcaggag	420

cacaaccaac	tggaatctat	caaaaatgac	ctggccattg	cgggagaaat	ccagcaaacg	480
attcttcccc	gttcttttcc	tccttttccg	gaactgacgg	aagtgggtga	tatttatgct	540
tccatgactc	cggcaaaaaga	tgtagggtggc	gatttttatg	atttcttcca	gattgacgat	600
gaacgtatcg	ggctgggtgat	tgctgacgta	tctgggaaaag	gggtgccggc	atccttgttc	660
atggcgggtta	gtcggaccct	gctccgtgca	actgctcttc	gggtgttttc	gtcggcagaa	720
tgccttactt	atgccaataa	gttactgtgt	aaagagagcc	tggactctat	gtttgttacg	780
gtcttttatg	ggatttatca	ttataaaaacc	ggcatgatgg	actataccaa	tgccgggcat	840
aatccccctt	atctccttcg	cggcggacgg	actgttgaat	gcttgccctgt	cgcttctaata	900
tttgtggtag	gcgtgttcga	tgatattgaa	tttgagagta	atacattgac	gttcggcatc	960
gggtgacactt	tacttctgta	tacggatggg	gtcacagagg	cttttaacga	caagcgggaa	1020
caattctcgg	aaagtaactt	acaggatata	ttggcgtcta	tgcacgaaag	tagttccgca	1080
aaagagggttg	ttacgagtgt	attgcagttc	gttaagactt	tctccggaga	ctatcctcag	1140
tccgatgaca	taaccctgct	ttctcttcaa	cgaatcaaat	aa		1182

<210> 1619

<211> 480

<212> DNA

<213> B.fragilis

<400> 1619

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ttgatggaaa	acggaatgaa	caagaaagtt	actgaacctt	atctcgtgga	tgcactcagc	120
tttacagaag	cagaagcacg	cattattgag	gagatgaccc	cgttcattac	aggagaattt	180
accgtatcgg	atatcaaacg	agccaaactat	agtgaacttt	tccccagcga	agaagaagct	240
gctgaccgct	ggtttaagtg	taaactgatt	tttatcacac	tagacgaaaa	aagtgggtgct	300
gagaaaaaaa	cgtcgacaca	agttctggta	caggcagctg	acctgcgcga	tgctgtaaaa	360
aagctggacg	aaggcatgaa	aggtacaatg	gctgattatc	agataggttc	tgttgctgaa	420
acagcaataa	tggatgtata	tccatatagt	tctgagccta	atgataaacc	ggaagtataa	480

<210> 1620

<211> 405

<212> DNA

<213> B.fragilis

<400> 1620

tttatgaaaag	agaattcaat	caaaccgtat	tgttattgtg	gtgagtcaga	aagctcattg	60
gtcgataatg	ctatttttgt	ttatttttgg	gatgaatata	gaagagtact	tctggatgaa	120
atcttatggc	tggaaagcatc	cggcagttat	tgtgtactct	gtatggagaa	cgggtgcagag	180
ataacagtca	gctatccttt	ggatcggatc	ttcaataatg	accttcctcg	cggcaagttt	240
cagagaattc	atcgttctta	cgctatcaat	gtgttcaagg	tgaccggatt	tgcaggtaac	300
tatgtacata	taggaaagaa	gatgttgccg	gtcagtgaat	ctcacaaaaa	gaatttttta	360
gcttgtttcc	ataaaaattta	ctcaaagcgt	gcattgggaa	aataa		405

<210> 1621

<211> 621

<212> DNA

<213> B.fragilis

<400> 1621

tataatatgg	ataataagaa	agttaggagc	actagtagcc	aggtaatgga	acttcagcaa	60
ttgattgccg	gtcctttgat	tgcaactatt	gaagcggatt	cattatcttc	acaaagatat	120
ctggattatc	tgatgaaaat	cgcatttgaa	tcctatgata	ctgtgacagg	acggaccggg	180
aagatacgta	tgcttacgtt	caactatcag	agtcaggatg	ccgggtggggg	aagaacgcaa	240
agtgtaaagta	taccgatact	gacatttgga	cctctgccac	tgttgcaagt	acaggaagca	300
gatttccgatt	tcgatattaa	aattctggat	gcactgtcgg	aaacagctga	agaaaaattt	360
tcactggaag	aaggtaaaaag	cgtgaaatgag	ccgcaaaagt	gaggaggatt	taaactccgg	420
gcttcactgg	ctcccaaaca	gggagaaggc	agcagcactt	cgaatgtgca	gcagagcttg	480
tccggcaata	tgaagtgaag	agtgaagatg	cgtcaggcag	atatgcctgc	ggggttgtct	540
aatctgttac	atctgacggc	gagcaatatg	caagtagaag	aaactgaagc	tgaagaaata	600

acggaaggag gaaataaatg a

621

<210> 1622

<211> 582

<212> DNA

<213> B.fragilis

<400> 1622

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<211> 573

<212> DNA

<213> B.fragilis

<400> 1623

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